



# TAGUNGSBAND

## 73. JAHRESTAGUNG DER ARBEITSGEMEINSCHAFT DER INSTITUTE FÜR BIENENFORSCHUNG E.V.



ARBEITSGEMEINSCHAFT  
DER INSTITUTE FÜR  
BIENENFORSCHUNG E.V.

*24.-26. März 2026 · Braunschweig*

## 73. Jahrestagung der Arbeitsgemeinschaft der Institute für Bienenforschung e. V.

### VERANSTALTER

Arbeitsgemeinschaft der Institute für Bienenforschung e. V.

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Bei Beiträgen mit mehreren Autorinnen und Autoren wird aus Gründen der Übersichtlichkeit ausschließlich die institutionelle Zugehörigkeit der präsentierenden Autorin bzw. des präsentierenden Autors angegeben.

# IMPRESSUM · ORGANISATION

TAGUNGSORT	<b>FORUM Medienhaus</b> , Hintern Brüdern 23, 38100 Braunschweig
TAGUNGSBÜRO	<b>FORUM Medienhaus</b> ( <u>WLAN Zugang</u> ) Öffnungszeiten: Dienstag 24. März 2026, 11:00 bis 16:00 Uhr Mittwoch 25. März 2026, 8:30 bis 16:00 Uhr Donnerstag 26. März 2026, 8:30 bis 14:00 Uhr
EINLASSKONTROLLE	Es wird darum gebeten, die Namensschilder gut sichtbar zu tragen, da sie der Einlasskontrolle dienen.
FOTOS WÄHREND DER TAGUNG	Während der Veranstaltung werden Fotoaufnahmen für die Dokumentation sowie für die Berichterstattung (z. B. Website und Tagungsrückblick) erstellt. Wenn Sie <b>nicht fotografiert werden möchten</b> , wenden Sie sich bitte vor Ort an das Organisationsteam. Sie werden entsprechend gekennzeichnet und bei Aufnahmen sowie beim Gruppenfoto nicht berücksichtigt.
POSTERPRÄSENTATIONEN	Die Poster werden ebenfalls im Gebäude des FORUM Medienhaus ausgestellt. Die Posterstellwände sind für das Format <b>DIN A0 im Hochformat</b> ausgelegt. Die Postersession mit Anwesenheit der Autorinnen und Autoren findet am <b>Mittwoch, 25. März 2026, von 13:30 bis 15:30 Uhr</b> statt. Bitte hängen Sie Ihr Poster bereits am <b>Dienstag</b> auf, damit es rechtzeitig zur Postersession präsentiert werden kann. Wir bitten Sie außerdem, Ihr Poster möglichst bis zum Ende der Tagung am <b>Donnerstag</b> hängen zu lassen.
ABENDVERANSTALTUNGEN  ( <i>BITTE TRAGEN SIE IHRE NAMENSSCHILDER GUT SICHTBAR</i> )	<b>Dienstag, 24. März 2026, ab 19:00 Uhr</b> Jubiläumsempfang – 10 Jahre Institut für Bienenschutz (JKI) Ort: Große Dornse, Altstadtrathaus Adresse: Altstadtmarkt 7, 38100 Braunschweig  <b>Mittwoch, 25. März 2026, ab 19:00 Uhr</b> Social Dinner Ort: Braunschweiger Parlament Adresse: Hannoversche Straße 60b, 38116 Braunschweig
REISEKOSTENZUSCHUSS FÜR STUDIERENDE	Für Studierende mit eigenem Beitrag (Vortrag oder Poster), deren Arbeit an einem Mitgliedsinstitut der AG Bienenforschung entstanden ist. Förderung durch den Deutschen Imkerbund (D.I.B.), vorrangig für Teilnehmende ohne verfügbare Projektmittel. Erstattet wird anteilig die studentische Tagungsgebühr (ohne Exkursionen oder Rahmenprogramm), abhängig vom verfügbaren Budget. Persönliche Teilnahme an der Tagung ist erforderlich. Der Antrag ist vollständig mit Belegen bis spätestens <b>9. Mai 2026</b> online einzureichen.  <b>Weitere Informationen &amp; Onlineformular:</b> <a href="https://ag-bienentagung.de/reisekosten-studierende/">https://ag-bienentagung.de/reisekosten-studierende/</a>
HINWEIS	Redaktioneller Stand: 25.03.2026 – Änderungen vorbehalten.

Sehr geehrte Damen und Herren,  
liebe Kolleginnen und Kollegen,

im Namen des Instituts für Bienenschutz des Julius Kühn-Institut freue ich mich sehr, Sie zur 73. Jahrestagung der Arbeitsgemeinschaft der Institute für Bienenforschung e. V. hier in Braunschweig begrüßen zu dürfen – zehn Jahre nach unserer Gründung und der letzten AG-Tagung an diesem Standort.

Unsere Jahrestagung ist eine zentrale Plattform für den Austausch über aktuelle Entwicklungen in der Bienenforschung. Angesichts vielfältiger Herausforderungen für Bestäuber – von Krankheitserregern über Veränderungen der Agrarlandschaft bis hin zu komplexen Umweltstressoren – ist eine interdisziplinäre, wissenschaftlich fundierte und praxisnahe Forschung wichtiger denn je. Forschung muss bewerten, beraten und Lösungen aufzeigen. Zugleich feiern wir das zehnjährige Bestehen unseres Instituts. Der Bienenschutz bleibt dabei untrennbar mit dem Pflanzenschutz verbunden. Viele Wirkstoffe sind vom Markt verschwunden, Vergiftungsfälle zurückgegangen – ein wichtiger Erfolg. Dennoch stellen Zulassung und Bewertung weiterhin hohe Anforderungen an wissenschaftliche Sorgfalt, Transparenz und Augenmaß, um eine wirtschaftliche und zugleich nachhaltige Landwirtschaft zu fördern.

Ein besonderer Dank gilt der Stadt Braunschweig für die Bereitstellung der historischen Dornse im Altstadtrathaus sowie für die enge Zusammenarbeit bei zahlreichen Maßnahmen zugunsten von Bienen, anderen Insekten und damit auch der Menschen. Wissenschaft dient nicht dem Selbstzweck – sie entfaltet ihren Wert in der praktischen Umsetzung. Braunschweig ist dadurch ein Stück lebenswerter und noch schöner geworden für Menschen und für Bienen.

Auch und gerade in Zeiten neuer politischer Prioritäten und Sparmaßnahmen dürfen wir den Bestäuberschutz nicht aus dem Blick verlieren. Kontinuität ist für den Bestäuberschutz und Wirksamkeit von Fördermaßnahmen entscheidend. Nachhaltiger Schutz – insbesondere für Wildbienen – erfordert verlässliche Rahmenbedingungen und dauerhaftes Engagement.

Die vergangenen zehn Jahre zeigen, was durch Expertise, Kooperation und Leidenschaft möglich ist. Lassen Sie uns diesen Weg gemeinsam weitergehen.

Mein herzlicher Dank gilt allen Autorinnen und Autoren sowie unseren Unterstützerinnen und Unterstützern und dem wissenschaftlichen Komitee. Ein besonders herzliches Dankeschön geht an das Organisationsteam und alle Mitarbeitenden des Instituts, die sich hier und auch sonst stets mit Leidenschaft und Engagement einbringen, und unsere gemeinsame Arbeit stark voranbringen.

Ich wünsche uns eine erfolgreiche und inspirierende Tagung mit lebendigen Diskussionen und neuen Impulsen für unsere gemeinsame Arbeit. Herzlichen Dank.

Dr. Jens Pistorius  
Leiter des Instituts für Bienenschutz



# PROGRAMM

## Dienstag

Zeit	Beitragstitel	Referent/in	Institution	SB*
12:30– 13:10	Eröffnung und Begrüßung			
	<b>Keynote</b>			
13:10– 14:00	<u>KN</u> : Honey bees as sentinels of environmental quality	Ivo Roessink	WUR	
	<b>Bienenschutz &amp; Pflanzenschutz</b> ▪ Chair Ivo Roessink			
14:00– 14:15	<u>V1.1</u> : Assessing the risks of biopesticide tank mixtures: Interspecific differences in sensitivity among three bee species	Marie Christine Seidel	JKI	SB
14:15– 14:30	<u>V1.2</u> : What are the effects of the copper-based pesticide Cuprozin® on the red mason bee <i>Osmia bicornis</i> ?	Ronja Einberger	UHOH	SB
14:30– 14:45	<u>V1.3</u> : Species, sex and behaviour shape sensitivity to thiamethoxam in bees	Domenic Camenzind	UNIBE	SB
14:45– 15:00	<u>V1.4</u> : Exposure comparison of honey bees and bumble bees in strawberry fields in Germany and Slovakia	Abdulrahim Alkassab	JKI	
15:00– 15:15	<u>V1.5</u> : Pesticide risk assessment for bees: use and benefit of colony and population models	Amelie Schmolke	Rifcon	
15:15– 15:45	<i>Pause</i>			
	<b>Physiologie &amp; Verhalten I</b> ▪ Chair Ingrid Illies			
15:45– 16:00	<u>V1.6</u> : Observations on drifting drones and worker bees – a comparison between <i>Apis m. mellifera</i> and hybrid Buckfast in Sweden	Finja Schaumann	UFZ	SB
16:00– 16:15	<u>V1.7</u> : Pollinator-mediated assembly of nectar yeast communities in sunflower	Yuliia Kovalova	DSMZ	SB
16:15– 16:30	<u>V1.8</u> : Interspecific differences in flight capacity and spermatozoa production in two European bumble bees	Manon Bovier	UNIBE	SB
16:30– 16:45	<u>V1.9</u> : The role of tailocins in interspecific bacterial communication in the honey bee gut	Elisa Kathe	JKI	SB
16:45– 17:00	<u>V1.10</u> : Establishing metabolomics and (meta)proteomics for analysing the age-dependent development of the metabolome in the honey bee gut and utilisation of protein	Martin von Bergen	UFZ	
ab 19:00	<b>Jubiläumsempfang</b> Dornse Altstadt – 10 Jahre Institut für Bienenschutz (Einlass ab 18:30 Uhr)			

