UNIVERSITY OF HOHENHEIM

5 KomBioTa

NATURAL HISTORY MUSEUM STUTTGART

SPRING MEETING 2026

5 Years of KomBioTa – Educate. Empower. Protect.

KomBioTa Coordination Office
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Looking Back: KomBioTa's 2026 Spring Meeting & 5th Anniversary Celebration

On behalf of KomBioTa's board of directors and coordination office, we would like to thank everyone who joined us for our anniversary celebration and 5th annual Spring Meeting. With a record attendance of 118 participants, the event was a fantastic reflection of the vibrant spirit of our network and the growing interest in biodiversity and taxonomy research.

Your engagement – whether through presentations, posters, lively discussion, or simply your presence – made this day truly special and highlighted the strength of our community. We are grateful for your contributions, your curiosity, and the new collaborations that took root during this meeting.

The Spring Meeting was followed by another exciting moment for KomBioTa: SWR visited us to produce a television feature about our network and its work. The piece includes two members of our Board of Directors and offers a glimpse into the people and research behind KomBioTa. You can watch the feature here.

Together, we have marked an important milestone for KomBioTa and set the stage for continued growth and cooperation. Thank you for being an integral part of our journey.

All the best from,
The KomBioTa Board of Directors & Coordination Office

WELCOME

14:00 **Prof. Dr. Lars Krogmann**, *KomBioTa Board of Directors, Scientific Director SMNS*

14:05 **Prof. Dr. Christoph Schneider**, *Rector of University of Hohenheim*

14:15 **Prof. Dr. Markus Röhl**, *KomBioTa Scientific Advisory Board, HfWU*

14:25 **Presentation of KomBioTa image film**

View on YouTube:

14:30 **Prof. Dr. Martin Hasselmann**, *KomBioTa Board of Directors:* Development of KomBioTa: Where do we come from, where do we go?

Diversity in research, teaching & knowledge transfer across the network

PART 1: BASIC RESEARCH PERSPECTIVES

14:45 **Prof. Dr. Frank Schurr**: Biodiversity research in the new Clusters of Excellence GreenRobust and TERRA

Biodiversity research (and KomBioTa members) plays a key role in the two recently established Clusters of Excellence GreenRobust and TERRA. GreenRobust aims to identify principles underpinning the robustness of plant life across perturbations, across organizational levels (from molecules to ecosystems) and across the plant kingdom. A key component of GreenRobust is the Plant Perturbation Atlas, an unparalleled experiment studying robustness to heat and drought in multiple plant species and from the molecular to the population level. TERRA aims at an integrated understanding of how interactions between the geosphere and the biosphere respond to environmental change, using evidence from the geological past and the present to improve projections of future global change impacts. The central hypothesis of TERRA is that diversity in the geosphere promotes biodiversity and stability in the biosphere, and that biodiversity promotes both diversity and stability in the geosphere. A key component of TERRA is the Diversitorium, a large field experiment that will manipulate the diversity of geological substrates to study effects on grassland dynamics. The two excellence clusters will also fund the establishment of three new professorships at the University of Hohenheim on biodiversity theory, eco-evolutionary theory and remote sensing of the biosphere. In summary, GreenRobust and TERRA will further enlarge the KomBioTa community and will provide exciting opportunities for biodiversity research.

15:05 **Dr. Niloofar Alaei Kakhki**: The genomic architecture of color pattern evolution in birds

Coloration is a key evolutionary trait that can drive speciation through mate choice and adaptation. Using birds as model systems, phylogenomic and population genomic analyses are combined based on whole-genome data across different bird groups to investigate the genetic architecture underlying diverse color patterns, how coloration evolves among species, and how these traits contribute to speciation. Integrating time-series genomic data from museum specimens aims to examine how color-related genes change over time and respond to environmental variation.

15:20 **Simon Müller**: Land use and its effects on body size and functional diversity

Pollinators are threatened by extensive land use changes, but both sublethal effects on bee fitness and the influence on functional trait communities remain underexplored. Those topics are addressed in this talk by evaluating data originating from the LUBW flying insect monitoring program in Baden-Württemberg.

15:35 **POSTER PITCHES** (see page 6)

15:45 **GROUP PHOTO & COFFEE BREAK**

16:15 **Tobias Pfeifer**: Phylogenomics and morphometrics reveal new species and signals of an adaptive radiation in Vanuatuan *Strumigenys* trap-jaw ants (Hymenoptera: Formicidae)

The South Pacific region harbors thousands of tropical islands and endemic species, making it one of the most geologically complex and biologically unique regions on the planet. In ecology, ants serve as important biodiversity indicators because they are highly abundant, diverse, and ecologically dominant insects in terrestrial habitats. Recent advances in biodiversity research in the South Pacific region have revealed the Vanuatuan archipelago as a novel ant biodiversity hotspot, with numerous newly discovered endemic species. Here, we employ an integrative taxonomic framework that combines phylogenomics using ultraconserved elements (UCEs) and quantitative morphometrics to delimit species, infer the evolutionary history, and explore the morphological diversity of *Strumigenys* trap-jaw ants in Vanuatu. The results reveal the presence of at least seventeen Strumigenys species, several of which are newly discovered and endemic to the archipelago, making *Strumigenys* the most species-rich ant genus in Vanuatu. Moreover, the UCE phylogeny revealed a clade of high elevation endemics that exhibit substantial morphological variation and whose evolutionary history indicates the first potential case of an endemic adaptive radiation in Vanuatuan ants.

PART 2: PRACTICE-ORIENTED PERSPECTIVES

16:30 **Dr. Patrick Kohl**: Population demography of wild honey bees (*Apis mellifera*) in Europe

Despite a long history of apiculture, the honeybee (*Apis mellifera*) has not been domesticated on the species level, and a large fraction of its world population still lives wild. In this talk, the current status of wild honeybee research in Europe will be presented.

16:45 **Prof. Dr. Martin Dieterich**: From Science (not) to practice - case example yellow-bellied toad

The presentation addresses the problems of integrating scientific data into species protection programs using the case example of the yellow-bellied toad (*Bombina variegata*). Research results have been integrated rather successfully into state forest management. In spite of interference by the scientific community, to integrate scientific results into statewide protection programs appears to be more difficult. The case will be described and obstacles for integrating science into practice will be discussed.

17:00 **Sri Dhanya Adusumilli**: Nature-based solutions in higher education

Since 2024, the University of Hohenheim's "Learn in Nature Lab" has been integrating nature-based solutions (NBS) into higher education. A core module, "NBS Case Study", enables students to address real-world challenges (climate change, biodiversity loss, urban resilience) by identifying and critically assessing NBS in interdisciplinary, practice-oriented settings, including visits to permaculture practitioners. Extracurricular "NBS 101" events cover topics such as duckweed, soil, bee diversity, biodiversity-friendly roadside management, RNA-based plant protection and Farmer-Managed Natural Regeneration. The Lab is embedded in the EU project "eNaBlS", which develops higher education curricula, open-access resources and training formats on NBS.

17:15 **Amelie Höcherl**: At the intersection of science, policy and society: Collective action as a basis for tackling invasive *Tapinoma magnum* ants

The spread of *Tapinoma magnum*, a supercolony-forming Mediterranean ant, is increasingly impacting infrastructure in Baden-Württemberg and beyond. Recognizing the urgent need for action, the TAPINOMA project was launched through an initiative in the state parliament and unites researchers, local collectors, policy makers, citizens, and practitioners in a dynamic partnership. By combining scientific investigation with crowd sourcing and stakeholder engagement, the TAPINOMA project not only advances our fundamental understanding of the species' invasion, but also demonstrates how science and society can work hand in hand to address emerging problems.

FAREWELL

17:30 **Prof. Dr. Lars Krogmann**

17:45 Networking with drinks and snacks

POSTERS:

Origilene Dantas & Anna Virginia Albano de Mello: International Collaborations and Training of Taxonomists on Evolution and Conservation

Verena Engl, Magdalena Pfeiffer, Erhard Strohm, Gernot Kunz & Robert Zimmermann: Selektive Zikadenjägerin oder Opportunistin? Beuteauswahl der Grabwespe *Alysson tricolor* (Hymenoptera, Bembicidae)

Lucas de Freitas Lacerda, Niloofar A. Kakhki, Heike Reise, John Hutchinson, Ira Richling & Ricardo J. Perreira: Slow Movers, Rapid Change: Introgression from Native Species Increases Genetic Variation in Invasive Slugs

David Grunicke, Kyle W. Gray & Christian Rabeling: Integrative taxonomy of Vanuatuan doryline ants reveals four new endemic species in the South Pacific

Louis Hausner, Niloorfar Alaei Kakhi, Maximilian Offermann, Ricardo J. Perreira: Dissecting genes of colour pattern in birds and their role in maintaining species boundaries in a moving hybrid zone

Moritz Hemmert: Ant communities and diversity in an arid protected biodiversity hotspot in South Africa

Daniel Hitzler, David Becker, Marit K. Kasten, Torben Weber, Ingo Grass & Thomas Hiller: Listening to invaders: Passive acoustic monitoring of American Bullfrogs

Dr. Sajad Noori, Sarah M. Gaugel, Michael C. Orr: A curated and integrated dataset for exploring global bee-plant interactions

Dr. Sajad Noori, Laura K. Steib, Tibor Sos, Dennis Rödder: A comparison between Static and Dynamic Species Distribution Models: case study of Romanian herpetofauna

Undine Schölkopf, Viktoria Ferenc, Maria Májeková, Richard Michalet & Pierre Liancourt: From Regional History to Local Mechanisms: Temporal Dynamics and Multi-Diversity in Baden-Württemberg's Grasslands

Maria Seiter: Diversified farming in Baden-Württemberg

Cristina Lupaşcu-Vasiliţa, Alexander Riedel, Daniela Mera-Rodríguez, Clement Tavakoli, Jenny Hein, Pauline Pfeiffer, Rebecca Spiecker, Janes Odar, Angelica Cecilia, Christian Rabeling, Tilo Baumbach, Lars Krogmann & Thomas van de Kamp: Integrating Synchrotron Micro-CT & DNA Sequencing (including digital displays)

Hannah Weinländer, Jens Hartung & Maria Müller-Lindenlauf: Effects of undersowing maize with a diverse annual flower mixture on insect abundance and diversity

Robert Zimmermann: Bees and stinging wasps in Schäffer's "Icones" (1766–1779)

KomBioTa Coordination Office: Bachelor of Science – Biodiversitätswissenschaften

KomBioTa Coordination Office: Feedback Station

Spring Meeting 2026

TRAINING TAXONOMISTS IN EVOLUTION AND CONSERVATION TO UNDERSTAND NEOTROPICAL BIODIVERSITY

Anna Mello, Origilene Dantas, Sofia Frey, Lucas Freitas, Ricardo J. Pereira

Biodiversity Monitoring

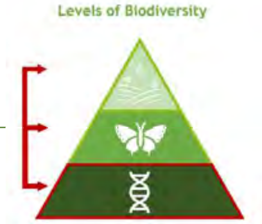
Our mission is to advance knowledge of biodiversity by understanding **genetic diversity** within species and how it affects species and ecosystems. Extending the value of collections using genomic tools, we aim to understand:
1) how species are **formed** and
2) how they **persist** in a changin environment.

Why Neotropics?

It is the most biodiverse region on Earth, first extensively explored by early naturalists, and crucial for understanding how biodiversity originates, diversifies, and is maintained.

Capacity Building

Training a **next generation of taxonomists** in the use of genomic data can open new possibilities for addressing evolutionary and conservation questions, while also strengthening international collaborations that will aid global conservation efforts.



1) How are species **formed?**

Understanding how historical processes shaped the origin, divergence, and hidden diversity of Neotropical lineages.

2) How do species **persist?**

Using genomic data to define, prioritize, and protect Evolutionarily Significant Units for effective conservation.

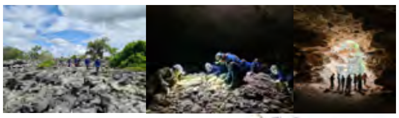
How can **genomic data** contribute to our understanding of Neotropical Biodiversity?

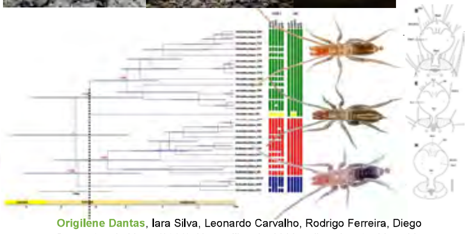
Integrative taxonomy leads to the **description** of seven new species.

Anna Mello, Renato Recoder, Antoine Fouquet, Miguel Rodrigues, Pedro Nunes (2024). Integrative taxonomy of the *Iphisa elegans* species complex (Squamata: Gymnophthalmidae) leads to the description of five new species. ***Zoological Journal of the Linnean Society***, 200(2), 477-504.

Integrative taxonomy leads to the **description** of two new species.

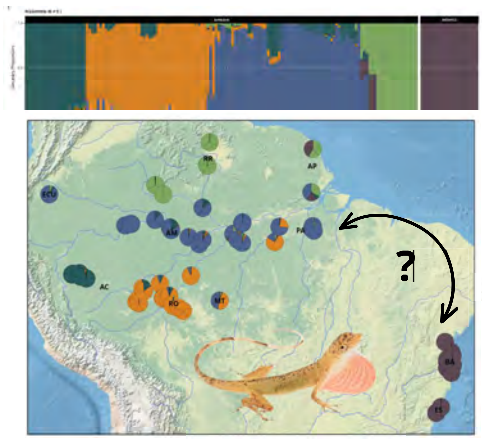
Hidden diversity in Caatinga Caves



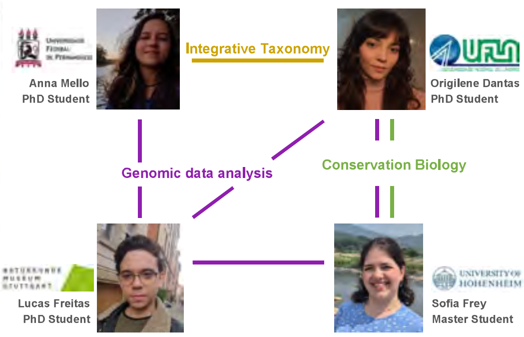


Origilene Dantas, Iara Silva, Leonardo Carvalho, Rodrigo Ferreira, Diego Bento, Sergio Lima. (2026). Unravelling the hidden diversity of schizomids (Arachnida: Schizomida: Hubbardiidae) in caves of the Brazilian semiarid. ***Zoological Journal of the Linnean Society***, 206(3), zlag010.

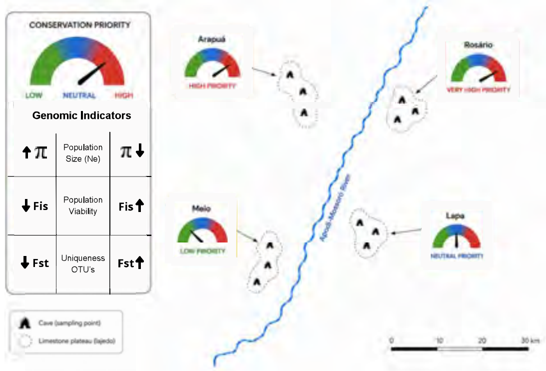
Genetic admixture in *Anolis fuscoauratus* reveals historical connections between **Amazon** and **Atlantic** forest populations



International collaboration



How to use genomic data to identify **priority areas** for conservation?



π: Nucleotide Diversity, Fis: inbreeding coefficients within populations,Fst: genetic differentiation among populations

Take home messages:

Genomic divergence between populations uncovers a potencial **hidden species** in the Atlantic Forest, showing that genomics can **accelerate biodiversity discovery** before it disappears.

Advancing our understanding of the origin and resilience of biodiversity requires **egualitary collaboration** across countries and career stages.

Genomic data will provide insights into the **adaptive potential** of cave populations, identifying priority areas for conservation of largely unknown ecosystems.

Baden-Württemberg
MINISTERIUM FÜR WISSENSCHAFT, FORSCHUNG UND KUNST

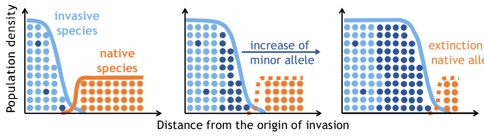
Slow Movers, Rapid Change: Introgression from Native Species Increases Genetic Variation in Invasive Slugs

Lucas de Freitas Lacerda[1,2*], Niloofar A. Kakhki[1], Heike Reise[3], John Hutchinson[3], Ira Richling[1], Ricardo J. Pereira[1,2]
[1]State Museum of Natural History Stuttgart; [2]University of Hohenheim; [3]Senckenberg Museum of Natural History Görlitz
*lucas.freitas@smns-bw.de

Invasive species often cause local extinctions and alter ecosystem functioning, driving significant macroevolutionary turnover. Their **rapid adaptation** to new environments depends on evolutionary processes such as selection acting on standing genetic variation shaped by their evolutionary history. Despite facing strong **founder effects** and **demographic bottlenecks** that reduce genetic diversity during colonization, invasive species frequently adapt quickly and thrive.

Understanding **how genetic variation is generated and maintained to enable such rapid adaptation** remains a key challenge at the intersection of micro- and macroevolution.

Reduction of genetic variation during a range expansion:



invasive species:

Arion vulgaris

native species:

Arion ater ater
Arion a. ruber
Arion a. rufus

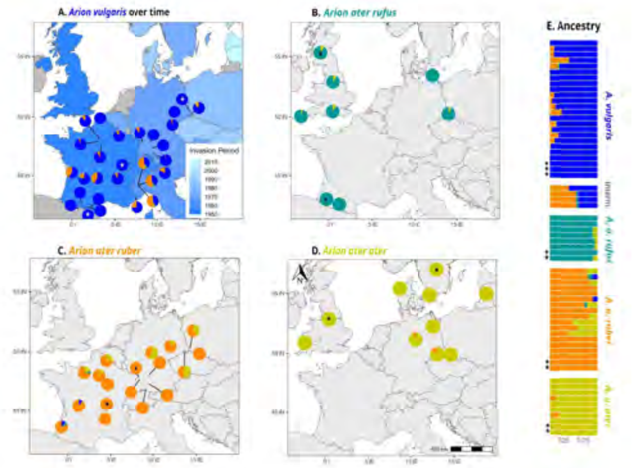
Native *Arion ater* subspecies of slugs were historically widespread across Europe. Since the 1950s, the invasive *Arion vulgaris* has rapidly expanded from southwestern France, driven largely by human-induced landscape changes. This invasion has caused local extinctions, species turnover, and significant economic damage to agriculture.

Although *A. vulgaris* and *A. ater* are known to interbreed, the evolutionary consequences of this hybridization remain unclear.

Does hybridization facilitate invasiveness?

Which taxa hybridize?

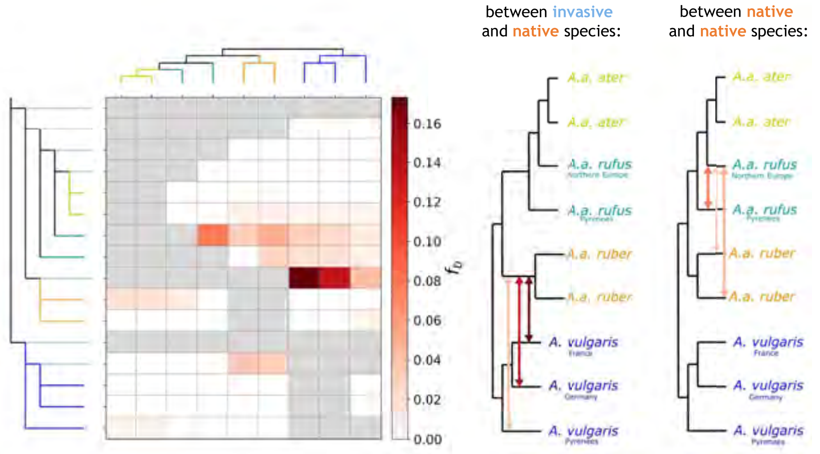
We sequenced 66 individuals at low (~6 x) coverage, representative of the entire known distribution of the 4 taxa. Using genotype likelihoods and a reference genome (~1.5 Gbp) we identify ~52 MM SNPs along the 26 chromosomes.



Hybridization is widespread across all 4 taxa, irrespective of the level mitochondrial divergence (up to 9 Mya between invasive and native species).

Where is introgression most common?

We sequenced 11 pure individuals* at high (~22 x) coverage, and called genotypes to estimate a multispecies coalescent tree and introgression among individuals.



Introgression is most common between the invasive and native species, **particularly within the invasive range**.

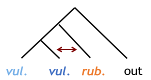
Can we detect adaptive introgression?

We scanned the genome for signatures of introgression and selection in pure populations of the native *A. a. ruber*, the invasive *A. vulgaris*, and the native *A. vulgaris*.

Expectation for **introgressed regions**:

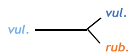
Introgression (F_{DM})

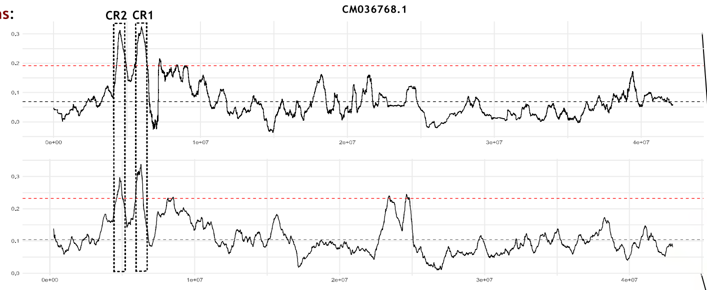
Excess of shared alleles between invasive *A. vulgaris* and native *A. a. ruber* (i.e. higher F_{DM}).



Population Branch Statistics (PBS)

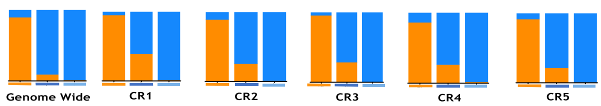
invasive *A. vulgaris* is more similar to native *A. a. ruber* than expected (i.e. higher PBS).

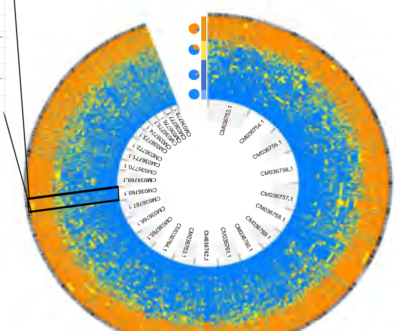




Chromosome Painting

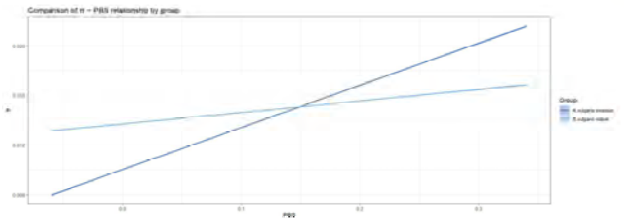
The proportions of *A. a. ruber* alleles in invasive *A. vulgaris* are higher in introgressed areas when compared to the whole genome



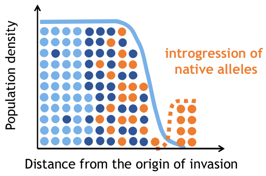


Diversity x Introgression

Higher PBS values correlate positively with population level diversity in invasive *A. vulgaris*. Showing that hybridization might increase diversity in certain genomic areas, what may counteract the genome wide bottleneck experienced during invasion



Take home message:



Our results show that hybridization challenges expectations of reduced genetic diversity in invasive species. Introgression from the native *A. a. ruber* into the invasive *A. vulgaris* may introduce locally adapted alleles into a novel genomic background facing new environmental pressures.

Adaptive introgression of locally adapted alleles may contribute to the rapid adaptation seen during species invasion.

Kompetenzzentrum Biodiversität und integrative Taxonomie
NATURKUNDE MUSEUM STUTTGART
UNIVERSITY OF HOHENHEIM

Integrative taxonomy of doryline ants reveals four new endemic species in Vanuatu

David Grunicke [1,2] , Kyle W. Gray [1,2] , Christian Rabeling [1,2]

[1] Department of Integrative Taxonomy and Biodiversity of Insects, Institute of Biology, University of Hohenheim, Stuttgart, Germany
[2] KomBioTa – Center for Biodiversity and Integrative Taxonomy, University of Hohenheim & State Museum of Natural History, Stuttgart, Germany

Background

Island ecosystems harbor many endemic species but are at severe risk due to habitat destruction and climate change. One of these regions, the South Pacific archipelago Vanuatu (Fig. 1), has recently been identified as an ant biodiversity hotspot, hosting dozens of endemic species, including undescribed members of the ant subfamily Dorylinae. This study used an integrative taxonomic framework including existing molecular data to delimit the Vanuatuan Dorylinae and explore their evolutionary history.

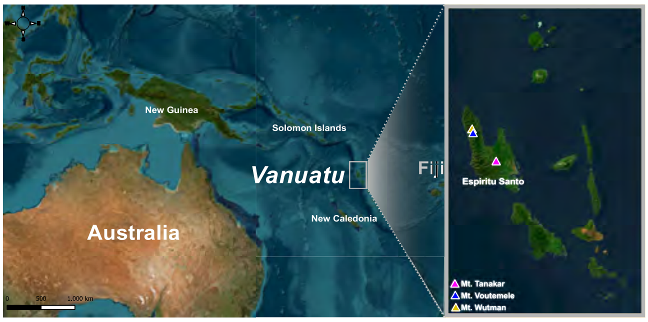


Figure 1: Regional map of Vanuatu including sampling sites.