\*SB = Studentischer Beitrag

# PROGRAMM

## Mittwoch

Zeit	Beitragstitel	Referent/in	Institution	SB
	<b>Physiologie &amp; Verhalten II • Chair Saskia Wöhl</b>			
09:00– 09:15	<u>V2.1</u> : When the colony fails: how thermal stress disrupts bumble bee development and survival	Christoph Kurze	UR	
09:15– 09:30	<u>V2.2</u> : Impacts of climate change on the overwintering of solitary bees	Henri Greil	JKI	
09:30– 09:45	<u>V2.3</u> : Influence of brood chamber volume on the water content of honey	Raphael Marx	UHOH	SB
09:45– 10:00	<u>V2.4</u> : Which hive type should I use? Results of a four-year systematic comparison of hive types with gradually different management options.	Jana Bundschuh	ZALF	
10:00– 10:15	<u>V2.5</u> : From temperature to data-fusion: effective monitoring of honey bee colony health	Maciej Bryś	UP-Lublin	SB
10:15– 10:40	<i>Pause</i>			
	<b>Bienenpathologie • Chair Sebastian Gisder</b>			
10:40– 10:55	<u>V2.6</u> : Activated charcoal: a highly potent legal alternative for <i>Vespa velutina</i> nest destruction	Ulrich Ernst	Independent	
10:55– 11:10	<u>V2.7</u> : Entrance guards as a protective measure against <i>Vespa velutina</i> : first results from Southwestern Germany	Ramona Wiedemann	UHOH	SB
11:10– 11:25	<u>V2.8</u> : From bench to hive: a lateral flow assay for rapid on-site detection of <i>Paenibacillus larvae</i>	Antonia Reinecke	LIB	SB
11:25– 11:40	<u>V2.9</u> : More than motility: flagella in the pathogenesis of <i>Paenibacillus larvae</i>	Josefine Göbel	LIB	
11:40– 11:55	<u>V2.10</u> : Influence of an extended brood break (trapping comb) on Varroa destructor-associated and non-associated viruses in honey bees ( <i>Apis mellifera</i> )	Paul Köhler	MLU	SB
11:55– 12:10	<u>V2.11</u> : Effects of multiple foundress infestation of <i>Varroa destructor</i> on pupal development and viral dynamics in the honey bee, <i>Apis mellifera</i> in Germany and in China	Yakun Zhang	UHOH	SB
12:10– 12:25	<u>V2.12</u> : BroodSense: a platform for scanner-based brood and varroa monitoring	Parzival Borlinghaus	BroodSense	
12:25– 12:30	<i>Gruppenbild</i>			
12:30– 13:30	<i>Mittagspause-parallel</i> : Filmvorführung: Menschen und wilde Honigbienen – Ein konfliktreiches Zusammenleben	im Vortragssaal		
13:30– 15:30	<b>Postersession</b>			
15:30– 17:30	<i>Exkursionen</i>			
ab 19:00	<i>Social Dinner</i> Braunschweiger Parlament (Einlass ab 18:30 Uhr)			

# PROGRAMM

## Donnerstag

Zeit	Beitragstitel	Referent/in	Institution	SB
	<b>Genetik &amp; Zucht • Chair Richard Bernstein</b>			
09:00– 09:15	<u>V3.1</u> : Implementation of an extended SNP Panel for the genetic monitoring of honey bees and its application to <i>A. mellifera mellifera</i> and <i>A. mellifera carnica</i> samples across Europe	Jana Vanessa Huml	Apigenix	
09:15– 09:30	<u>V3.2</u> : Insights into transcriptomic data of early-stage honey bee larvae from an inbred crossing	Michelle Jung	UHOH	SB
09:30– 09:45	<u>V3.3</u> : Effective population size of the Central European Carnica population from SNP data	Richard Bernstein	LIB	
	<b>Ökologie, Wildbienen, Bestäubung • Chair Volker Grimm</b>			
09:45– 10:00	<u>V3.4</u> : Buzzing tramways – a comparative analysis of wild bee diversity on tram tracks in four German cities	Felix Rosenbaum	JKI	SB
10:00– 10:15	<u>V3.5</u> : Penthouse for pollinators? – How attractive are pollinator-friendly balconies at various heights?	Michael Glück	UHOH	SB
10:15– 10:30	<u>V3.6</u> : Fungal associates of the ground-nesting wild bee <i>Andrena vaga</i> and their potential role in oligolecty	Hanna Gardein	JKI	
10:30– 11:00	<b>Pause</b>			
11:00– 11:15	<u>V3.7</u> : Citizen scientists, DNA traces and empty nests: Three years of volunteer-based eDNA sampling for the detection of cavity-nesting wild bees – lessons learned so far	Wiebke Sickel	THÜNEN	
11:15– 11:30	<u>V3.8</u> : Strengthening long-term monitoring of bee communities in agricultural landscapes by surveying wing morphotype abundance	Severin Polreich	JKI	
11:30– 11:45	<u>V3.9</u> : Site-specific weed management can boost food resources for pollinators	Anke Dietzsch	JKI	
11:45– 12:00	<u>V3.10</u> : Monitoring of bumble bees in agricultural landscapes in Germany: nationwide data on population trends, phenological patterns and floral resource use	Felix Kirsch	THÜNEN	
12:00– 12:15	<u>V3.11</u> : Honey bees vs. wild bees: time to act now!	Peter Neumann	UNIBE	
	<b>Evenius-Preis &amp; Abschluss</b>			
12:15– 12:30	Preisverleihung und Verabschiedung	Jury		
	Ausgabe Lunchpakete			
13:00– 14:00	<b>Mitgliederversammlung</b> (nicht öffentlich)			

# WLAN-ZUGANG (FORUM MEDIENHAUS)

## Kostenfreies WLAN

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# VORTRÄGE

## KN: Honey bees as sentinels of environmental quality

*Honigbienen als Bioindikatoren der Umweltqualität*

**Ivo Roessink\***

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### ABSTRACT

The INSIGNIA project established a pan-European citizen science network of beekeepers to biomonitor environmental quality using honey bee colonies. In total, 315 apiaries across 27 European countries participated. Bee-collected pollen was sampled biweekly using pollen traps and analysed by DNA metabarcoding. Overall, 2,508 samples revealed pollen from 501 plant genera. Pollen diversity differed among land-use types, with higher mean diversity in urban landscapes than in agricultural and forest areas, and distinct regional patterns, particularly in Mediterranean countries. Seasonal trends showed increasing numbers of visited plant genera during spring and early summer. Environmental contaminants were monitored non-invasively using APIStrips placed in the brood nest and exposed for two-week periods. Of 450 target compounds, 202 pesticides were detected in 5,524 samples. Residues were ubiquitous, with higher numbers per sample in agricultural landscapes and frequent exposure of colonies to pesticide mixtures. Several compounds occurred in most countries, and banned substances were occasionally detected. In contrast, polar pesticide residues in honey were found in only about 6% of samples and generally at low concentrations. Spatial modelling revealed clear seasonal and geographic patterns, with increasing pesticide diversity during periods of intensive agricultural activity. The INSIGNIA network demonstrates the potential of standardised honey bee-based monitoring for large-scale assessment of environmental quality and for evaluating land-use and pesticide policies across Europe.

*Keywords* honey bee, biomonitoring, citizen science, pesticide exposure, pollen diversity

← ZURÜCK

## V1.1: Assessing the risks of biopesticide tank mixtures: Interspecific differences in sensitivity among three bee species

*Bewertung der Risiken von Tankmischungen aus biologischen Pestiziden: Interspezifische Unterschiede in der Empfindlichkeit zwischen drei Bienenarten*

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### ABSTRACT

Bees are vital ecosystem service providers, yet they face pressure from agricultural practices and several environmental factors. Although biopesticides are central to organic farming, the potential synergistic or additive risks of tank mixtures (TMs) containing multiple biocontrol agents are frequently understudied. Here, we investigated how such mixtures affect three model bee species with diverging life histories: the highly eusocial honey bee *Apis mellifera*, the primitively eusocial bumble bee *Bombus terrestris*, and the solitary bee *Osmia cornuta*. Through standardised laboratory contact exposure assays, we examined the lethal and sublethal impacts of two insecticidal TMs, including a combination of azadirachtin and sulphur and a combination of sulphur and potassium hydrogen carbonate. The results show clear differences in how each species responds to the mixtures. *A. mellifera* was the most sensitive species, showing mortality rates of up to 22.4% and severe behavioural abnormalities in up to 78% of the tested individuals. Conversely, the other two bee species demonstrated higher resilience; both *B. terrestris* and *O. cornuta* exhibited mortality below 7% and minimal behavioural changes (< 10%). These results suggest that lethal and behavioural responses to biopesticide tank mixtures are not uniform across the tested bee species. To build on these findings, subsequent research should expand from adult contact exposure to include oral and larval pathways, ensuring a holistic evaluation of biopesticide impacts across all life stages and social structures.

*Keywords* biopesticide, tank mixtures, *Osmia cornuta*, *Bombus terrestris*, *Apis mellifera*

## V1.2: What are the effects of the copper-based pesticide Cuprozin® on the red mason bee *Osmia bicornis*?

*Welche Auswirkungen hat das kupferbasierte Pestizid Cuprozin® auf die rote Mauerbiene *Osmia bicornis*?*

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### ABSTRACT

Global insect declines have increased concern about agricultural stressors affecting pollinators, particularly in intensively managed cropping systems. Copper-based fungicides are widely used in perennial fruit orchards, viticulture and organic agriculture to control fungal diseases, yet little is known about the effects of copper residues in pollen on the larval development and survival of solitary wild bees. This study investigated the effects of increasing copper-based fungicide concentrations in pollen provisions on the survival and larval development of the red mason bee (*Osmia bicornis*) using combined in vivo and in vitro approaches. In vivo experiments were conducted under natural field conditions using five replicated nesting blocks within the same meadow area, where copper solutions derived from Cuprozin® Progress were applied directly to pollen provisions in newly established brood cells. In parallel, an in vitro rearing experiment enabled precise control of pollen mass and copper exposure under standardised laboratory conditions. Copper was applied at four concentrations (25, 50, 75 and 250 mg Cu kg<sup>-1</sup> pollen) and compared to a water control. Larval development and mortality were monitored every two days throughout development and pupation (in vivo n = 1548; in vitro n = 238). Overall, copper exposure had a significant effect on larval survival and development under in vivo conditions (n = 1548, p < 0.001). These effects were primarily observed at the highest concentration (250 mg Cu kg<sup>-1</sup> pollen), representing a worst-case scenario, and included reduced larval survival, delayed development, and reduced pollen consumption. In addition to this, the adult emergence rate and weight measured in the following season will give insights into further effects of Cuprozin® Progress on the development of *O. bicornis*.