Materials and Methods

The ants for this study were collected in 2011 and 2012 by Christian Rabeling, Simone Cappellari-Rabeling, and Edward O. Wilson, from the largest island in Vanuatu, Espiritu Santo (Fig. 1). Morphometric measurements of 15 traits from 18 specimens were taken and analyzed using a shape PCA (results not shown). Molecular UCE data from previous studies[1,2] were used to infer a coalescent species tree in IQ-TREE 2 using ASTRAL-III (results not shown), as well as a maximum-likelihood species tree from a concatenated alignment partitioned with SWSC-EN. Lastly, a divergence dating analysis using MCMCtree in paml was conducted, calibrated based on a recent Dorylinae phylogeny (Fig. 2).

Results and Discussion

All phylogenetic analyses recovered four reciprocally monophyletic clades with both qualitative morphology and morphometry supporting these lineages as distinct species across two genera. Preliminary insights into their evolutionary history suggest **three independent dispersal events to Vanuatu**. Two species in the genus *Parasyscia* indicate a case of ***in situ* speciation**, occurring in sympatry on Espiritu Santo. Morphological and phylogenetic data suggest that Vanuatuan Dorylinae are closely related to Fijian members of the subfamily.

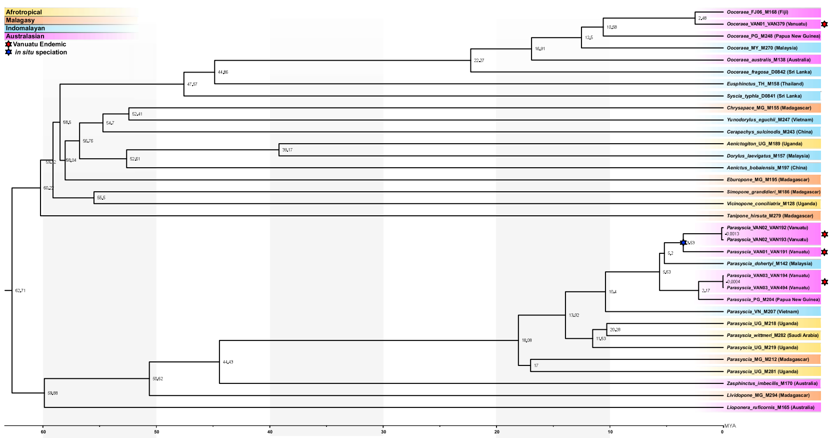


Figure 2: Time calibrated phylogeny of selected Old World Dorylinae. Vanuatuan endemics are marked with a red star and a potential *in situ* speciation with a blue star.

Figure 3: Workers of A) *Ooceraea* VAN01, B) *Parasyscia* VAN01, C) *Parasyscia* VAN02 and D) *Parasyscia* VAN03.

References:
1. Borowiec, M. L. Convergent Evolution of the Army Ant Syndrome and Congruence in Big-Data Phylogenetics. Systematic Biology 68, 642–656 (2019).
2. Gray KW (2023) Biodiversity and Biogeography of Myrmecosymbioses and Vanuatuan Ants. Doctoral Dissertation, Arizona State University

CONTACT
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Rabeling Lab:

Dissecting genes of colour pattern in birds and their role in maintaining species boundaries in a moving hybrid zone

Louis Hausner[1,2]*, Niloofar Alaei Kakhki[1], Maximilian Offermann[2], Ricardo J. Pereira[1,2]

[1]Biodiversity Monitoring, State Museum of Natural History Stuttgart, Germany, [2]University of Hohenheim

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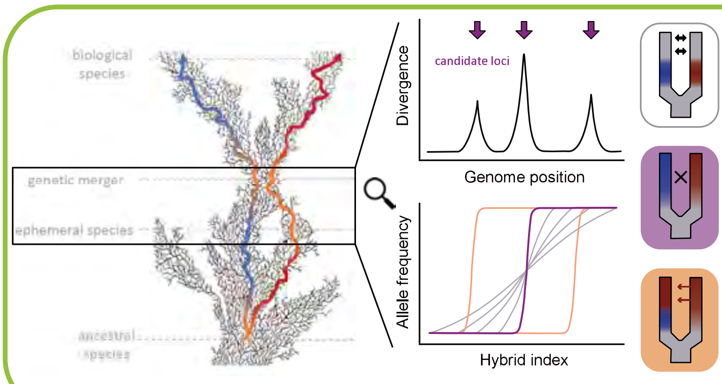


from Pereira & Singhal 2022

adjusted from Schield et al. 2024

Speciation is a continuous process. Populations may split and diverge in isolation. Upon secondary contact, incomplete reproductive isolation (RI) can produce hybrid zones. Even with incomplete RI, species boundaries may persist if selection acts strongly enough on certain phenotypes (e.g. **sexually selected colour patterns**).

The strength needed is determined by the **genetic architecture of underlying loci**. For instance, functionally linked linked loci will require stronger selection compared to physically linked loci.

Studying hybrid zones allows to infer whether highly divergent loci resist gene flow (**barrier loci**) whereas neutral parts of the genome become homogenized. Additionally, loci might move from one species into the other if they provide a selective advantage (adaptive introgressed loci).

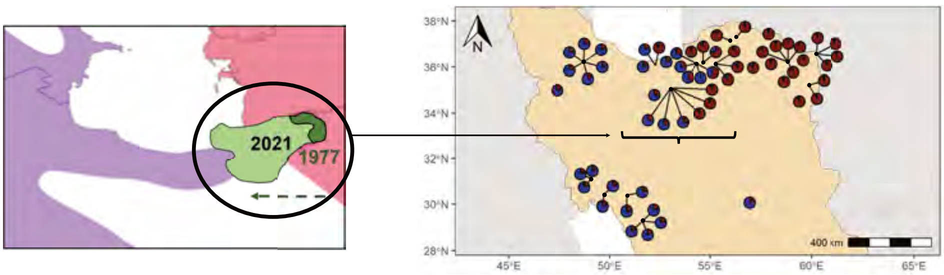
Using the Bunting-Zone we want:

1. to address whether plumage colouration effectively acts as a barrier to gene flow to maintain species boundaries and uncover underlying loci.
2. to test whether those barriers are stable over time.

The Bunting-Zone

The **black-headed bunting** and the **red-headed bunting** differ in several discrete colouration traits with hybrids showing different degrees of intermediate but also novel phenotypes.

We will capitalize on the ongoing movement of the hybrid zone (Gholamhosseini et al. 2017) expecting greater homogenization compared to stable hybrid zones.

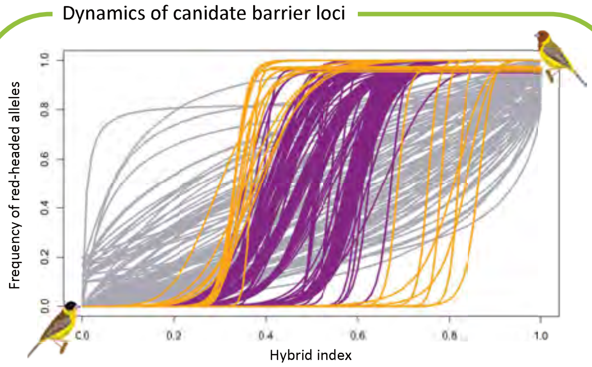


Current state of the hybrid zone in Iran. Pie charts depict the hybrid index per individual. **Blue** proportions correspond to alleles inherited from the **black-headed bunting**, **red** proportions to alleles inherited from the **red-headed bunting**.

We find **various degrees of admixture** in the centre of the hybrid zone leaning to the parental species in the West and East.

Even regions believed well-outside the hybrid zone (e.g. South-West Iran) show signs of admixture.

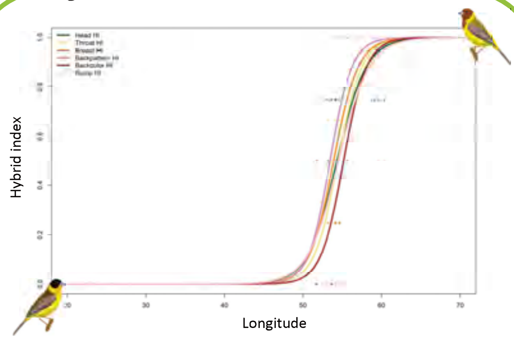
Dynamics of canidate barrier loci



We find loci exhibiting **steep clines** compared to genome average suggesting strong natural or sexual selection.

➡ Some loci show **restricted introgression** along the hybrid index indicating strong selection against gene exchange between the **black-** and the **red-headed bunting**. Others show bi-directional adaptive introgression from either species into the other.

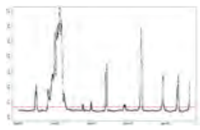
Signals of sexual selection?



Phenotypic clines for the hybrid index based on colouration scores broadly coincide with clines for barrier genes indicating **plumage colouration** acts as a **barrier to gene flow**.

➡ Sexual selection likely plays a role in maintaining species boundaries!

Curious to learn about previous findings from the Bunting-Zone?



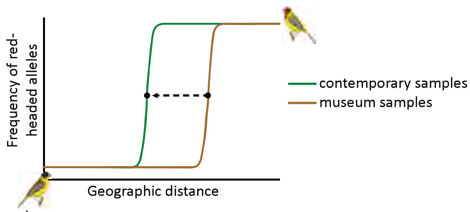
Visit poster board:
P02.333

If you are interested in other projects from our working group, SCAN:

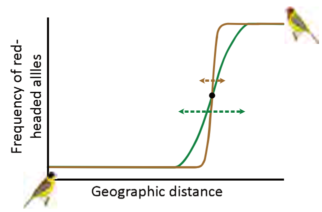
Outlook

By using **museum specimens** sampled in the hybrid zone 50 years ago (~25 generations) we want to test whether barriers to gene flow are **stable over time:**

- Has **functional** and **physical linkage** involving barrier genes decreased over time?
- Is the rate of introgression of barrier genes similar in contemporary and museum samples?



➡ Barriers are stable but the centre of the hybrid zone shifted.



➡ The centre of the hybrid zone remains constant but barriers decreased in stability

References

- Gholamhosseini et al., 2017. An expanding hybrid zone between Black-headed and Red-headed Buntings in northern Iran. *Ardea*
- Pereira & Singhal, 2022. A lizard with two tales: What diversification within Sceloporus occidentalis teaches us about species formation.
- Schield et al., 2024. Sexual selection promotes reproductive isolation in barn swallows. *Science*

ESEB2025 BARCELONA 17-22 AUGUST 2025 CONGRESS OF THE EUROPEAN SOCIETY FOR EVOLUTIONARY BIOLOGY

UNIVERSITY OF HOHENHEIM

Ant communities and diversity in an arid protected biodiversity hotspot in South Africa

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FG 1900 Integrative Taxonomie der Insekten

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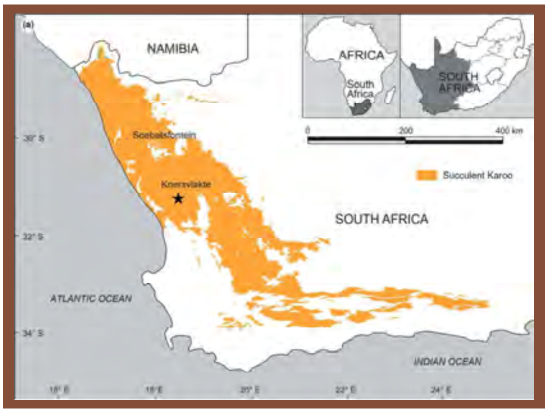
SCAN ME

Introduction

The Succulent Karoo region of South Africa's Western Cape is an arid biome characterised by sparse winter rainfall and low productivity. Despite these conditions, it is recognised as a global biodiversity hotspot, harbouring over 2,000 endemic plant species (Hilton-Taylor, 1996). In contrast to the known plant diversity, the region's insect communities remain poorly understood.

In this project, we used ants (Formicidae) as bioindicators to investigate how microhabitats, vegetation, and geographic factors shape insect communities, and we provide an updated, comprehensive species inventory of this understudied region. These findings contribute valuable ecological data to support and guide conservation efforts in this unique biome.