*Keywords* copper-based fungicides, solitary wild bees, larval development and survival

## V1.3: Species, sex and behaviour shape sensitivity to thiamethoxam in bees

*Spezies, Geschlecht und Verhalten beeinflussen die Sensitivität gegenüber Thiamethoxam in Bienen*

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### ABSTRACT

Ubiquitous pesticide contamination is a major driver of global wild insect declines and losses of managed pollinators. Yet current environmental risk assessment (ERA) frameworks largely ignore biological and behavioural sources of variation in pesticide sensitivity, potentially underestimating hazards to non-target insects. Here, we demonstrate pronounced inter- and intraspecific differences in sensitivity to chronic neonicotinoid exposure. Using modified OECD 245 protocols, we chronically exposed female and male honey bees (*Apis mellifera*), bumble bees (*Bombus terrestris*), and solitary bees (*Osmia bicornis*) to the neonicotinoid thiamethoxam and measured mortality and feeding behaviour. Feeding rates were unaffected at field-relevant concentrations ( $<40 \text{ ng g}^{-1}$ ) across all species. In contrast, sensitivity differed markedly, with *A. mellifera* exhibiting the highest mortality, followed by *O. bicornis* and *B. terrestris*. Within species, males were consistently more sensitive than females, consistent with haploid susceptibility increasing vulnerability to xenobiotics. Moreover, honey bee workers engaged in male-tending behaviour experienced significantly elevated mortality compared with non-tending workers, indicating that increased energetic demands constrain detoxification capacity while elevating exposure. Our results demonstrate that sex-specific genetic architecture and behavioural energy allocation strongly modulate pesticide sensitivity. Although reliance on female honey bees in ERA reflects a precautionary approach, excluding males and behavioural context from early-tier testing risks systematic underestimation of pesticide impacts. Incorporating both sexes and ecologically relevant behaviours into Tier-1 laboratory testing would substantially improve the ecological relevance and robustness of pollinator risk assessment.

*Keywords* ecotoxicology, neonicotinoids, behaviour, haplodiploid susceptibility, thiamethoxam

## V1.4: Exposure comparison of honey bees and bumble bees in strawberry fields in Germany and Slovakia

*Vergleichende Untersuchung zur PSM-Exposition von Honigbienen und Hummeln während Erdbeerblüte (Deutschland vs. Slowakei)*

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### ABSTRACT

Recent studies have reported interspecific differences in the exposure level to pesticide residues among bee species. These differences may be related to bees' foraging activity and performance in collecting nutrients like pollen and nectar from different crops. The current study investigated the pollen-foraging preferences of honey and bumble bees under field conditions. Totally, five fields of strawberry, two in Germany and three in Slovakia, were selected. Three bumble bee colonies and one honey bee colony were placed at the edge of each strawberry field. Various matrices, such as collected and stored pollen, stored nectar, and forager bees, were sampled weekly over the flowering period. The exposure levels of both bee species were compared by analysing the residues in the collected matrices. Furthermore, palynological analysis of the collected and stored pollen was conducted to correlate the detected residues with the origin of plants. The preliminary results showed that fungicides are the most commonly detected residues, with higher residue concentrations in pollen compared to nectar or bee bodies. The exposure level of both bee species varied over the flowering time. Our study highlights possible differences in pesticide exposure levels between honey and bumble bees. Ongoing analyses aim to provide a deeper understanding of the relationship between both bee species' foraging behaviour and realistic field pesticide exposure.

*Keywords* residue, strawberry, bees, pesticides

← ZURÜCK

## V1.5: Pesticide risk assessment for bees: use and benefit of colony and population models

*Kolonie- und Populationsmodelle für Bienen: Bedeutung und Anwendung in der Risikobewertung von Pestiziden*

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### ABSTRACT

Ecological pesticide risk assessments in the EU have evolved in the past decades to address ecological complexity and scientific knowledge. It also means that risk assessments are increasingly complex by considering the species diversity and the context of agricultural landscapes. The complexity of the risk assessments is, for example, reflected in the revised guidance on the risk assessment of plant protection products on bees (EFSA 2023). In this guidance, ecological effect models are identified as valuable tools for risk assessments of bees, particularly in the context of higher-tier assessments which focus on potential effects on colonies of honey bees and bumble bees and populations of solitary bees. Ecological effect models have the potential to expand and complement available study data. This is particularly important in light of different landscapes and the corresponding potential exposure patterns, the great diversity of bee species, their different levels of sociality and their ecological traits. In the context of the risk assessment for bees exposed to plant protection products, colony and population models have already been developed. Model applications include, for instance, the extrapolation of exposure-effect responses from organism to colony or population level, the estimation of observed effects in semi-field and field studies to other species or environmental conditions as well as the comparison of possible mitigation scenarios. We will present and discuss different models for honey bees, bumble bees and solitary bees that are currently available. We will provide an overview of the current state of the art, show examples and discuss how bee models can be used in combination with study data from laboratory and (semi-)field studies. Furthermore, we will also address acceptance of effect models as tools in pesticide risk assessments.

*Keywords* ecological effect models, pesticide risk assessment, bee diversity, agricultural landscapes

← ZURÜCK

## V1.6: Observations on drifting drones and worker bees - a comparison between *Apis m. mellifera* and hybrid Buckfast in Sweden

*Beobachtungen zu driftenden Drohnen und Arbeiterbienen – ein Vergleich zwischen Apis m. mellifera und Buckfast in Schweden*

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### ABSTRACT

Drifting behaviour in honey bees, defined as the entry of individuals into non-natal colonies, is well recognised but remains insufficiently studied, despite its potential role in pathogen transmission and reduced colony productivity. A better understanding of drifting dynamics is therefore important for effective colony management and the conservation of locally adapted honey bee populations, particularly given the widespread use of non-local breeds in modern apiculture. We investigated drifting behaviour in drones and worker bees of the native honey bee *Apis m. mellifera* (Mel) and the hybrid Buckfast (Buck) within an apiary in Sweden. Using Radio-Frequency Identification (RFID) technology, we continuously monitored individual flight activity and lifespan in four colonies over an entire mating season (May–August). Despite the use of coloured and angled hive entrances, drifting occurred repeatedly throughout the study period. Overall, drones drifted more frequently than worker bees, and Mel bees showed higher drifting rates than Buck bees. Drifting was generally associated with increased lifespan compared to non-drifters, particularly in drones. Drift events occurred predominantly between colonies of the same subspecies, while inter-subspecies drifting was rare, especially among worker bees. Colony size further influenced acceptance patterns, with smaller colonies accepting more non-natal drones but fewer non-natal workers. Our findings suggest that drifting may be linked to altered activity patterns or reduced exposure to high-risk behaviours in both drones and worker bees. However, drifting was more frequently observed in drones, possibly due to caste-specific roles within the colony and differences in nestmate recognition at the hive entrance. The observed differences between Buck and Mel bees indicate local adaptation of Mel to Swedish environmental conditions, characterised by a short summer (i.e. mating season) and a long winter.

*Keywords* drifting behaviour, drones, worker bees, *Apis mellifera mellifera*, Buckfast

## V1.7: Pollinator-mediated assembly of nectar yeast communities in sunflower

*Einfluss der Bestäuber auf die Zusammensetzung von Nektarhefen in der Sonnenblume*

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### ABSTRACT

Floral nectar, along with pollen, is a central resource for bees and simultaneously a habitat for microorganisms that may influence nectar quality and bee foraging behaviour. This study investigates how bee visitation shapes nectar yeast communities in sunflowers (*Helianthus annuus*). Field experiments were conducted on four commercial sunflower cultivars using a pollinator-exclusion design that allowed access to day-active pollinators, night-active pollinators, both, or none, as well as controlled pollination by *Bombus terrestris*. Nectar, air, and bumble bee gut samples were analysed using cultivation-based methods combined with MALDI-TOF MS and DNA sequencing. Nectar yeast communities were species-poor and strongly dominated by the nectar specialist *Metschnikowia reukaufii* in flowers visited by day-active pollinators. In contrast, flowers exposed only to night pollinators or fully excluded from insects contained few or no yeasts. The absence of *M. reukaufii* from air samples indicates that bees are the primary vectors of this yeast in sunflower nectar. Fungal communities in bumble bee guts differed depending on diet, suggesting links between floral yeast availability and gut mycobiome composition. These results demonstrate that bee visitation is a key driver of nectar microbial communities and highlight nectar-dwelling yeasts as an underexplored component of bee-flower interactions, with potential implications for bee nutrition and pollinator health in agricultural landscapes.

*Keywords* nectar, yeasts, mycobiome, sunflower, bumble bee

## V1.8: Interspecific differences in flight capacity and spermatozoa production in two European bumble bees

*Interspezifische Unterschiede in der Flugfähigkeit und Spermienproduktion bei zwei europäischen Bienenarten*

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### ABSTRACT

Bumble bees (*Bombus spp.*) are essential pollinators, yet many species are declining under increasing anthropogenic pressures. Although female worker and queen bumble bees have been studied extensively, male physiology remains poorly understood despite its importance for mating success and population dynamics. Here, we report first year results of a two-year study examining interspecific variation in male flight performance and reproductive traits in two widespread, but ecologically distinct European bumble bee species, *Bombus terrestris* and *B. pascuorum*. Males were collected from multiple sites in Bern, Switzerland, and assessed for flight duration, distance and speed ( $N_{B. terrestris} = 41$ ,  $N_{B. pascuorum} = 20$ ) using tethered flight mills, as well as for spermatozoa quantity ( $N_{B. terrestris} = 75$ ,  $N_{B. pascuorum} = 49$ ) and pathogen presence ( $N_{B. terrestris} = 70$ ,  $N_{B. pascuorum} = 50$ ) using standard dissecting methods. Pathogen screening indicated no detectable effects of parasite infestations on either flight performance or reproductive traits. By contrast, pronounced species-specific differences were observed: *B. terrestris* males exhibiting 35% higher mean flight speeds, 42% higher maximal speeds, and 58% greater spermatozoa quantities than *B. pascuorum*. Maximal flight distances approached 20 km for *B. terrestris* and exceeded 12 km for *B. pascuorum*, indicating substantially greater dispersal capacities than previously assumed. These findings suggest that male flight performance and reproductive investment differ markedly between species, likely reflecting divergence in morphology, mating behaviour and life-history strategy. Data from the second study year are currently being analysed and will increase sample sizes, allowing assessment of the robustness of these patterns as well as epidemiological patterns and pathogen effects on male physiology.

*Keywords* conservation, fitness, flight-mills, physiology, *Bombus*

← ZURÜCK

SB

## V1.9: The role of tailocins in interspecific bacterial communication in the honey bee gut

*Die Rolle von Tailocinen bei der interspezifischen bakteriellen Kommunikation im Darm der Honigbiene*

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### ABSTRACT

Flowers are hotspots for diverse microbial communities and important hubs between plants, insects, and microorganisms. During foraging, honey bees ingest a variety of plant-associated bacteria and pathogens. Maintaining a stable and functional gut microbiome therefore necessitates effective antagonistic strategies to protect both the microbial community and its host. One well-studied mechanism that mediates interspecific bacterial interactions in the honey bee gut is the type VI secretion system (T6SS), which enables bacteria to kill competitors by injecting toxic effectors into neighbouring cells. Another antagonistic mechanism involves tailocins, a subtype of contractile phage tail-like particles (CPTPs) produced by certain bacteria. In contrast to T6SS, tailocins are released in large numbers upon bacterial lysis and kill closely related bacteria by puncturing their cell wall and membranes, leading to a collapse of the target's proton motive force. Despite their potential antibacterial activity, the role of tailocins in shaping interactions between honey bee gut symbionts, ingested plant-associated bacteria, and pathogens remains largely unknown. In this study, we investigate the diversity and distribution of tailocin-producing bacteria associated with honey bees and their environment. Using a combination of bioinformatic analyses and experimental approaches, we identified tailocin gene clusters in bacterial genomes, screened for candidates capable of producing tailocins, and assessed their antagonistic potential. Preliminary results reveal a highly diverse molecular repertoire of antagonistic systems among honey bee-associated bacteria, highlighting tailocins as a potentially important, but underestimated factor in bee gut microbiome dynamics.

*Keywords* tailocins, gut microbiome, *Apis mellifera*

### V1.10: Establishing metabolomics and (meta)proteomics for analysing the age-dependent development of the metabolome in the honey bee gut and utilisation of protein

*Etablierung von Metabolomik und (Meta)Proteomik zur Analyse der altersabhängigen Entwicklung des Metaboloms im Darm der Honigbiene und der Verwertung von Protein*

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#### ABSTRACT

The microbiome-host interaction is essential for honey bee health. During the development of worker bees from hatching to foraging, their nutrition changes, but how the microbiome responds to these nutrient shifts remains poorly understood and for assessing the molecular effects in honey bees, we established a broad range of techniques from metagenomics, (meta)proteomics and metabolomics of several organs of honey bees. Here we will show examples how the microbiome as well as the corresponding metabolome is changing in an age dependent manner from day 2 to day 18. Extracellular metabolome analysis was conducted using LC-TOF-MS in both positive and negative ionisation modes. Peak identification was performed with Progenesis software. A total of 930 metabolites were identified: 338 in the midgut, 124 in the ileum, and 468 in the rectum. Quantification was relative across measurements. To identify age- or development-specific metabolite patterns, we applied k-means clustering to the data. We discovered four distinct clusters across all three gut sections, corresponding to different microbiome stages: day 2 (establishment), days 2- 14 (in-hive activities), and days 14-24 (foraging). We further established the workflow for mass spectrometry for (meta-) proteomic and metabolomic of the guts and brains which allowed insights into the global structural and functional dynamics of the microbiota, as well as the functional and metabolic alterations in the host gut and brain, and their interactions. We observed a correlation between concentrations of tryptophan and its metabolic products between honey bee brain and gut. These results indicate the relevance of molecular analyses for the analysis of microbiome-host research in honey bees.

*Keywords* honey bee, microbiome, gut-brain interaction, metabolomics, metaproteomics

← ZURÜCK

### V2.1: When the colony fails: how thermal stress disrupts bumble bee development and survival

*Wenn die Kolonie versagt: Wie Hitzestress die Entwicklung und das Überleben von Hummeln beeinträchtigt*

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#### ABSTRACT

Heatwaves are becoming more frequent and intense due to climate change, posing a significant threat to global biodiversity. While the decline of crucial pollinators like bumble bees is well-documented, the specific impact of heatwaves on their developmental stages remains largely unknown. We investigated the effects of varying thermal stress durations and intensities on *Bombus terrestris* pupae in vitro, as well as the carry-over effects of cyclic thermal stress. Our findings highlight the profound consequences of thermal stress on bumble bee pupal development and deferred mortality, with potential cascading effects on colony fitness. Ultimately, this research emphasises the need for stage-specific data to better understand how environmental stressors scale from the individual to the colony level.

*Keywords* climate change, metamorphosis, development, survival, deformations

← ZURÜCK

### V2.2: Impacts of climate change on the overwintering of solitary bees

*Auswirkungen des Klimawandels auf die Überwinterung von Solitärbiene*

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#### ABSTRACT

The climate has been warming at an unprecedented rate for decades. Local winter temperatures in central Germany (Braunschweig) are set to rise 3-4°C, based on the IPCC's RCP8.5 scenario. Soil temperatures may increase at an even faster rate. Declines in abundance and diversity of bees as pollinators impose a threat on biodiversity. The majority of bees live solitary and nest in the ground. And spring-flying adult wintering bees are most vulnerable to warmer winter temperatures. To compare the effects of climate change on the overwintering of ground-nesting and above-ground nesting bees, the ground-nesting species *Andrena vaga* and the above-ground nesting species *Osmia bicornis* were overwintered under 'historical', 'current' and 'future' temperature conditions. Under the future temperature regime, weight loss was mostly elevated. The ground-nesting species *A. vaga* was more strongly affected than *O. bicornis*, and males generally more affected than females. Mortality was generally high in *A. vaga* and significantly higher in females. Spring emergence of *O. bicornis* was advanced in future temperatures, which may lead to temporal mismatches with food plants. Under current local temperature conditions, overwintering success does not seem to be impaired yet but will be severely affected in the future.

*Keywords* climate change, solitary bees, bee decline, ground nesting bees, overwintering

← ZURÜCK

### V2.3: Influence of brood chamber volume on the water content of honey

*Einfluss des Brutraumvolumens auf den Wassergehalt im Honig*

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#### ABSTRACT

Water content that is too high in honey not only presents beekeepers with the problem of limited shelf life, but also significantly restricts marketability. The water content of honey is the result of water evaporating from nectar during the maturation process. This process is significantly influenced by the air humidity and air temperature in the colony. Drying nectar into honey is very labour-intensive and energy-depleting for the bees. Since honey may not be dried by beekeepers post harvesting, it is all the more important that the bees have adequate conditions for the ripening process. One of the conditions that beekeepers impose on their colonies is the choice of hive type and thus the volume of space the bees have to thermoregulate. To investigate whether the volume of the brood chamber affects the water content of the honey, we conducted an experiment with 24 colonies. Twelve colonies were located at each of two sites, with six colonies having a single brood chamber and six colonies having two brood chambers. The experiment was conducted from May to July, 2025 in Stuttgart-Hohenheim. One honey super was provided per colony. Sensors were placed in each brood chamber and honey super to measure air temperature and humidity. Honey was harvested twice during the experiment (June and July). All the honey combs were extracted separately for each colony and the mass (kg) of the harvested honey determined. The honey extractor was cleaned after each colony-wide honey extraction. To avoid influencing colony size during the experiment, we neither removed any brood nor used drone frames. To prevent swarming, we only removed swarm cells. The colonies with two brood chambers had a significantly higher honey yield overall ( $p < 0.05$ ). In both harvests, colonies with one brood box had honey with a significantly lower water content ( $p < 0.05$ ). Measurement data from the iButtons showed that colonies with one brood box had significantly lower humidity in both the brood chamber and honey super ( $p < 0.05$ ).

*Keywords* honey quality, water content, beekeeping, brood chamber

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← ZURÜCK

### V2.4: Which hive type should I use? Results of a four-year systematic comparison of hive types with gradually different management options.

*Welche Beute soll ich nehmen? Ergebnisse aus vier Jahren Systemvergleich zwischen Beutentypen unterschiedlicher Eingriffsmöglichkeiten*

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#### ABSTRACT

The question of adequate housing is a basal question continuously discussed by beekeeping beginners and professionals alike. To see whether natural honey bee swarm housed into different hive types performed differently, we conducted a field experiment in two regions in Germany (Allgäu and North-east Germany) from 2022-2025. Four swarms were housed into four new boxes of each of the four hive systems in the experiment on both study sites (total n=32). Hive systems were chosen to be relevant in the context of the “natural” beekeeping discourse in Germany and ranging on a gradient covering most known intrusive management options (Dadant magazine hive) to no intrusive management options (Schiffertree), with Bienenbox and Bienenkiste in between. For data collection, continuous weight measurement with automated scales, annual laboratory testing and continuous management records were used. Response variables included health parameters (survival, varroa, nosema, virus prevalence), energy balance (feed consumption and foraging behaviour, workload related to hive management, pollen composition in honey and residues in honey and wax. Results including a survival analysis will be presented and the usability of these hive systems in the context of farm beekeeping will be discussed.