South African Succulent Karoo and the Knersvlakte (modified from Weber et al., 2018)

Methods

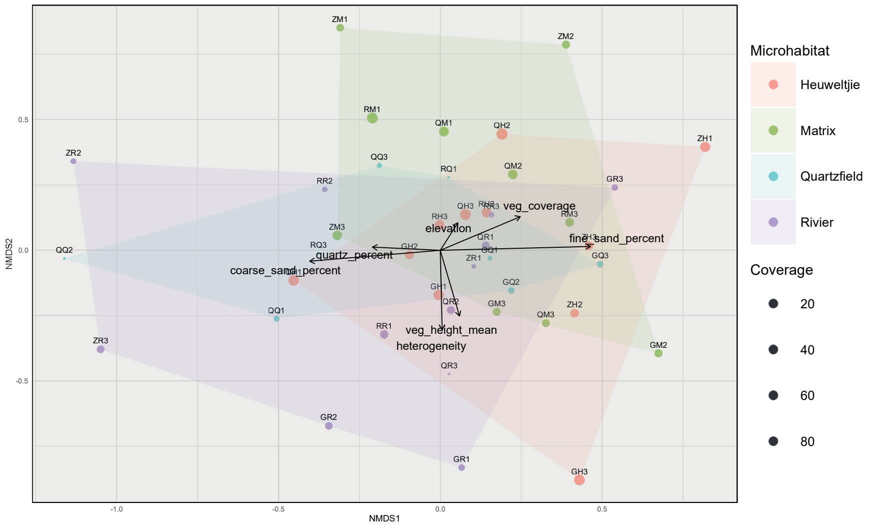
1 habitat sampling using pitfall traps

2 specimens were sorted by morphospecies and mounted on pins for further examination

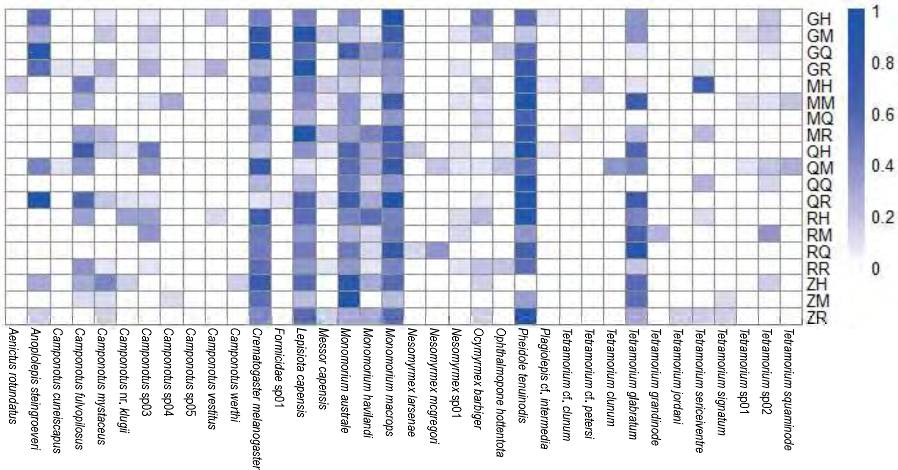
3 ants were identified, digitally imaged and an incidence based database was established

4 NMDS and relative abundance heatmap for community composition in relation to environmental variables

Results



NMDS ordination shows overlap in ant community composition across microhabitats. This suggests shared species assemblages, influenced by vegetation structure, soil characteristics and elevation.



Relative abundance heatmap of ant communities across sites and microhabitats. This illustrates the contrast between highly abundant dominant species and rare taxa recorded only at specific sites.

Conclusion

Ants served as bioindicators for studying insect community composition. Statistical analysis revealed that habitat characteristics had a low influence on community compositions, suggesting a relatively low heterogeneity across different sites. This is likely due to the high mobility of foraging ants, which weakens microhabitat boundaries while nesting sites may still be microhabitat specific. Species abundance was highly uneven, with a few dominant taxa and many rare ones. Although pitfall traps provide standardised sampling they are prone to underrepresent species closely linked to vegetation or nesting sites.

This project established a baseline incidence database for future research in this area, discovered two new species, and rediscovered a species not documented for nearly a century. This underscores the ecological value of the region and highlights the importance of continued research and conservation.

References: Weber, B. Tamm, A., Maier S. & Rodriguez-Caballero, E. (2018). Biological soil crusts of the Succulent Karoo: a review. - *African Journal of Range & Forage Science*, 35: pp. 335-350.

Hilton-Taylor, C. (1996). *Patterns and characteristics of the flora of the Succulent Karoo Biome, southern Africa.* In: The Biodiversity of African Plants, pp. 58-72.

Humboldt reloaded

Listening to Invaders: Passive Acoustic Monitoring of American Bullfrogs

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Motivation

The **invasive American bullfrog** (*Lithobates catesbeianus*) is spreading across Europe. Due to its high reproductive output, omnivorous diet, and tolerance of human modified habitats, it poses a **serious threat to native species and freshwater ecosystems**. In southwestern Germany near Karlsruhe, a population has been established since approximately 1990 and **continues to thrive in a number of gravel pit lakes**. Many invaded sites are located in proximity to protected areas and further expansion along a network of water bodies in the Upper Rhine region is easily possible. Since the control of established populations is **labor intensive and costly, early detection is critical**. However, traditional survey methods often fail to detect low density or newly colonizing populations. Therefore, we aim to test and evaluate **acoustic monitoring as a tool** to bridge this gap.

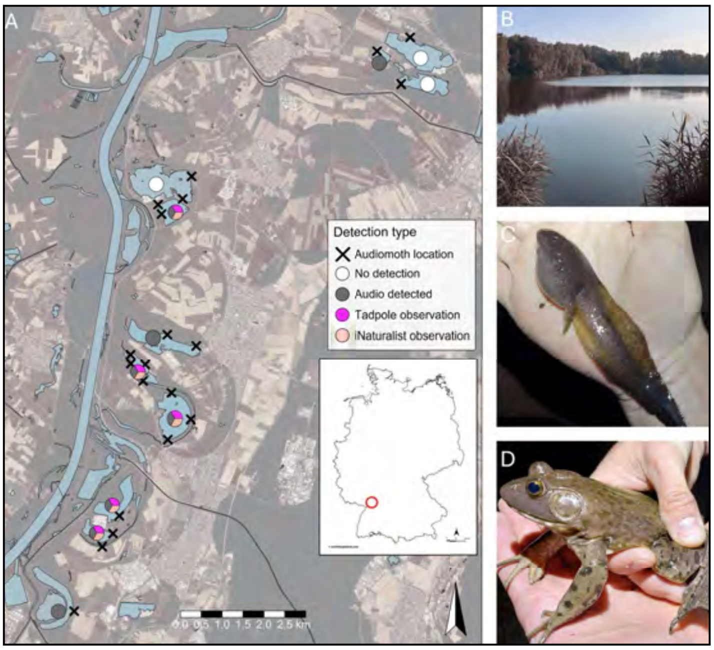

Figure 1. A: Spatial overview of citizen-science and pilot-study observations within invaded waterbodies. B: Source pool Lake Streitköpflesee (C). Tadpole and (D) adult American bullfrog (by Lennhard Hudel)

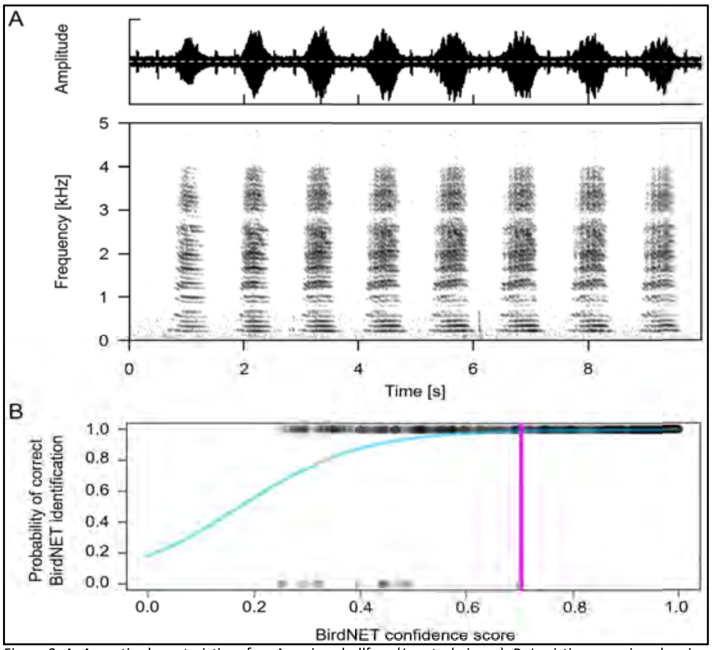

Figure 2. A: Acoustic characteristics of an American bullfrog (*L. catesbeianus*). B: Logistic regression showing BirdNET confidence score thresholds at which the probability of a correct identification was 99%.

Proof of concept

In 2025, we conducted a pilot study using AudioMoths as passive acoustic monitoring **(PAM)** devices in combination with BirdNET automatic species identification to assess the occurrence of invasive American bullfrogs at eleven water bodies near the source population.

The results were as follows:

- Bullfrog calls **detected at 8 of 11** monitored lakes
- Detection **near the protected area NSG Erlich**
- Tadpoles observed at 5 sites, confirming reproduction
- **1,600 hours of audio recordings** over 2 months
- **56,298 call detections** using BirdNET analysis
- Validation of 500 random samples, with 485 correct identifications and 15 incorrect identifications
- Logistic regression model showed that identifications of American bullfrogs with a confidence score above 0.703 had a **99% probability of being correctly identified**

Objectives moving forward

1. Develop and deploy **real-time acoustic monitoring devices**
2. Enable **early detection** before breeding events
3. Expand **spatial monitoring coverage**
4. Assess potential **dispersal pathways** via river systems
5. Provide a monitoring **concept for conservation authorities**

Methodology 2026

In 2026, we will **install five real-time monitoring stations (BirdWeather PUC)** alongside five previously tested PAM devices at highly invaded lakes **to further improve and evaluate the method**. Additionally, we will **monitor 30 water bodies with PAM** devices to increase spatial coverage. These are located on both sides of the Rhine, as well as up/- and downstream of the river, to assess its **potential role as a dispersal corridor.** Others are situated within or close to protected nature reserves to evaluate **potential ecological impacts.**

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Funded by KomBioTa
Center for Biodiversity and Integrative Taxonomy

Effects of undersowing maize with a diverse annual flower mixture on insect abundance and diversity

Hannah Weinläder[1], Jens Hartung[2], Maria Müller-Lindenlauf[1]

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Weinläder, H., Hartung, J., & Müller-Lindenlauf, M. (2026). Effects of undersowing maize with a diverse annual flower mixture on insect abundance and diversity. Basic and Applied Ecology, 90, 109–119. https://doi.org/10.1016/j.baae.2025.12.009

Introduction

Background:

- Silage maize cultivation occupies large areas (21 % in Germany, Eurostat (2024)) but provides low ecological benefits, particularly for pollinators
- Biodiversity decline → requires the development of sustainable cropping systems

flower strip (FS) – land sparing

(Foto: HfWU)

- well-established conservation measure on arable land with proven biodiversity effects (Haaland et al., 2011; Lowe et al.,2021; Scheper et al.,2015)
- typically occupy only a small proportion of the field
- arable land out of production

undersown maize (MU) – land sharing

(Foto: HfWU)

- rather „novel“ conservation measure
- wide row spacing in maize enables intercropping with flowering plants
- biodiversity effect on larger area
- no arable land out of production
- impacts on maize yield and quality?

Wild bees (Apoidae) **Ground beetles** (Carabidae) **Rove beetles** (Staphylinidae)

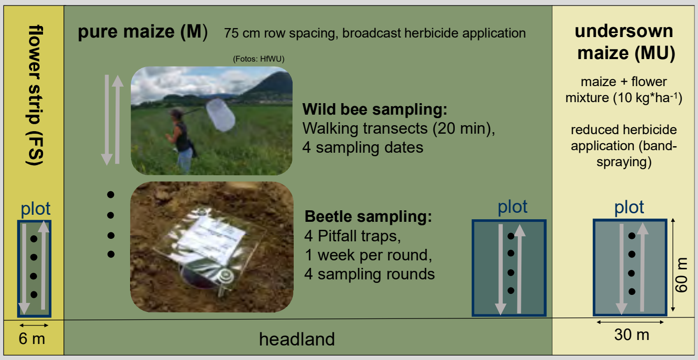
→  ?

Wild bee: @ James K. Lindsey, wikimedia commons, Ground beetle: @ JonRichfeld, wikimedia commons, Rove beele: @ Francisco Welter-Schultes, wikimedia commons

Material and Methods

Study design:

- 2 years (2022-2023), 12 trial sites on 11 conventionally managed farms, Baden-Württemberg, Germany
- flower strips only 2023 (*n* = 6), sown autumn 2022

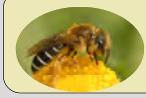


Data analysis:

- Pooling: farm × year × system (across sampling rounds & traps)
- Metrics: Total abundance (wild bees) / activity density (beetles), species richness, and Shannon Diversity Index (SDI)
- Count data → GLMM (poisson, log-link), SDI → LMM (normal distribution)
- Fixed effects: system, year, system × year, random effects: farm, farm × system, farm × year; residual error effects with year-specific variance
- Post-hoc: Fisher`s LSD test (α = 0.05)

Results and Discussion

Does undersowing maize with diverse annual flower mixtures increase insect abundance and diversity compared to pure maize?