*Keywords* bee hive types, honey bee boxes, foraging behaviour, beekeeping systems

← ZURÜCK

### V2.5: From temperature to data-fusion: effective monitoring of honey bee colony health

*Von der Temperatur zur Datenfusion: effektives Monitoring der Gesundheit von Honigbienenvölkern*

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#### ABSTRACT

Honey bee colony is a superorganism whose health and functioning can be described by physiological and behavioural processes of all its specimens. In this context, the in-hive temperature is a key homeostatic parameter regulated through collective thermoregulatory behaviour and reflects colony level-metabolic activities as well as brood conditions. This presentation discusses the usefulness of continuous in-hive temperature measurements as a non-invasive method for monitoring colony health characteristic behavioural changes. Temperature data from the hives were analysed and correlated with selected honey bee colony statuses. Obtained results indicate that differences from the colony's thermal set-point are biologically informative: increased daily variability and a downward shift in temperature can precede brood diseases. It is noticeable the most clearly for the *Ascosphaera apis*, where brood chilling to approximately 18°C, followed by maintaining sealed brood at suboptimal temperatures markedly increases larval mummification process. Additionally, the temperature instability is reported to trigger American foulbrood. On the contrary, in Central Europe conditions, a sustained rise and stabilisation of in-hive temperature is an indicator of the onset and intensification of spring brood rearing, as colonies expand. The analysis proves that temperature measurement is useful yet insufficient while used alone to reliably distinguish between various colony states, as similar thermal responses may result from multiple stressors. Therefore, effective diagnostics requires a multiparameter monitoring approach. Integrating temperature with additional data, e.g. volatile organic compounds, can significantly improve the ability to differentiate between diseases and behavioural conditions. Data-fusion techniques support more accurate colony assessment and represent a key step toward advanced precision beekeeping and sustainable apiculture.

*Keywords* temperature measurements, remote sensing, honey bee disease, swarming

SB

← ZURÜCK

### V2.6: Activated charcoal: a highly potent legal alternative for *Vespa velutina* nest destruction

*Aktivkohle als hochwirksame legale Alternative für die Vespa velutina Nestbekämpfung*

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#### ABSTRACT

The invasive yellow-legged hornet *Vespa velutina nigrithorax* has spread across Europe following its accidental introduction into France in 2004. This species adversely affects biodiversity, apiculture, pomiculture and viticulture, and human health. Current management relies predominantly on nest destruction; however, manual removal is often logistically challenging and costly because nests are typically located high in trees (up to 30 m), frequently necessitating vehicle-mounted lifts. Ground-based application of biocides using long injection lances is comparatively rapid and inexpensive, but in many countries, insecticides are not permitted because products are not specifically authorized for hornet control. Consequently, alternative approaches are needed. Here, we evaluated the efficacy of activated charcoal for nest destruction in *V. v. nigrithorax*. We injected 150 nests with 50–100 g of activated charcoal and subsequently destroyed the nests. One week later, we assessed worker survival and the establishment of new nests. Emergency nest construction by surviving workers was observed in 3 of 150 cases (2.0%). This rate was comparable to that observed following insecticide treatment (2 of 136 cases; 1.5%). Activated charcoal therefore appears to be similarly effective to insecticide-based control while offering advantages in terms of environmental compatibility, user safety, ease of handling, and legal applicability in Europe. Activated charcoal may represent a practical alternative to manual nest removal and unauthorised insecticide use.

*Keywords* invasive species, biodiversity, pest management, biocide, hornets

← ZURÜCK

### V2.7: Entrance guards as a protective measure against *Vespa velutina*: first results from Southwestern Germany

*Fluglochgitter als Schutzmaßnahme gegen Vespa velutina: Erste Ergebnisse aus Südwestdeutschland*

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#### ABSTRACT

The invasive Asian hornet (*Vespa velutina nigrithorax*) first arrived in Germany in 2014 and has spread rapidly since 2023. This invasive predatory hornet poses an increasing threat to honey bee colonies, due to its aggressive hunting at hive entrances. Persistent predation at the flight entrance or even intrusion into the hives can disrupt foraging activity and even lead to colony losses of honey bees (*Apis mellifera*). Entrance guards (muzzles) are increasingly implemented as a protective measure, but their effectiveness and practicality have not yet been sufficiently investigated. Initial preliminary tests were carried out at the end of 2025 with two different entrance guards (Wooden entrance muzzle with a galvanized metal grid and a plastic flight entrance box with large, layered entrance holes) in Stuttgart and in Karlsruhe. These tests examined the ease of handling for such entrance guards, their functionality, and the effects on the behaviour of honey bees and Asian hornets. Data was collected through flight entrance observations. Additionally, two online surveys were conducted among beekeepers in October and December 2025 to assess the current use of entrance guards, experiences with other protective measures against *Vespa velutina*, and document beekeeper observations on the behaviour and interactions of Asian hornets and honey bees. Evaluation of the trial and survey data is ongoing and will be presented at the conference.

*Keywords Vespa velutina, entrance guards, invasive species, protection, online survey*

## V2.8: From bench to hive: a lateral flow assay for rapid on-site detection of *Paenibacillus larvae*

*From bench to hive: Ein Lateral Flow Assay für den schnellen Vor-Ort Nachweis von Paenibacillus larvae*

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### ABSTRACT

American Foulbrood (AFB) is a globally occurring and fatal brood disease of the Western honey bee (*Apis mellifera*), caused by the gram-positive, spore-forming bacterium *Paenibacillus larvae*. AFB is a serious threat to colony health and productivity, leading to severe economic losses in apiculture. The spores of *P. larvae* are very resistant and spread very quickly within and between apiaries. AFB is therefore highly contagious, making early and accurate diagnosis essential for effective disease control. However, conventional laboratory diagnosis for detecting *P. larvae* can take up to two weeks, during which valuable time is lost before control and hygiene measures can be implemented to contain the further spread of the disease. In order to achieve a more rapid diagnosis of AFB, we developed, in collaboration with fzmb GmbH, a duplex lateral flow assay (duplex-LFA) for the detection and differentiation of the clinically relevant *P. larvae* genotypes ERIC I and II. Based on our results of basic research conducted over the past two decades, two target antigens were selected for the generation of monoclonal antibodies, comprising one antigen specific for *P. larvae* and a second antigen specific for the ERIC II genotype. The target antigens were produced recombinantly or purified directly from *P. larvae* culture supernatants. Highly specific monoclonal antibodies directed against these antigens formed the basis for the development of two sandwich enzyme linked immunosorbent assays (ELISAs) and, building on these, the duplex-LFA. Both immunoassay formats were evaluated using experimentally infected larvae samples, while the duplex-LFA was further validated using field samples. The assays achieved high levels of specificity, sensitivity, and accuracy, ensuring reliable detection of *P. larvae* and differentiation between the genotypes ERIC I and II. The lateral flow assay provides a rapid on-site diagnosis, facilitating early intervention and effective disease control.

*Keywords* American Foulbrood, *Paenibacillus larvae*, diagnostics, LFA, ELISA

### V2.9: More than motility: flagella in the pathogenesis of *Paenibacillus larvae*

*Mehr als Motilität: Flagellen in der Pathogenese von Paenibacillus larvae*

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#### ABSTRACT

*Paenibacillus larvae*, the causative agent of American foulbrood (AFB), is typically described as rod-shaped, Gram-positive, spore-forming bacterium, based on its appearance under a light microscope. However, light microscopy does not reveal that the surface of this bacterium is covered by a multitude of hair-like structures, the so-called flagella. Due to their extreme thin structure, these elements only become visible when subjected to specific staining methods. The cellular appendages are capable of rotating in a propeller-like manner, thereby enabling the bacteria to move forward. Their function is based on a highly complex architecture consisting of three main domains: a membrane-anchored basal body containing the motor, a hook, and the long filament. Consequently, the synthesis of flagella is an energy-expensive process, leading to the hypothesis that flagella may play an important role in the pathogenesis of *P. larvae*. In order to investigate this hypothesis, a flagella-deficient mutant of *P. larvae* ERIC II was generated and subsequently tested in both in vitro and in vivo studies. Our findings demonstrate that, in the absence of flagella, *P. larvae* manifests not only a non-motile and non-swarmer phenotype, but also showed alterations in biofilm formation. Furthermore, survival assays using honey bee larvae revealed that flagella are essential for the full virulence of *P. larvae*. Subsequent analysis of sections of infected larvae by fluorescence in situ hybridization (FISH) indicated a role for flagella during various steps of the infection process, especially during the invasion of the hemocoel. Accordingly, the flagellum can be classified as a virulence factor of this *P. larvae* genotype.

*Keywords Paenibacillus larvae, flagella, virulence, biofilm, motility*

← ZURÜCK

### V2.10: Influence of an extended brood break (trapping comb) on *Varroa destructor*-associated and non-associated viruses in honey bees (*Apis mellifera*)

*Einfluss eines verlängerten Bannwabentaschenverfahrens auf Varroa destructor assoziierte und nicht assoziierte Viren der Honigbiene Apis mellifera*

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#### ABSTRACT

*Varroa destructor* (varroa mite) is widely recognised as the major threat to Western honey bees (*Apis mellifera*), particularly due to its role as a vector of viral pathogens such as deformed wing virus (DWV). This study investigated whether an extended brood break using a double-framed Trapping Comb to reduce varroa mite numbers in a colony could reduce virus loads of DWV genotype B (DWV-B), black queen cell virus (BQCV), sacbrood virus (SBV), and acute bee paralysis virus (ABPV). Twenty Buckfast colonies, located at two sites in Germany (Leipzig and Zeitz), were divided into a treatment (extended brood break for 47 days) and a control group (no brood break). Virus loads were quantified by RT-qPCR before and after the treatment intervention. Statistical analyses (Mann-Whitney U test, Generalized Linear Models) revealed a highly significant effect of the brood break on the intensity of infection (viral titre) of DWV-B. In contrast, no significant changes were observed in the prevalence or intensity of infection of the viruses BQCV, SBV, and ABPV, likely due to their lower prevalence in the sampled colonies. Location did not show any significant influence on virus levels, nor did it modulate the treatment effects. In conclusion, these results demonstrate that a prolonged brood interruption by means of the Trapping Comb method is effective in reducing not only varroa mites but also the DWV-B load in honey bee colonies. Moreover, this approach does not involve chemical treatments, thus providing a promising and residue-free strategy to mitigate varroa-induced damages. Future research could be expanded to investigate potential impacts of a brood break on other viral or bacterial pathogens.

*Keywords* pathogen, deformed wing virus, prevalence, load

### V2.11: Effects of multiple foundress infestation of *Varroa destructor* on pupal development and viral dynamics in the honey bee, *Apis mellifera* in Germany and in China

*Effekte eines Mehrfachbefalls durch Muttermilben von Varroa destructor auf die Puppenentwicklung und Virusdynamik der Honigbiene Apis mellifera in Deutschland und China*

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#### ABSTRACT

The ectoparasitic mite, *Varroa destructor* is widely recognised as one of the most serious threats to the health of the western honey bee, *Apis mellifera*, as *Varroa* not only feeds on bees' fat body and haemolymph, but also transmits multiple viruses. While extensive research has documented the impacts of single mite infestation at the individual and colony levels, the biological impact of multiple infestations within a single brood cell remains poorly understood, particularly whether multiple mites exert additive or non-additive effects on developing pupae. In this study, we artificially infested worker brood cells just after capping with a single, two and four-foundress mites and evaluated pupal development, physical wounding, viral prevalence and viral loads at 4-day and 10-day post capping (4 dpc, 10 dpc). Experiments were conducted in both Germany and China to understand host responses from different geographic populations. We demonstrated that pupal mortality, and the size of the feeding site wound increased significantly with the number of mites, while pupae weight at 10dpc was significantly reduced. Our temporal analysis in China revealed a divergent pattern in viral dynamics during pupal development. Specifically, the titres of Deformed Wing Virus (DWV) increased significantly from 4 dpc to 10 dpc. In contrast, Israeli Acute Paralysis Virus (IAPV) loads decreased substantially over the same period, especially in the highly infestation pupae. Taken together, our results reveal that multiple mite infestation negatively influences bee development, with enlarged feeding wounds and mite-mediated amplification of acute and chronic viruses potentially accelerating pupal mortality. These findings underscore the importance of considering multiple mite infestation dynamics, especially in the late summer season, when assessing the outcome of *Varroa*-virus-host interactions.

*Keywords* *Varroa destructor*, multiple infestation, honey bee viruses, Germany, China

### V2.12: BroodSense: a platform for scanner-based brood and varroa monitoring

*BroodSense: Eine Plattform für scannerbasiertes Brut- und Varroa-Monitoring*

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#### ABSTRACT

Non-destructive monitoring of honey bee brood under field conditions remains methodologically challenging. Building on a previously published proof-of-concept study demonstrating that modified flatbed scanners integrated into brood frames allow continuous observation of individual brood cells, we present recent methodological developments aimed at improving reproducibility and accessibility of this approach. The scanner-based system enables repeated imaging of brood cells at short temporal intervals, allowing the detection of larval development, food storage, hygienic brood removal, and the presence of brood-associated parasites such as *Varroa destructor*. Over the past year, the hardware configuration was extended by software for controlling the device and managing the data in a scalable way. We will outline practical considerations for deployment under apiary conditions, demonstrate the data management platform, and discuss limits related to resolution, scan frequency, and colony acceptance. The contribution emphasises the methodological potential of scanner-based brood phenotyping as a research tool for studying brood dynamics, parasite reproduction, and hygienic behaviour in honey bee colonies.

*Keywords* brood monitoring, *Varroa destructor*, automated phenotyping, research instruments

← ZURÜCK

### V3.1: Implementation of an extended SNP Panel for the genetic monitoring of honey bees and its application to *A. mellifera mellifera* and *A. mellifera carnica* samples across Europe

*Implementierung eines erweiterten SNP Panels für das genetische Monitoring von Honigbienen und dessen Anwendung auf A. m. carnica und A. m. mellifera Proben in Europa*

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#### ABSTRACT

In this project, we evaluate a 70K SNP-array based on Jones et al. (2021) for the routine genetic monitoring of honey bees. This SNP-array includes previously published marker sets for subspecies differentiation, as well as markers that reflect phenotypic differences, such as variation in immune response or associations with traits such as hygienic behaviour, honey production and varroa tolerance. The inclusion of markers that show intra-subspecies variation of functional relevance, as well as the higher marker density compared to previous honey bee SNP-chips, makes this a promising tool including a wide range of applications. These are the estimation of genetic diversity, inbreeding and effective population size, parentage analysis and possible genomic selection in breeding programs. Further, the analysis of introgression was optimized to distinguish between six clusters comprising of the A-, O- and Y-Lineages, *A. mellifera mellifera*, *A. mellifera carnica* and *A. mellifera ligustica*, using a comprehensive database of 1270 reference samples, built considering a total of 20 subspecies and ~4600 samples across Europe, the Middle East and Africa. Here, we report on the optimization and validation of these applications on the basis of the 70K SNP-array and present results on ~4200 samples targeting *A. m. mellifera* and *A. m. carnica* across 20 European countries.

*Keywords* genetic monitoring, genetic diversity, inbreeding, hybridization, introgression

[← ZURÜCK](#)

## V3.2: Insights into transcriptomic data of early-stage honey bee larvae from an inbred crossing

*Einblicke in Transkriptomdaten früher Honigbienen-Larvenstadien einer Inzuchtkreuzung*

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### ABSTRACT

The molecular basis of sex determination of the western honey bee *Apis mellifera* is controlled by the complementary sex determiner (*csd*) gene which acts as the primary signal of the following downstream gene regulatory cascade. This signal is based on the allelic endowment of *csd*. Heterozygosity at *csd* initiates female development, while hemi- and homozygosity leads to male development. *Csd* homozygous individuals develop into diploid drones which have zero fitness, as they are recognized and removed by worker bees within hours after hatching. The signal which triggers this behaviour is still unknown, whereas cuticular hydrocarbons (CHC) have been proposed to play an important role in the discrimination of diploid drone larvae. The aim of this project is to gain insights into the underlying genetic mechanism that leads to this remarkable phenotype. We used different early larval stages (12h, 24h, 36h, 48h after hatching, six samples for each group) from an inbred cross reared in-vitro for transcriptome sequencing to investigate gene expression differences between diploid females, diploid males and haploid males. The results show a remarkable number of differentially expressed genes (DEG) between the sexes linked to different metabolism and biosynthesis pathways. In addition, DEGs encoding for cuticular proteins support the hypothesis that the detection might be linked to differences in the CHC profiles between the distinct larvae.

*Keywords* *Apis mellifera*, *csd*, diploid drones, transcriptome, different expressed genes

### V3.3: Effective population size of the Central European Carnica population from SNP data

*Effektive Populationsgröße der mitteleuropäischen Carnica-Population auf Basis von SNP-Daten*

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#### ABSTRACT

*Apis mellifera carnica* is native to Austria and the Balkans but gained worldwide popularity, due to its gentleness and high honey yield. The Central European breeding program is based on a network of breeders from Germany, Austria and neighbouring countries who use morphometrical checks to guarantee the purity of their bees. The pedigree and phenotypical data is maintained at, and breeding values are published on beebreed.eu. Managing the genetic diversity in breeding populations relies on close attention to genetic data. Whilst levels of genetic diversity and inbreeding can give valuable insights on the current status of a population, estimates of effective population size give a better prediction of the longer-term ability of a population to retain genetic diversity. This is the size of an ideal, panmictic population with the same increase of inbreeding per generation as the population under consideration. Although methods were established for haplodiploid species, selection and the use of mating stations in honey bee breeding pose considerable challenges for the estimation. We conducted a forward in time simulation of a population under selection. Five settings were simulated over 55 years and each was repeated 100 times. In the standard setting, 1,000 breeding queens per year, and 50 mating stations were simulated. In the 4 other settings, the mating scheme was changed in year 30 by increasing or decreasing either the number breeding queens or the number of mating stations by 40%. The effective population size was estimated via the linkage-based implemented in GONE and the temporal method from NeEstimator\_v2. Both methods were compared to estimates from inbreeding reported by the simulation software. About 3,000 queens were genotyped on a 70-k-SNP-chip (HONEYBEE\_2021) via their flight muscle, queen cells, or drone samples. Estimates of effective population size were generated and discussed in the context of simulation results.

*Keywords* breeding, SNP chip, genomics, *Apis mellifera carnica*, genetic monitoring

[← ZURÜCK](#)

## V3.4: Buzzing tramways - a comparative analysis of wild bee diversity on tram tracks in four German cities

*Buzzing tramways - Untersuchung der Wildbienen Diversität von Straßenbahngleisen in vier deutschen Städten*

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### ABSTRACT

Wild bee populations have severely declined over recent decades due to habitat loss and deteriorating habitat quality. Despite the decline, it has been shown that cities can provide suitable habitats for bees, particularly through elements of urban green infrastructure. In this context, green tram tracks as linear structures could be promising habitats for bees, yet their benefit remain largely untested. In this study, we conducted the first quantitative assessment of wild bee diversity on differently managed tram track types (gravel, turf, flower tracks). Standardized pan trap surveys were performed on 48 plots across four German cities in 2025. Potential drivers of bee diversity were recorded on both the habitat scale (flowering resources, temperature, field layer) and on the landscape scale (urbanization, surrounding land use). In total, 4,510 bee individuals of 109 species were recorded, including 26 species listed on the Red List of Germany. Preliminary results reveal a high within plot-type variability in both vegetation characteristics and bee abundance. Management types do not appear to be reliable predictors of bee diversity. Instead, open flower coverage influences both bee abundance and diversity on the tracks. These results indicate that the actual development of tram tracks can be more important than a specific a priori biodiversity-oriented design. Our findings highlight the potential of tram tracks as habitats for wild bees and suggest that future management of existing track systems should focus on maximizing floral resources through extensive management regimes.