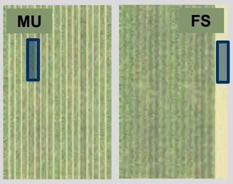


- MU → significant positive effects on abundance and diversity
- promotes wider range of species compared to maize-bean intercropping (Hüber et al., 2022)
- but rather unspecialized, polylectic species

- no significant effects, except for increased activity density of rove beetles
- ground beetle community dominated by the 20 most widespread farmland species (Trautner, 2017) in the region (95 % of individuals in both systems)
- highest ground beetle activity density in M, possible bias due to methodology?
- short duration of cropping system may have limited observed effects

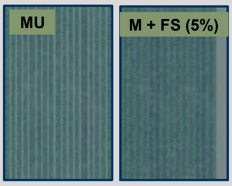
How does the "novel" undersowing system compare with the "well-established" flower strips? (data from 2023 only)

Per sampling area

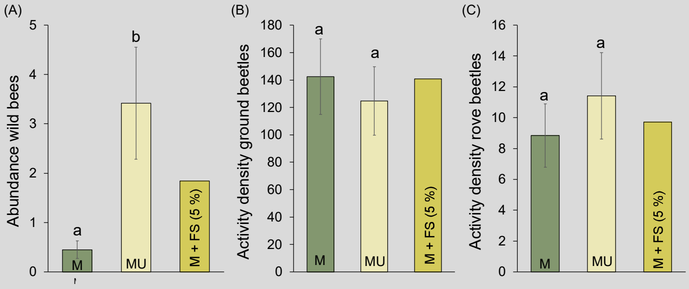


- FS with significantly higher species richness per unit area across all insect groups
- FS with significantly higher abundance of wild bees and rove beetles
- effects particularly pronounced for wild bees
  - 8-fold higher abundance
  - 4-fold higher species richness
- highest ground beetle activity density in M

Scenario: 5 % flower strip coverage of a maize field



- M + FS (5%) shows lower abundance/ activity density than MU (wild bees, rove beetles)
- ground beetle activity density higher in M + FS (5%) (driven by high values in M)
- FS coverage needed to match MU: 11 % for wild bees, 15 % for rove beetles
- trade-off: high FS coverage → loss of productive land
- Species richness not scalable (dependent on habitat quality)



Abundance of wild bees (A) and activity density of ground beetles (B) and rove beetles (C) per sampling area in pure maize (M), undersown maize with a flower mixture (MU) and in a scenario with 5 % flower-strip coverage (M + FS (5 %)) of a maize field. All values are based on year x system estimates for 2023. The 5 % flower-strip scenario was approximately calculated as a weighted mean of abundance estimates from M (*n* = 12 trial sites) and FS (*n* = 6 trial sites). MU values were obtained from MU *n* = 11 trial sites. Values represent total counts pooled across all sampling rounds and were standardized using an offset for the number of sampling rounds.

Conclusion

- Undersowing maize with diverse annual flower mixtures enhances biodiversity
- Benefits mainly generalist wild bee species
- Advantage: provides resources across a larger area, scalable without reducing crop area (unlike flower strips)
- Limitation: provides floral resources, but no nesting/overwintering habitats → limited effect on species richness
- Potential trade-offs with crop productivity; further research needed

The project "Diversification of silage and energy maize cultivation in conventional and organic farming systems" (01 May 2018 – 31 December 2025) was funded by the Ministry of Rural Affairs and Consumer Protection (MLR) as part of the "Special Program for Strengthening Biodiversity." Project partners include Nürtingen-Geislingen University (HfWU), the Agricultural Technology Centre Augustenberg (LTZ), the Agricultural Centre Baden-Württemberg (LAZBW), and the Competence Centre for Organic Farming Baden-Württemberg (KÖLBW).

References: Eurostat (2024), Eurostat—Crop production in eu standard humidity, https://ec.europa.eu/eurostat/databrowser/view/apro_cpsh1__custom_15788746/default/table?lang=en; Haaland, C., Naisbit, R. E., & Bersier, L.-F. (2011). Sown wildflower strips for insect conservation: A review. Insect Conservation and Diversity, 4(1), 60–80. https://doi.org/10.1111/j.1752-4598.2010.00098.x; Hüber, C., Zettl, F., Hartung, J., & Müller-Lindenlauf, M. (2022). The impact of maize-bean intercropping on insect biodiversity. *Basic and Applied Ecology*, *61*, 1–9; https://doi.org/10.1016/j.baae.2022.03.005; Lowe, E. B., Groves, R., & Gratton, C. (2021). Impacts of field-edge flower plantings on pollinator conservation and ecosystem service delivery – A meta-analysis. *Agriculture, Ecosystems & Environment*, *310*, 107290. https://doi.org/10.1016/j.agee.2020.107290; Scheper, J., Bommarco, R., Holzschuh, A., Potts, S. G., Riedinger, V., Roberts, S. P. M., Rundlöf, M., Smith, H. G., Steffan-Dewenter, I., Wickens, J. B., Wickens, V. J., & Kleijn, D. (2015). Local and landscape-level floral resources explain effects of wildflower strips on wild bees across four European countries. *Journal of Applied Ecology*, *52*(5), 1165–1175. https://doi.org/10.1111/1365-2664.12479; Trautner, J. (2017). *Die Laufkäfer Baden-Württembergs [2 Volumes]*.

A curated and integrated dataset for exploring global bee-plant interactions

Noori, S., Gaugel, S. M., Orr, M. C.

Eltonian shortfall

- There are a lot of **gaps in our knowledge** about biodiversity
- Eltonian shortfall ➔ knowledge gap on **biotic interactions**
- Interactions between different organisms can help understanding **community function** & **ecosystem services**
- Disruptions to **interaction network** can cause negative, cascading impacts on ecosystems network

The solution

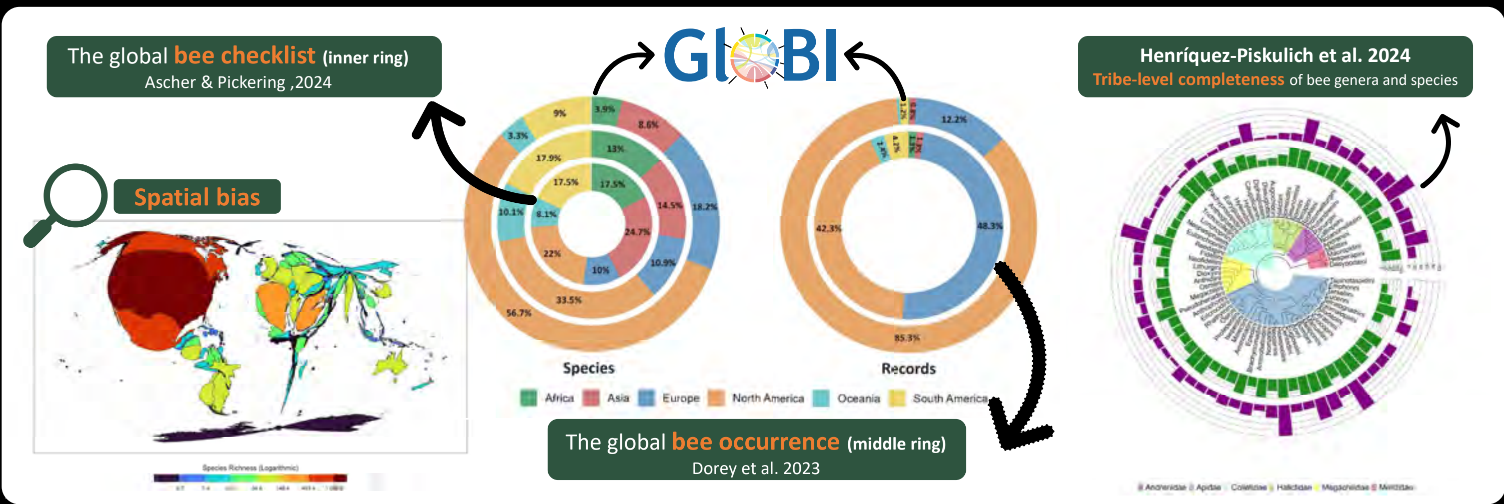
- **Compiling current knowledge** about species interactions from different sources ➔ **GloBI** did this step! (Poelen et al. 2014)
- **Harmonize** and **standardize** these data into a human and machine readable format
- Assess taxonomic, phylogenetic and geographical **biases**
- **Integrating metadata** from other sources to enrich the dataset

Our approach

- **Bee-plant interactions** from GloBI > 2 M records
- **Multi-step quality control** based on global checklists for bees and plants ➔Harmonizing the taxonomy
- Intergrade with:
  - Global **bee** checklist Ascher & Pickering ,2024 ➔ 21 k species
  - Global **plant** checklist Brown et al. 2023& POWO, 2025 ➔ 308 k species
  - Global bee **occurrences** Dorey et al. 2023 ➔ 11 k species, 7 M records

The curated dataset

- **982 k** unique bee-plant interactions
- For **5,537** bees & **12,699** plants
- **> 80%** with coordinate data
- + **Endemism** for bee and plants at national level
- + Metadata for **human plant use**
- + Metadata for **phylogenomic distance**



Taxonomic biases

- Apidae family ➔ **> 53%** of the records
- Bombini, Apini, and Halictini tribes ➔ **> 70%** of records
- Bombus ➔ **> 30%** of records
- western honey bee (*Apis mellifera*) ➔ **7%** of records
- Interactions mainly with **common human-used plants**
- **Non-endemic** bees/plants are better represented

Geographical biases

- North America ➔ **> 48%** of its bee fauna
- North America ➔ **> 85%** of all records
- UK, USA, Canada, and Germany ➔ **>65 to 45%** of their fauna
- e.g., South Africa, Peru, Türkiye ➔ **< 3%** of their fauna
- **Disproportionately underrepresented** ➔ Africa and Asia, Central Asia, and South America

Applications

- '**fit for use**' but still heavy taxonomic and geographic biases
- To explore the diversity and structure of the **bee-plant interaction networks** across North America and Europe
- Patterns of specialization, robustness and modularity in **pollination networks** globally
- To investigate their environmental and anthropogenic **drivers** of bee-plant network patterns

If you want to know more about my work!

A comparison between Static and Dynamic Species Distribution Models: case study of Romanian herpetofauna

Sajad Noori[1], Laura Karolin Steib[2], Tibor Sos[3,4], Dennis Rödder[2]

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[3] Babeş-Bolyai University, Cluj-Napoca, Romania
[4]Milvus Group Bird and Nature Protection Association, Tîrgu Mureş, Romania

- Biodiversity is not a stable entity and shifts toward **suitable habitats** in response to fluctuations in environmental conditions.
- Classical **Species Distribution Models (SDMs)** assumes climate stability and overlooks variability and trends, especially under anthropocentric climate change.

➢ Assess the efficiency of **Dynamic** and **Static** SDMs in capturing spatio-temporal **occupied climate variations** by species .

➢ Using SDMs results to investigate the **Conservation Gap** of Romanian protected areas for its herpetofauna.

19 amphibians **19 reptiles**

Occurrences ➔ **45,887** (2002-2023)

Habitat mask ➔ Using suitable **IUCN** terrestrial habitats

Variables ➔ Relevant **WorldClim** (1988-2023) variables

Background points ➔ **Weighted** based on sampling **bias** layer

Protected areas (PAs) of Romania ➔ **1,615**

Climate scenarios

Average (Static), each year (Dynamic), every 3- and 5-year

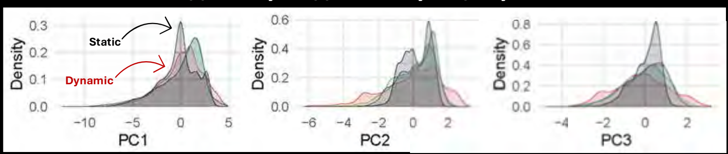
SDMs

Maximum Entropy (**MAxEnt**) optimal setting ➔
All feature classes (L, P, Q, H, T, and their combinations)
AUC_{test} > 0.7 // 80/20 split // 100 runs // 10% omision

Principal Component Analysis (**PCA**) + **Hypervolum** ➔
To assess the occupied climate space vs. Background

Climate coverage

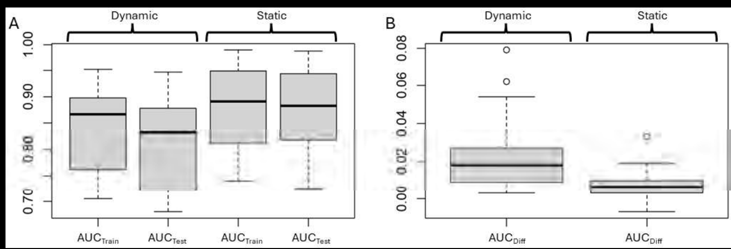
Static narrowest //Five-year// Three-year/ Dynamic broader



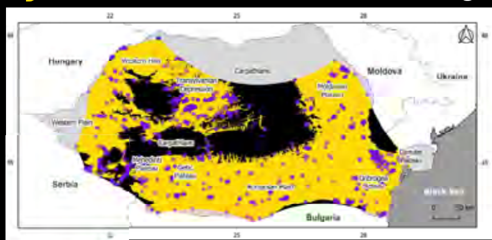
Hypervolume size

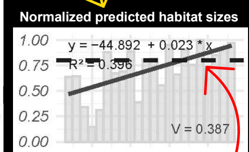
	Background	Records
Dynamic	422	356
Static	48	52

Higher $AUC_{Test/Train}$ for Static (p > 0.001) + Lower AUC_{Diff}

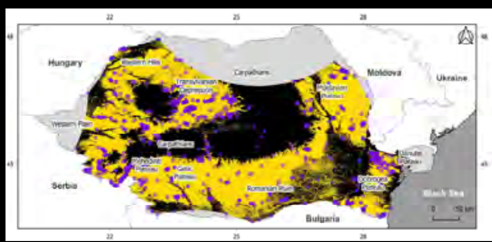


Dynamic ➔ broader and fluctuated range!