*Keywords* Wild bees, tram tracks, urban green infrastructure, bee diversity

## V3.5: Penthouse for pollinators? – How attractive are pollinator-friendly balconies at various heights?

*Penthouse für Bestäuber? - Attraktivität von bestäuberfreundlichen Balkonbepflanzungen in unterschiedlichen Höhen*

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### ABSTRACT

Wild bees and pollinators in urban areas need suitable food resources, often supplied through diverse green spaces and flowering areas. In dense urban environments, however, horizontal spaces for pollinator-friendly plantings are limited and vertical greening systems are often not a viable alternative due to their high costs. Pollinator-friendly balcony plantings could therefore be a simple and cost-effective approach to support a diverse pollinator community, although their actual use by wild bees and other pollinators, and the influence of balcony height on its attractiveness, have not yet been investigated in a scientific study. In our study, we investigated the attractiveness of two planting concepts (wild perennials and cultivars) across a total of five floors along the southern side of a building complex at the University of Hohenheim. To record the exact number of flower-visiting insects, we performed five-minute pollinator observation bouts over a 14-week period from June to August on each of the 30 plant boxes. Additionally, we recorded important environmental factors such as the temperature, solar irradiation, wind speed, and the number of flowers per plant species during each observation. In total, we were able to perform 736 individual plant box observations with over 9,200 pollinator visits. Our preliminary results demonstrated the general attractiveness of both planting concepts for a wide variety of pollinator groups and showed a significant effect of height on the honey bee visitation rate ( $N=4,989$ ;  $p < 0.001$ ), with the 5th floor visited less frequently. In contrast, there was no significant height effect on the visitation rates of wild bees ( $N=4,013$ ;  $p=0.245$ ). The results highlight the attractiveness of balcony plantings at different heights and their great potential as urban flowering resources.

*Keywords* pollinator-friendly plantings, urban pollinators, foraging behaviour, pollinator observation

## V3.6: Fungal associates of the ground-nesting wild bee *Andrena vaga* and their potential role in oligolecty

*Pilze in Assoziation mit der bodennistenden Wildbiene Andrena vaga und ihre mögliche Rolle bei der Oligolectie*

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### ABSTRACT

To understand fundamental questions of the bee's biology and ecology, it is essential to gain knowledge about their associated (micro-)organisms. Currently, functional descriptions of bee-fungi-interactions of solitary bee species, particularly ground-nesting bees, are scarce. So far, most studies were conducted with managed social bees and their bacterial associates. In our study, we characterise the yeast community composition associated with the oligolectic mining bee *Andrena vaga*. We examined seven matrices of the early nest stage, using both classical cultivation and ITS2 DNA-metabarcoding. Remarkably, the only cultivated yeast from all egg samples was *Triodomyces crassus*, a smut-related dimorphic yeast species. It assimilates salicin and produces antimicrobial glycolipids, potentially used for pollen detoxification and brood cell disinfection. This suggests that yeast associates might be a key factor enabling oligolectic bees to specialise on toxic pollen sources. The ecology and functionality of other identified yeasts like *Starmerella bombicola* are discussed here. In accordance with recent research, our findings suggest that solitary bees can possess core microbiomes and provide initial indications of vertical symbiont transmission for solitary bees, a phenomenon previously documented only in social bees. Our study sheds light on the critical role of associated microorganisms and may serve as the missing link to unravel the uncertainties regarding the origin of oligolecty.

*Keywords* solitary bee, microbiota, mutualism, bee-fungi interaction, symbiont transmission

← ZURÜCK

### V3.7: Citizen scientists, DNA traces and empty nests: Three years of volunteer-based eDNA sampling for the detection of cavity-nesting wild bees – lessons learned so far

*Bürgerwissenschaftler\*innen, DNA-Spuren und leere Nester: Drei Jahre eDNA-Probenahme durch Ehrenamtliche zum Nachweise holhraumnistender Wildbienen - bisherige Erkenntnisse*

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#### ABSTRACT

Modern pollinator monitoring approaches should harness the power of modern methods, such as citizen science and environmental DNA (eDNA). As part of a wild bee monitoring program, eDNA sampling of nesting observation boxes (NOBs) for cavity-nesting bees, performed by volunteers, has been explored since 2023. Volunteers were introduced to eDNA analysis during webinars, with a clear focus on practical aspects during sampling. Subsequently, they received a sampling kit containing most required materials and detailed sampling instructions. Volunteers sampled the NOBs independently and sent the samples to the laboratory. Sampling correctness was monitored based on photographs taken before and after sampling. Organic material collected from NOBs was processed for (e)DNA-based detection of cavity-nesting hymenopterans and other arthropods. Volunteers were actively asked for feedback, which informed potential changes to the process for the following year. Each year, more than 90% of sampling kits were returned to the lab, and sampling correctness was 86% and above. Volunteer feedback was highly positive, but sampling took up to 120 minutes per NOB, which was perceived as too effort-intensive by approximately one third of the volunteers. After the first year, online training was extended to two webinars, an optional online exercise was developed and the sampling kit was amended based on the feedback received. Volunteers were highly motivated and training provided by webinars proved sufficient to guarantee a smooth sampling process. Results obtained from eDNA analysis allowed resolving species aggregates, but failed to detect some rare species. Time-effort required for sampling and subsequent DNA analysis, practical aspects of sampling in the field and the inability to control for DNA degradation remain a challenge. In summary, communication, feedback and volunteer appreciation are key to successful combination of citizen science and eDNA-based approaches.

*Keywords* cavity-nesting wild bees, citizen science, eDNA, monitoring

← ZURÜCK

## V3.8: Strengthening long-term monitoring of bee communities in agricultural landscapes by surveying wing morphotype abundance

*Unterstützung des Langzeitmonitoring von Bienengemeinschaften in Agrarlandschaften durch Erfassung der Häufigkeit von Flügelmorphotypen*

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### ABSTRACT

In long-term monitoring, linking absolute diversity with the abundance dynamics of insect taxa remains challenging due to limited taxonomic expertise, financial constraints, and the need for rapid sample processing. However, such data are essential for assessing population trends and the status of pollinators. Within the MonViA project (Monitoring of Biodiversity in Agricultural Landscapes), we developed an efficient method to survey the morphological diversity of bee wings and integrate these findings with DNA metabarcoding data. Our study utilized 576 pan-trap samples, collected at phenologically determined dates between April and August 2024 across 16 sites. We extracted the right forewings of 7,858 bees and generated high-resolution scans for further analysis and a digital archive. Using twenty-one descriptors derived from specialist literature, we identified fifteen wing morphotypes associated with specific bee genera and, in some cases species. These data were compared with 1,180 OTU matches generated via BLAST analysis of the corresponding metabarcoding data. Approximately 60% of the samples were assigned to *Lasioglossum*, followed by *Andrena*, *Apis*, and *Bombus*. Ten percent represented morphotypes associated with over eleven other genera. Preliminary results show a Shannon index from 1.01 to 1.76 and evenness between 0.41 and 0.72. However, these values were strongly influenced by temporal dynamics; for instance, *Lasioglossum* counts fluctuated between 11 and 2,158 individuals per site. Overall, this approach effectively complements baseline diversity data with abundance information through standardized wing characterization. Future integration of AI with the digitized archive could identify additional species-related descriptors, further enhancing the efficiency of monitoring programs.

*Keywords* bee diversity, abundance, DNA-metabarcoding, wing morphology, shannon index

← ZURÜCK

## V3.9: Site-specific weed management can boost food resources for pollinators

*Standortangepasstes Unkrautmanagement fördert Nahrungsangebot für Bestäuberinsekten*

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### ABSTRACT

Diverse weed communities can play a key role in providing resources for pollinators and other beneficial insects in agricultural landscapes. One novel approach to enhance weed diversity in conventional agriculture combines site-specific weed management (SSWM) with ecosystem service capacity. This modified SSWM uses fine-scaled, in-field weed distribution maps to differentiate between areas that potentially provide ecosystem services (high service potential) and areas that pose high risks of yield losses (high disservice potential) restricting weed control only to the latter. Such SSWM decisions rely on knowledge about species-specific (functional) weed traits. To test and improve the categorization of (dis-)service potential, we investigated weed diversity, traits, and pollinator visitation at two fields grown with winter wheat. By means of distribution maps for each weed species and their functional traits derived from the literature, we picked ten 1 m<sup>2</sup> plots per site along a (dis-)service potential gradient. In each plot, we recorded floral phenology, abundance and flower visitors of all weed species for 15 min every fortnight between April and July 2025. We also monitored pollinators along two transects per site per sampling date and with pan traps. Body-bound pollen of individually caught flower visitors were prepared, and insects were pinned before identification. Pollinator abundance varied significantly between sampling dates and weed species. Bumble bees showed a preference for common poppy (*Papaver rhoeas* L.) and were recorded otherwise at low counts. Honey bees were absent during the majority of observation sessions. We used pollinator diversity, abundance, and flower abundance as parameters for modelling (dis-)service potential in the application of SSWM. We will investigate whether this novel SSWM contributes to the preservation of ecosystem services without negatively affecting yield.

*Keywords* flower visitation, flower density, weeds, bee diversity, floral resources

← ZURÜCK

### V3.10: Monitoring of bumble bees in agricultural landscapes in Germany: nationwide data on population trends, phenological patterns and floral resource use

*Hummel-Monitoring in Agrarlandschaften: bundesweite Daten zu Populationstrends, phänologischen Mustern und zur Nutzung von Nahrungsressourcen*

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#### ABSTRACT

Bumble bees are vital for essential ecosystem functions, particularly the pollination of crops and wild plants. However, their populations are declining globally, with intensive agricultural land use identified as a major contributing factor. To understand how bumble bee populations are changing in agricultural landscapes, long-term and large-scale data are essential, but currently lacking. For this reason, we have implemented a nationwide bumble bee monitoring scheme in agricultural landscapes in Germany (<https://wildbienen.thuenen.de>). The program integrates a standardized sampling design with a citizen science-based transect approach, supported by data validation by species experts. Due to monthly transect surveys, the program enables robust assessments of bumble bee abundance, species diversity, bumble bee-plant interactions, as well as the detection of interannual variation in phenological patterns. We present data from the first five years (2021 - 2025) of the monitoring program, which includes over 1,000 surveys conducted at 100 monitoring sites across Germany. Our findings reveal a clear dominance of three species or species aggregates in agricultural landscapes, which together accounted for approximately 75% of all observations. However, bumble bees used a wide variety of food plants, with records from over 120 different plant genera. Across the five-year period, bumble bee abundance and species richness remained stable, but phenological patterns varied between years. These results provide first insights into the status of bumble bees in Germany's agricultural landscapes and underscore the critical importance of repeated sampling throughout the year for a robust assessment of bumble bee populations.