Static



***Lacerta viridis* (LAURENTI, 1768)**

Static

Beter performance, compact climate space, smaller hypervolume, nested within Dynamic, smoothing the extreme variations

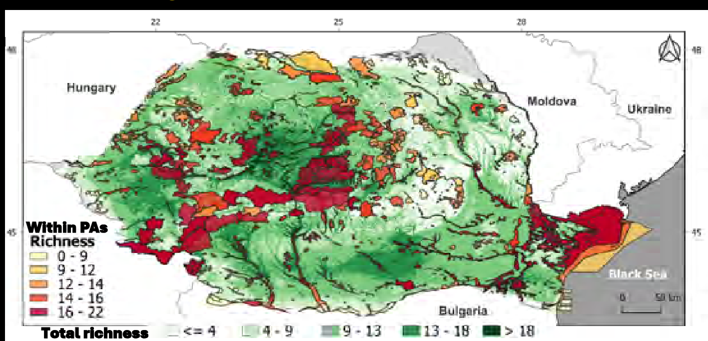
Dynamic

Capturing the spatio-temporal variabilities, broader climate space and hypervolume

Conservation coverage

	Amphibians	Reptiles
> 40%	5	10
> 20 < 40%	8	7
< 20%	6	2

Good coverage (> 40%) for IUCN threatened species by **PAs**!



Regional species loss, local functional retention: contrasting patterns across calcareous and siliceous grasslands

Undine Schöllkopf[1,2,3], Viktoria Ferenc[1,2,3], Maria Májeková[4], Richard Michalet[5], Pierre Liancourt[1,3,4]
1: State Museum of Natural History Stuttgart 2: University of Hohenheim 3: KomBioTa – Center for Biodiversity and Integrative Taxonomy 4: University of Tübingen 5: University of Bordeaux

BACKGROUND

- Calcareous and siliceous grasslands are among Europe's most species-rich habitats, both legally protected yet declining. Both face climatic drying, but vulnerability may differ.
- The two grassland types differ in soil properties and water availability:

Siliceous: high soil moisture, deep & acidic soils

Calcareous: dryer, more shallow soil, alkaline

Fig. 2: Study system. Siliceous grassland (left) and calcareous grassland (right)

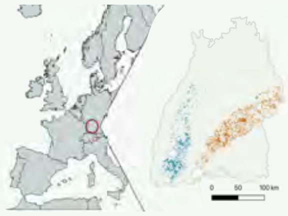
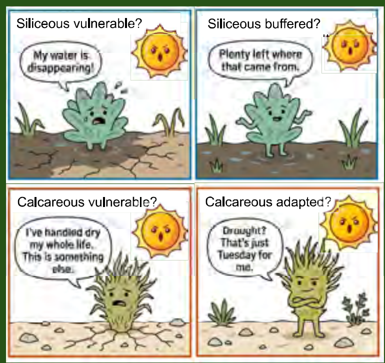


Fig. 1: Study region. State of Baden-Württemberg in southwest Germany. Typical locations of siliceous grasslands (blue) and calcareous grasslands (orange)

QUESTION & HYPOTHESES

Are siliceous and calcareous grasslands equally threatened by increasing drought?



H1: Siliceous grasslands are more vulnerable. Their moisture-demanding flora cannot cope with increasing drought.

H2: Calcareous grasslands are more vulnerable. They are already at the dry extreme, further drying exceeds tolerance thresholds.

RESULTS

HISTORIC DATA REGIONAL SCALE

1972-2023

Grid-level change in occurrence

Fig. 3: Extent (Baden-Württemberg) and grain (5 × 6 km grid cells) of historic regional floristic mapping analysis

Stronger declines in siliceous grassland species pool

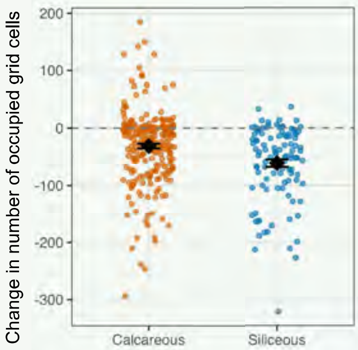


Fig. 4 Regional species change: Change in occurrence of characteristic grassland species by grassland type

Moisture-demanding species declined more in both grassland types

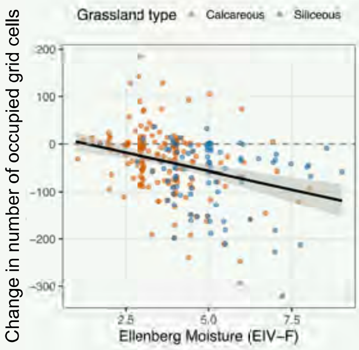


Fig. 5 Moisture predicts decline: Relationship between Ellenberg moisture and change in species occurrence. No interaction between grassland type and EIV M

RECENT DATA LOCAL SCALE

2025

24 local plots

Fig. 6: Location of 24 local grassland plots (2 × 2 m, sampled 2025)

Simpsons Diversity marginally higher in siliceous grasslands

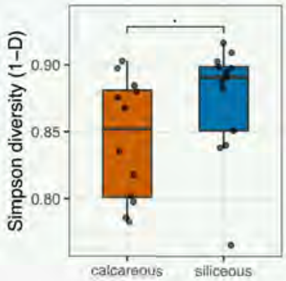


Fig. 7: Simpson's diversity (1−D) by grassland type. Wilcoxon test, p = 0.053

Functional dispersion higher in siliceous grasslands

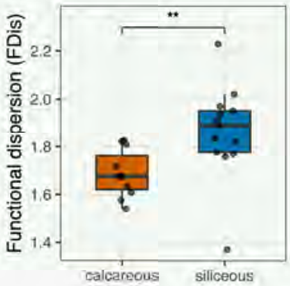


Fig. 8: Functional dispersion. Wilcoxon test, p < 0.01. Functional dispersion = mean distance of species to the community centroid in trait space; higher values indicate a wider range of coexisting strategies.

Ellenberg moisture median and variance higher in siliceous grasslands

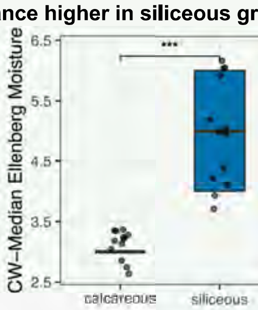


Fig. 9: Community-weighted median Ellenberg moisture (EIV-M) by grassland type. Median: Wilcoxon test, p < 0.001. Variance: Levene's test, p = 0.036.

DISCUSSION & CONCLUSIONS

- Siliceous grasslands lose more species regionally (supporting H1), but retain higher functional dispersion locally
- Weaker environmental filtering likely permits broader coexistence in siliceous grasslands; drought-tolerant species may partially compensate for specialist losses
- Calcareous grasslands have lower functional dispersion and (for now?) a narrower colonizer pool, limiting buffering under continued drying (supporting H2)

METHODS

Regional:

- Change in species occurrence across floristic mapping grid cells in Baden-Württemberg (period 1: 1972–2000, period 2: 2000–2023).
- Characteristic species defined following the Natura 2000 habitat manual.
- Ellenberg indicator values used as predictors of species occurrence change

Local:

- 24 grassland plots (12 calcareous, 12 siliceous) sampled in 2025.
- Species cover recorded in 2 × 2 m plots.
- Trait measurements: Height, specific leaf area, leaf dry matter content, and turgor loss point measured on species with cover ≥ 2%.

Undine Schöllkopf
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5 Kom Bio Ta

UNIVERSITY OF HOHENHEIM

NATURAL HISTORY MUSEUM STUTTGART

Diversified Farming works!
But Bees do not like Familie Workers?

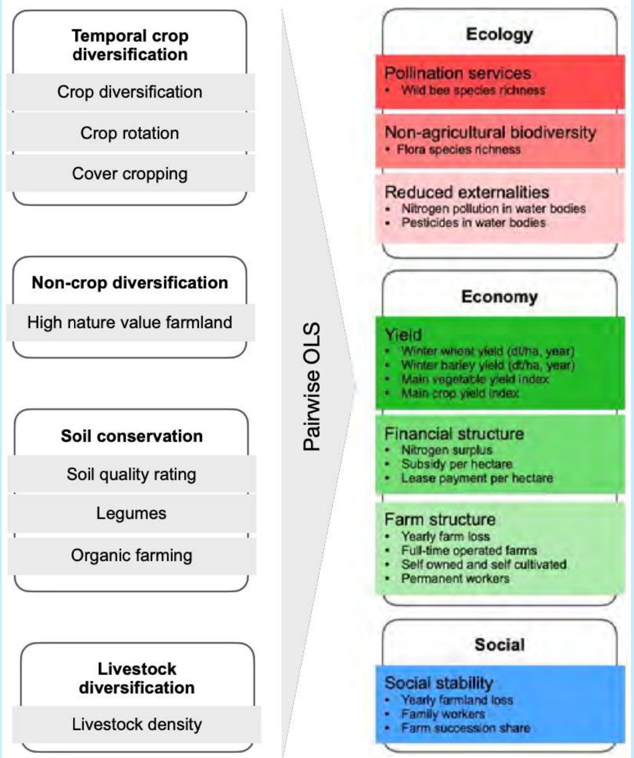
Maria Seiter | MSc Applied Environmental Studies, University of Koblenz

1. Motivation

Agricultural systems face the challenge of balancing productivity with ecological sustainability. Diversified farming systems (DFS) are increasingly discussed as a strategy to enhance biodiversity and ecosystem services. However, empirical evidence at larger spatial scales remains limited. This study investigated how different dimensions of diversification in farming relate to ecological, economic, and social outcomes at the district level.

2. Methods & Framework

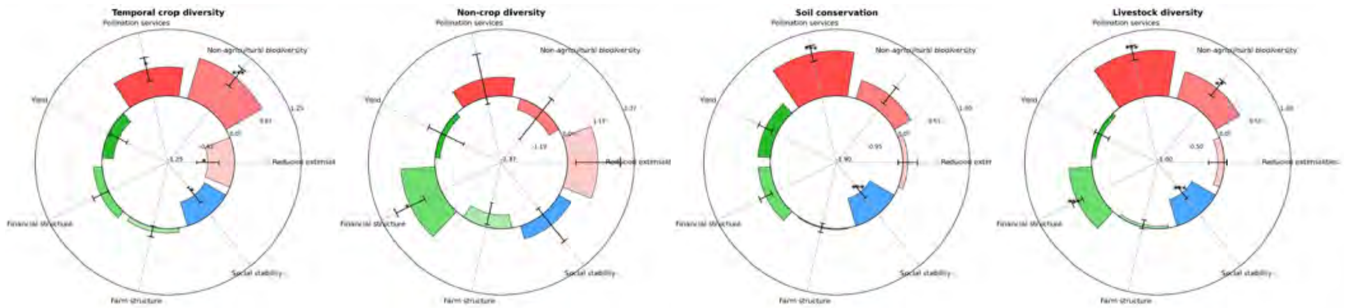
- Spatial unit: 44 districts in Baden-Württemberg
- Data sources: Open data, remote sensing, agricultural statistics
- Indicators: Multiple diversification metrics and outcome variables
- Analysis: Correlation analysis and exploratory OLS regression



Important! Livestock density is inverted (lower livestock density is a more favorable condition).

3. Results

- 28 OLS estimates tested; 11 significant ($p < 0.05$), including 6 highly significant ($p < 0.001$)
- Majority show positive associations (7 positive vs. 4 negative)
- Diversification shows consistent ecological benefits, but effects are strategy-dependent
- Economic outcomes remain limited: yield and financial indicators show weak responses
- Social stability exhibits negative patterns
- Ecological gains occur without reductions in environmental externalities (paradox)
- Temporal diversification practices vary strongly across districts and show substitution patterns
- Wild bee richness declines with higher family labor share via livestock system linkage
- Livestock intensity increases nitrogen pressure and reduces biodiversity indicators



4. Discussion

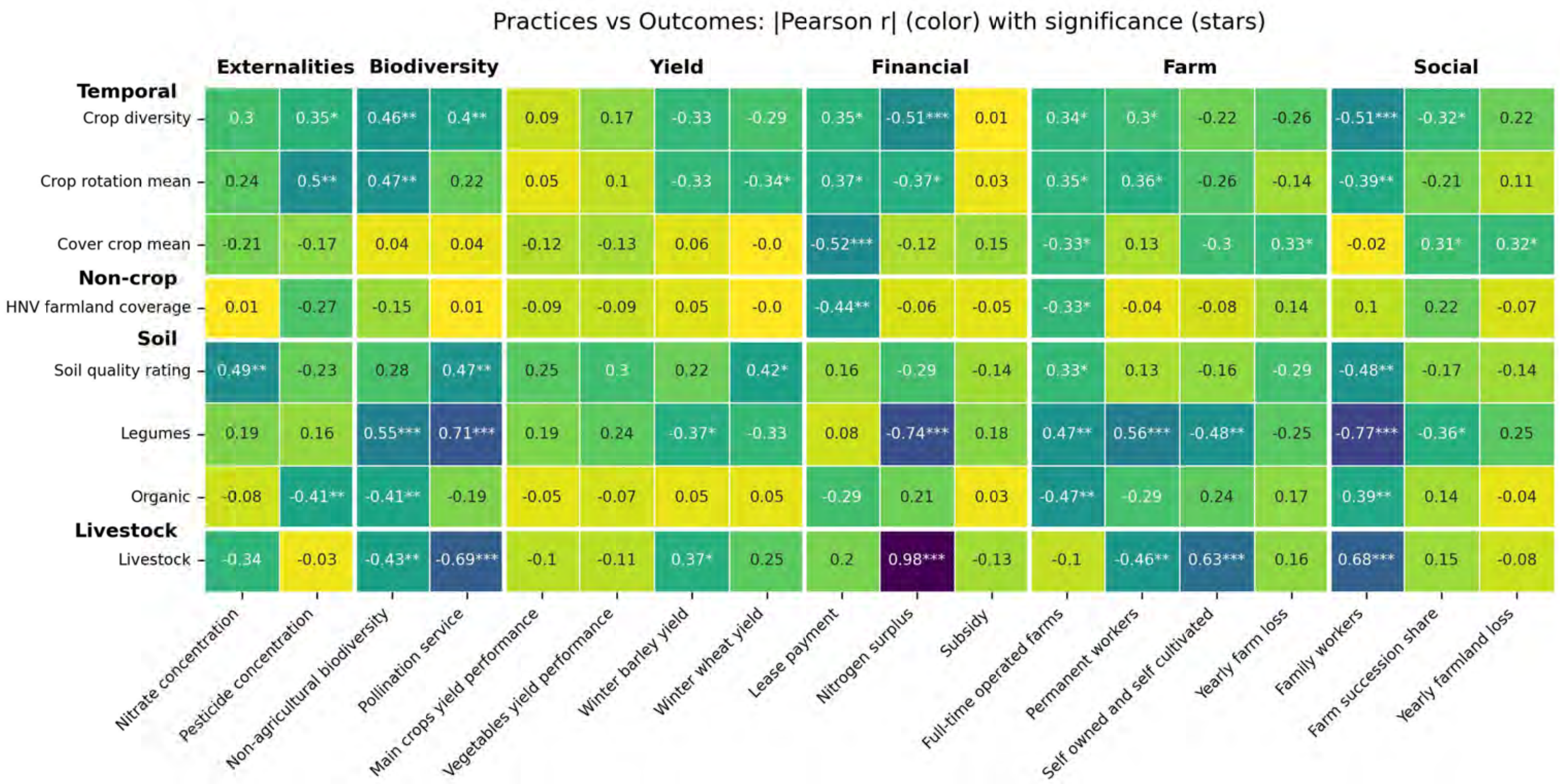
- Diversification operates as a structural system pattern that improves ecological outcomes but produces trade-offs and remains constrained by input-intensive production dynamics.
- Biodiversity ↑ but externalities not consistently ↓ (not only beneficial species supported?)
- Nitrogen is the underlying pattern which mediates many effects (Wild bees, Pollination Service) and is reduced by applying DFS (Crop diversity***, Crop rotation*)
- Legumes have many benefits & seem to be economic valuable for farmers
- Wild bees don't like family workers because they tend to work in animal husbandry systems (and are a mediator for nitrogen)

5. Conclusion

Diversified farming systems show consistent ecological benefits without clear yield gains, indicating that their value lies beyond productivity increases. The results suggest that diversification practices are already embedded in conventional farming systems, despite low organic shares, and contribute to system functioning. At the same time, effects remain shaped by underlying structural drivers such as nitrogen inputs. The study demonstrates that diversification patterns are detectable at regional scale using open data, providing a basis for monitoring agricultural system development over time.
Eat more lentils and reduce your meet and dairy consumption.

6. References

Beillouin, D., et al. (2021). Positive but variable effects of crop diversification on biodiversity and ecosystem services. Global Change Biology, 27(19), 4697–4710.
Rasmussen, L. V., et al. (2024). Joint environmental and social benefits from diversified agriculture. Science, 384(6691), 87–93.
Rosa-Schleich, et al. (2019). Ecological-economic trade-offs of Diversified Farming Systems – A review. Ecological Economics, 160, 251–263.


Practices vs Outcomes: |Pearson r| (color) with significance (stars)
Externalities
Biodiversity
Yield
Financial
Farm
Social
Temporal
Crop diversity
0.3 0.35* 0.46** 0.4** 0.09 0.17 -0.33 -0.29 0.35* -0.51*** 0.01 0.34* 0.3* -0.22 -0.26 -0.51*** -0.32* 0.22
Crop rotation mean
0.24 0.5** 0.47** 0.22 0.05 0.1 -0.33 -0.34* 0.37* -0.37* 0.03 0.35* 0.36* -0.26 -0.14 -0.39** -0.21 0.11
Cover crop mean
-0.21 -0.17 0.04 0.04 -0.12 -0.13 0.06 -0.0 -0.52*** -0.12 0.15 -0.33* 0.13 -0.3 0.33* -0.02 0.31* 0.32*
Non-crop
HNV farmland coverage
0.01 -0.27 -0.15 0.01 -0.09 -0.09 0.05 -0.0 -0.44** -0.06 -0.05 -0.33* -0.04 -0.08 0.14 0.1 0.22 -0.07
Soil
Soil quality rating
0.49** -0.23 0.28 0.47** 0.25 0.3 0.22 0.42* 0.16 -0.29 -0.14 0.33* 0.13 -0.16 -0.29 -0.48** -0.17 -0.14
Legumes
0.19 0.16 0.55*** 0.71*** 0.19 0.24 -0.37* -0.33 0.08 -0.74*** 0.18 0.47** 0.56*** -0.48** -0.25 -0.77*** -0.36* 0.25
Organic
-0.08 -0.41** -0.41** -0.19 -0.05 -0.07 0.05 0.05 -0.29 0.21 0.03 -0.47** -0.29 0.24 0.17 0.39** 0.14 -0.04
Livestock
Livestock
-0.34 -0.03 -0.43** -0.69*** -0.1 -0.11 0.37* 0.25 0.2 0.98*** -0.13 -0.1 -0.46** 0.63*** 0.16 0.68*** 0.15 -0.08
Nitrate concentration
Pesticide concentration
Non-agricultural biodiversity
Pollination service
Main crops yield performance
Vegetables yield performance
Winter barley yield
Winter wheat yield
Lease payment
Nitrogen surplus
Subsidy
Full-time operated farms
Permanent workers
Self owned and self cultivated
Yearly farm loss
Family workers
Farm succession share
Yearly farmland loss

Karlsruhe Institute of Technology

FROM MATTER TO MATERIALS AND LIFE
Building Blocks of Life: Structure and Function

Integrating Synchrotron Micro-CT & DNA Sequencing

Cristina Vasilița[1,3], Alexander Riedel[4], Daniela Mera-Rodríguez[5], Clement Tavakoli[1], Jenny Hein[1], Pauline Pfeiffer[1], Rebecca Spiecker[1], Janes Odar[1], Angelica Cecilia[1], Christian Rabeling[5], Tilo Baumbach[1,2], Lars Krogmann[3], Thomas van de Kamp[1,2]

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[3]Center for Biodiversity and Integrative Taxonomy Research, University of Hohenheim & State Museum of Natural History Stuttgart, Stuttgart, Germany
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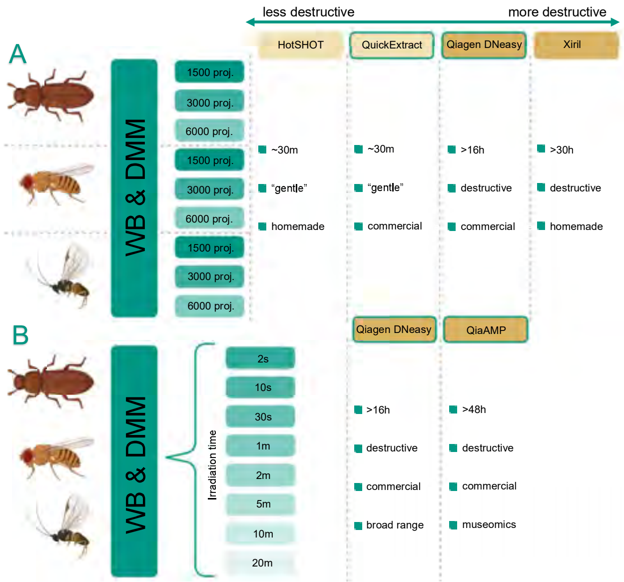
3D reconstruction of *Drosophila suzukii* and *Sitophilus granarius* with exposed internal morphology

Background

- The integrity of morphological internal and external structures, as well as genetic data is paramount in taxonomic and evolutionary studies [1].
- The majority of insects are very small (<2mm size [2]), therefore the entire insect body needs to be subjected to DNA extraction.
- The digestion steps during DNA extraction potentially affect soft tissues, rendering it impossible to digitize the internal morphology of insects post-extraction, while the extent to which DNA is compromised after a specimen has been scanned is unclear.
- A digital repository of both morphology and DNA is essential for the future of natural history collections, that currently host >500M insects [3]. It will provide permanent, high-resolution records and access to phenotypic and genotypic data without further physical handling of the specimen.

Experimental set up



Scope

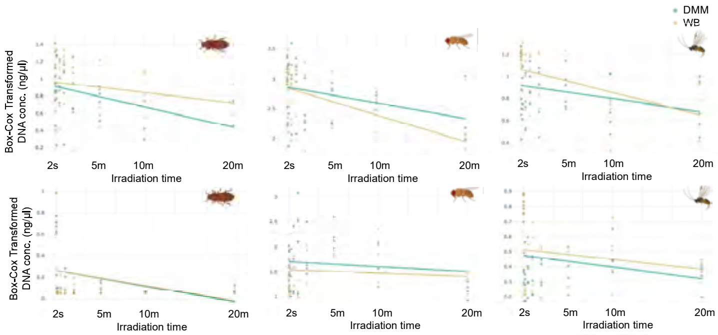
- Examine the effects of DNA extraction on the internal structures of insect specimens, particularly soft tissues.
- Evaluate the impact of high-dose radiation µCT scanning on DNA quality and integrity in insects.
- Establish an optimal workflow for combining synchrotron CT scanning and DNA extraction.

Results

- DNA extraction methods impact soft tissue to varying degrees, but all methods are inherently destructive.

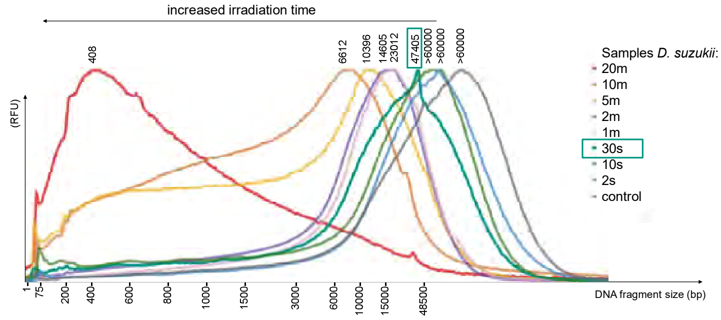
Slices, sagittal plane through insect bodies before and after DNA extraction: *Sitophilus granarius, Drosophila suzukii* and *Leptopilina japonica*

- The quantity of DNA decreases with longer irradiation.



Trend lines for DNA concentration values in samples post-irradiation. Method of DNA extraction: above – QiaAMP, below Qiagen DNeasy.

- The optimized workflow at IMAGE enables the efficient recovery of high-quality DNA.



References
[1] Meier, R. et al. . *Annu. Rev. Entomol.* 70 (2025)
[2] Srivathsan, A. et al. *Nat. Ecol. Evol.* 7 (2023)
[3] Short, A.E.Z. at al. *Annu. Rev. Entomol.* 63 (2018)

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Kompetenzzentrum Biodiversität und Integrative Taxonomie
NATURKUNDE MUSEUM STUTTGART

Selektive Zikadenjägerin oder Opportunistin?
Beuteauswahl der Grabwespe *Alysson tricolor* (Hymenoptera, Bembicidae)

Verena Engl[1], Magdalena Pfeiffer[1], Erhard Strohm[1], Gernot Kunz[2], Robert Zimmermann[1]

[1]Universität Regensburg, Institut für Zoologie, AG Evolutionäre Ökologie; verena.engl@stud.uni-regensburg.de

[2]Karl-Franzens University of Graz, Department of Biology (Zoology)

I Hintergrund

- Solitäre Grabwespe (0,6 – 1,0 cm), ursprünglich Mittelmeerraum → breitet sich nach Norden aus
- Weibchen legen Nester im Boden an, versorgen Brut mit gelähmten Cicadellidae (Zwergzikaden)
- Bisher bekannte Beute: 10 Arten (Eurymelinae & Deltocephalinae)
- **Unklar:** Jagdverhalten selektiv oder opportunistisch?

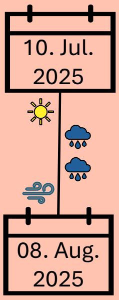
II Fragen

1. Wie groß ist das Beutespektrum der Wespen einer Aggregation?
2. Unterschiedet sich das Beutespektrum von der Habitatfauna? Jagt *A. tricolor* selektiv oder opportunistisch?

III Material und Methoden

Zwei Erfassungsgebiete im **Botanischen Garten der Universität Regensburg**:

- Nestaggregation von *A. tricolor* – Fang eingetragener Beute
- Umgebende Vegetation (Bäume) – Fang potenzieller Beute



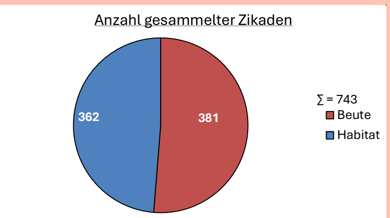
- Entspricht der Hauptflugzeit von *A. tricolor*
- Wetter im Sommer 2025 regnerisch

Datenanalyse:

Einteilung in zwei Gemeinschaften: (a) „Beute" (b) „Habitat“

Analyse: **Chi-Quadrat-Mehrfelder-Test, Binomialverteilung, Simpson/Shannon Index**

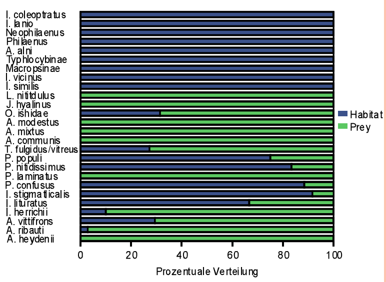
IV Ergebnisse



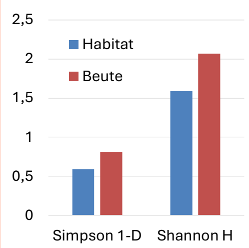
IV.1 Beutespektrum A. tricolor

Unterfamilie	Art	n (Beute)	n (Habitat)
Deltocephalinae	Allygus communis	11	0
Deltocephalinae	Allygus mixtus	18	0
Deltocephalinae	Allygus modestus	24	0
Deltocephalinae	Lamprotettix nitidulus	14	0
Deltocephalinae	Thamnotettix dilutor	0	0
Deltocephalinae	Fieberiella sp.	0	0
Deltocephalinae	Orientus ishidae	48	22
Deltocephalinae	Japananus hyalinus	2	0
Eurymelinae	Acericerus heydenii	33	0
Eurymelinae	Acericerus ribauti	137	4
Eurymelinae	Acericerus vittifrons	12	5
Eurymelinae	Idiocerus herrichii	63	7
Eurymelinae	Idiocerus stigmaticalis	3	33
Eurymelinae	Idiocerus lituratus	2	4
Eurymelinae	Populicerus nitidissimus	1	5
Eurymelinae	Populicerus confusus	3	23
Eurymelinae	Populicerus laminatus	1	0
Eurymelinae	Populicerus populi	1	3
Eurymelinae	Tremulicerus vitreus	5	2
Eurymelinae	Tremulicerus fulgidus	3	1
		∑ 381	∑ 109

IV.2 Artennutzung als Beute vs. Habitat



IV.3 Diversitätsvergleich



IV.1:

- Beutespektrum[4] um 10 Arten erweitert(rot)
- Im Vergleich zeigen sich deutliche Unterschiede in den Häufigkeiten → Nur 109 Individuen (30%) aus dem Habitat gehörten auch zum Beutespektrum.

IV.2:

- Einige Zikadenarten konnten nur als Beute und nicht im Habitat nachgewiesen werden ($n = 26$, $Chi^2 = 585.68$, $p < 0.000001$)

IV.3:

- Beuteprobe mit höherer Diversität als im Habitat (Shannon H_{Beute}: 2,07; Shannon $H_{Habitat}$: 1,59; Simpson 1-D_{Beute}: 0,812; Simpson 1-$D_{Habitat}$: 0,593)

IV.4:

- Deutliche Präferenz für *A. ribauti*, *A. heydenii* und *O. ishidae*
- Häufige Habitat-Arten wie *I. stigmaticalis* wurden kaum erbeutet (Binomialverteilung < 0,05)

V Diskussion

- *A. tricolor* zeigt **selektives Jagdverhalten**; Beuteverteilung weicht deutlich von Habitatfauna ab
- Bevorzugt werden *A. ribauti*, *A. heydenii* und *O. shidae*
- Höhere Diversität der Beute → **breites, aber gezieltes Beutespektrum**
- Neue Beutearten belegen womöglich **Flexibilität** und **Anpassung** an lokale Fauna während der Arealausbreitung
- **Fazit: Selektiv, aber anpassungsfähig – *A. tricolor* wählt seine Beute gezielt, erweitert womöglich sein Spektrum aber lokal**

Quellenangaben:

1. BERTSCH, L. (2021): *Alysson tricolor* Lepeletier & Serville, 1825 neu für Bayern sowie ergänzende Angaben zur Biologie (Hymenoptera: Spheciformes). – Ampulex 12: 46–49.
2. BERTSCH, L. (2023): Bemerkenswerte Bienen- und Wespenfunde aus Bayern (Hymenoptera: Aculeata). – Ampulex 14: 34-41.
3. BIEDERMANN, R. and NIEDRINGHAUS, R. (2004): Die Zikaden Deutschlands Bestimmungstafeln für alle Arten. – Scheeßel WABV-Fründ
4. ZIMMERMANN, R. et al. (2025): Five new prey species of *Alysson tricolor* Lepeletier & Serville, 1825 (Hymenoptera: Bembicidae). – Integrative Systematics 8 (2): 133-135.

Bildquellen:

Acericerus ribauti: G. Kunz, https://www.inaturalist.org/observations/41387729;
Allygus mixtus: G. Kunz, https://www.inaturalist.org/observations/63705534;
Idiocerus herrichii: G. Kunz, https://www.inaturlist.org/observations/65714888;
Erfassungsgebiet: Google Maps, Rest: Verena Engl

Universität Regensburg

Bees and stinging wasps in Schäffer's "Icones" (1766–1779)

Critical review of one of the oldest faunistic data sets of its kind

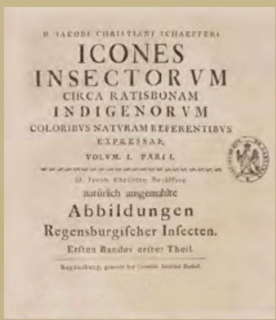
(Hymenoptera: Aculeata excl. Formicidae)

Robert Zimmermann

Introduction

- The current threat to biodiversity requires a good understanding of faunal change and detailed assessments of species' endangerment
- Historical faunistic data is as important as recent data
- Jacob Christian Schäffer in 1766–1779 published over 3,000 illustrations of insects found in the Regensburg area; his original insect collection is lost

Jacob Christian Schäffer (1718–1790)



Cover page of Volume I of the "Icones"

Methods

- Schäffer's works[1)2)3)] were scanned for bee and aculeate wasp illustrations and those were identified to the lowest possible taxonomic level
- All species that have ever been reported from Germany or an eastern neighbor country were considered for identification

?

Andrena cineraria (Linnaeus, 1758)

Andrena danuvia Stöckhert, 1950

Andrena barbareae Panzer, 1805

Results

- Of **166** bee and aculeate wasp illustrations **57** could be identified to a total of **33** distinct species

From left to right: *Andrena fulva* (Müller, 1766) (♀); *Anthidium manicatum* (Linnaeus, 1758) (♂); *Bombus campestris* (Panzer, 1801) (♂); *Bombus humilis* Illiger, 1806 (♀); Bombus hypnorum (Linnaeus, 1758) (♀); *Bombus pomorum* (Panzer, 1805) (♂); *Bombus pratorum* (Linnaeus, 1761) (♀); *Bombus pratorum* (Linnaeus, 1761) (♂); *Bombus rupestris* (Fabricius, 1793) (♀).

From left to right: *Bombus terrestris* s.l.; *Halictus quadricinctus* (Fabricius, 1776) (♂); *Megachile parietina* (Geoffroy, 1785) (♀); *Megachile parietina* (Geoffroy, 1785) (♂); *Melecta albifrons* (Forster, 1771); *Melecta luctuosa* (Scopoli, 1770); *Systropha planidens* Giraud, 1861 (♂).

From left to right: *Sphecodes albilabris* (Fabricius, 1793); *Chrysura cuprea* (Rossi, 1790); *Mutilla europaea* Linnaeus, 1758 (♀); *Mutilla europaea* Linnaeus, 1758 (♂); *Batozonellus lacerticida* (Pallas, 1771); *Ceropales maculata* (Fabricius, 1775), *Sapyga quinquepunctata* (Fabricius, 1781); *Scolia hirta* Schrank, 1781 (♂); *Scolia sexmaculata* Mueller, 1766 (♀); *Crabro cribrarius* Linnaeus, 1758 (♀).

From left to right: *Crabro cribrarius* Linnaeus, 1758 (♂); *Lestica clypeata* (Schreber, 1775) (♂); *Oxybelus lineatus* (Fabricius, 1787) (plus thorax dorsal); *Philanthus triangulum* Fabricius, 1775 (♀); *Sceliphron destillatorium* (Illiger, 1807) (♀); *Tiphia femorata* (Fabricius, 1775); *Dolichovespula media* (Retzius, 1783).

From left to right: *Euodynerus notatus* (Jurine, 1807); *Vespa crabro* Linnaeus, 1758; *Vespula germanica* (Fabricius, 1793); *Vespula rufa* (Linnaeus, 1758) (♀).

Can you find more identifiable figures? Scan the QR code!

→ Most notable species recorded by Schäffer

Bombus pomorum (Panzer, 1805)	(almost) extinct from Bavaria
Megachile parietina (Geoffroy, 1785)	extinct from Bavaria
Systropha planidens Giraud, 1861	extinct from Bavaria
Batozonellus lacerticida (Pallas, 1771)	extinct from Germany
Scolia hirta Schrank, 1781	extinct from Bavaria
Scolia sexmaculata Mueller, 1766	not known from the wider area
Oxybelus lineatus (Fabricius, 1787)	extinct from Bavaria
Sceliphron destillatorium (Illiger, 1807)	not known from Bavaria

Conclusions and outlook

- About one third of examined illustrations could be identified to species level
- To this day, **only** the Aculeata and the Lepidoptera have been exhaustively reviewed

Contact

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Acknowledgments

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John Ascher, Leander Bertsch, Casey Borowski Jr., Paul Geisendörfer, Justyna Kierat, Hanno Korten, Michael Kuhlmann, Alexander Kumpanenko, Johann Neumayer, Ozren Polašek, Johannes Schuberth, Andreas Segerer, Stefan Tischendorf, Johannes Voith, Kevin Williams

References

1) Schäffer JC (1766–1979) Icones insectorum circa Ratisbonam indigenorum: Coloribus naturam referentibus expressae: Vol. I–III. Regensburg.
2) Schäffer JC (1764) Die Maurerbiene in einer Rede. Johann Leopold Montag, Regensburg.
3) Schäffer JC (1779) Die Springfederbiene. In: Schäffer JC (Ed.), Abhandlungen von Insecten. Montagische Buchhandlung, Regensburg, 127–130.

UNIVERSITÄT HOHENHEIM

KomBioTa

NATURKUNDE MUSEUM STUTTGART

Bachelor of Science Biodiversitätswissenschaften

Studiengang zweier Fakultäten: Naturwissenschaften und Agrarwissenschaften

Studienverlauf

Sem. 1-3: Grundlagen

Biodiversität, Evolutionsbiologie, Systematik, Ökologie, Statistik, Mathe & Ökosystemchemie.

Sem. 4: Projektstudium

Biodiversitätsprojekt: Feldforschung, Datenauswertung & wissenschaftliches Schreiben.

Sem. 5-6: Vertiefung & Thesis

Wahl- und Wahlpflichtmodule beider Fakultäten (48 ETCS), Mobilitätsfenster für Auslandsaufenthalte & Anfertigung der Bachelorarbeit (12 ETCS).

Start
WS 2027/28

Studienplätze
50

Regelstudienzeit
6 Semester

Ziel

Erhaltung, Wiederherstellung und nachhaltigen Nutzung der biologischen Vielfalt.
Vertiefte Kenntnisse der Arten, der Ökologie, der Evolutionsbiologie, der Datenanalyse, des Naturschutzmanagements und des Umweltrechts.
Praktische Fähigkeiten in der Feldforschung, im Artenschutz und in der Umweltbildung.

Deine Zukunft

- ✓ Planungs- & Gutachterbüros
- ✓ Naturschutz-Organisationen
- ✓ Museen & Bildung
- ✓ Fachverlage & Presse
- ✓ Behörden & Ministerien
- ✓ Pharma-Industrie (z.B. Weleda)
- ✓ Forschungsinstitute (iDiv, Senckenberg)
- ✓ Universitäten

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