*Keywords* wild bees, trend monitoring, citizen science

← ZURÜCK

## V3.11: Honey bees vs. wild bees: time to act now!

*Honigbienen und Wildbienen: höchste Zeit zu agieren!*

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### ABSTRACT

Honey bees have increasingly been suggested to drive declines of wild bees via competition for food and pathogen transmission. This has already resulted in respective policy making. However, the opposition between honey bees and wild bees is not correct because: 1) only two species of the genus *Apis* are managed: western honey bees (*Apis mellifera*) and eastern honey bees (*Apis cerana*) and 2) most eastern and western honey bee colonies globally are wild and in their native range. Accordingly, they deserve the same protection as any other wild bees. Therefore, it is obvious that the term “honey bees” is wrong in this context and that conservation of wild honey bees should be advocated more strongly in the ongoing public debate. Irrespective of potential competition for resources and pathogen transmission between bees, the key drivers for global insect decline are pesticides, habitat destruction, invasive species and climate change. We here argue that research efforts and conservation policies should focus on the main drivers. The current focus on interactions between bees is distracting attention and resources from the main stressors and is thus detrimental for the conservation of all insects. It seems high time for the honey bee community to act now accordingly. We therefore propose that the interactions between bees need to be communicated to the general public urgently in a more appropriate fashion to limit wrong policy decision making.

*Keywords* honey bees, wild bees, declines, policy making

← ZURÜCK

# POSTER

## A01: Entomopathogenic nematodes reduce hibernation success of bumble bee queens, *Bombus terrestris*

*Entomopathogene Nematoden verringern den Überwinterungserfolg von Hummelköniginnen, *Bombus terrestris**

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### ABSTRACT

Entomopathogenic nematodes (EPNs) are increasingly promoted as sustainable alternatives to synthetic plant protection products, yet their effects on non-target organisms remain poorly characterized. This gap is particularly relevant for soil-dwelling bees that nest and hibernate in soil, where EPNs are commonly applied. Here we show that two commercially used EPN species, *Steinernema carpocapsae* and *Heterorhabditis bacteriophora*, can infest and markedly reduce survival of hibernating buff-tailed bumble bee (*Bombus terrestris*) gynes. Freshly mated queens were exposed to field-realistic EPN concentrations (0.25–1 million infective juveniles m<sup>-2</sup>) under simulated hibernation conditions (14 °C, 60% relative humidity) for 28 days. Both EPN species significantly reduced gyne survival relative to controls (95%), with survival declining to 40–60% for *S. carpocapsae* and 55–80% for *H. bacteriophora* (log-rank test,  $P = 0.4$ ), whereas mortality from *H. bacteriophora* increased significantly with dose ( $P < 0.01$ ). Both nematode species reproduced successfully within bee cadavers, indicating that hibernating gynes can serve as alternative hosts, although reproduction did not differ among species or concentrations. These findings demonstrate that hibernating bumble bee queens are susceptible to EPN exposure and reveal an overlooked risk to pollinators, particularly given the seasonal overlap between EPN application and queen hibernation. Our results underscore the need for systematic non-target risk assessment of biological control agents.

*Keywords* biological control, non-target effects, pollinators, sustainable agriculture, *Steinernema carpocapsae*

## A02: Analysis of influencing factors of the climate change on apiary and development of recommended procedures for beekeeping

*Analyse von Einflüssen des Klimawandels auf die Imkerei und Entwicklung von Handlungsoptionen für die Imkerschaft*

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### ABSTRACT

Climate change is leading to higher temperatures and reduced humidity in our latitudes. In this study we analysed the influence of different humidity and a single short heat stress on drones of *Apis mellifera*. Parameters such as the overall quantity of sperm, the quantity of living / dead sperm and the life span of the drones were measured. The quantity of sperm (Mann-Whitney-U test;  $U = 217$ ;  $Z = -5,736$ ;  $p = 0,001$ ) as well as the number of living sperm (Kruskal-Wallis test;  $p = 0,001$ ) is significantly higher in the control group compared to the ones stressed at 40°C and 30% humidity for 3 h during their development (capped brood). Drone larvae which were stressed at younger stages (4.-6. Larval stage, 1.-3. Larval stage) didn't survive long enough for the sperm to be examined. Throughout multiple test setups not even ten drones survived 13 days. The life span of the stressed group in every age group (capped brood, 4.-6. larval stage, 1.-3. larval stage) was up to 38 days shorter compared to the control group (Cox-Regression;  $\chi^2(5) = 1354,809$ ;  $p = 0,001$ ).

*Keywords* climate change, drones, *Apis mellifera*

## A03: Analysis and Evaluation of honey samples from the Beekeepers Association Westphalia-Lippe regarding residue data of plant protection products and varroacides (2018 - 2025)

*Analyse und Auswertung von Rückstandsdaten aus dem Einsatz von Pflanzenschutzmitteln und Varroaziden in Honigproben des Landesverbandes Westfälischer und Lippischer Imker in den Jahren 2018 bis 2025*

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### ABSTRACT

Food can be contaminated by residues or contaminants. Residues are components of substances that are deliberately used, for example in food production. The present study examines residue data of honey samples from the Beekeepers Association Westphalia-Lippe, which were collected in the years 2018 to 2025. The aim is, to analyse residues from plant protection products and varroacides in order to assess their occurrence, concentrations and temporal development. The samples were examined for the relevant ingredient groups neonicotinoids, pyrethroids, thiazoles, organophosphates, strobilurins, repellents, spinosyns, imidazoles, formamidines, dicarboximides, quinones, carboxamides, and anilinopyrimidines. The chemical analysis of the honey samples (2018 n = 300; 2019 n = 420; 2020 n = 610; 2021 n = 624; 2022 n = 650; 2023 n = 1.254; 2024 n = 100; 2025 n = 246) was carried out at LUFA NRW in Münster, Germany. The samples were homogenized and prepared using the QuEChERS extraction method. The statistical analysis of the data was conducted using the R Project for Statistical Computing software. In each sample cycle, the active ingredients azoxystrobin und boscalid were detected as representatives of the active ingredient groups of strobilurins, and carbonic acids. These are ingredients, for example, in the plant protection products Amistar and Cantus. The active ingredient boscalid is also used as a fungicide in vegetable and viticulture. In addition to amitraz and diethyltoluamide, the active ingredient Coumaphos has also been detected. The results provide important insights into the residue problem of plant protection products and varroacides in honey.

*Keywords* honey, residues, plant protection

SB

## A04: Improvement of plant protection product residue analysis in bees and bee matrices – Is dispersive solid-phase extraction really necessary?

*Verbesserung der Rückstandsanalytik von Pflanzenschutzmitteln in Bienen und Bienenmatrizes – Ist die dispersive Festphasenextraktion wirklich notwendig?*

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### ABSTRACT

Cases of bee poisoning are reported every year, requiring a specific chemical analysis of the causative substance. One possible cause is the inexperienced use of plant protection products (PPPs). An efficient and reliable method of analysis is required to detect residues of PPPs to which bees are exposed. The QuEChERS method is a popular tool in analytical chemistry for over 20 years, originally being developed for the analysis of pesticides in food. However, the basic QuEChERS extraction often results in sample extracts that are not clean enough for high sensitivity. Therefore, an additional purification step using dispersive solid-phase extraction (dSPE) was often considered necessary. Our aim was to develop an improvement of the existing QuEChERS method based on honey bees and using 273 active ingredients, and to determine differences between purification with dSPE and without. Analytical analysis was performed with LC- and GC-MS(/MS). The results show that 271 substances can be detected using either the dSPE, without purification, or both. Pentachlorophenol and Dichlobenil were the only substances that were not detectable using both methods. Over 70% of pesticides achieved acceptable recovery rates between 70% and 120% for both approaches. However, it turned out that there were more substances that could not reach the limit of acceptable recovery after purification with dSPE. The very good sensitivity of both methods was demonstrated by the limit of detection and quantification (LOD & LOQ), which coincided in approximately 40% of cases. For the remaining 60% of substances, the LODs and LOQs differed by only one calibration point up or down for both methods. Finally, it can be concluded that by using the improved method further purification steps are not necessarily required to reliably determine the ingredients within our analytical spectrum. In fact, it even turned out that for substances that are sometimes toxic to bees, it is better not to further purify the samples.

*Keywords* QuEChERS, multi method pesticide analysis, LC-MS/MS, GC-MS/MS, honey bee

SB

## A05: BEE-GUARDS – Impact of oral pesticide exposure on the survival and the immune system of the red mason bee (*Osmia bicornis*)

*BEE-GUARDS - Auswirkungen der oralen Aufnahme von Pflanzenschutzmitteln auf das Überleben und das Immunsystem der roten Mauerbiene (Osmia bicornis)*

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### ABSTRACT

Solitary bees are important pollinators, but both species diversity and population density are threatened by a wide range of environmental stressors. One major stress factor in modern agricultural landscapes is the exposure to plant protection products (PPP). Therefore, we investigated the effects of PPP exposure on the survival and immune responses in male and female red mason bees (*Osmia bicornis*) under laboratory conditions. For this purpose, the systemic butenolide insecticide Flupyradifurone (FPF; 4.8 mg/kg) and the triazole fungicide Tebuconazole (TEB; 0.14 mg/kg) were used. Since TEB belongs to the group of ergosterol biosynthesis inhibitors, which can impair detoxification processes in insects and thus inhibit the degradation of insecticides in bees, a combination of both active ingredients (T+F) was tested in addition. Survival assays showed that oral exposure to FPF and to the combined treatment (T+F) significantly reduced the lifespan of male red mason bees (Kaplan-Meier, FPF:  $p < 0.001$ , T+F:  $p < 0.001$ ). Additionally, we investigated the immune system of red mason bees. We were able to demonstrate that, in both males and females, the number of haemocytes was significantly reduced in the PPP-exposed groups compared to the control group. This effect was observed in all treatment groups (Mann-Whitney U-Test, Males: TEB:  $p = 0.012$ ; FPF:  $p = 0.023$ ; T+F:  $p = 0.023$ ; Females: TEB:  $p = 0.007$ ; FPF:  $p < 0.001$ ; T+F:  $p = 0.012$ ). In the further course of the study, functional analyses of the immune system will be conducted by measuring melanisation and encapsulation. Furthermore, the antibacterial activity of the haemolymph will be assessed using the inhibition zone assay. Finally, the expression of immune-related genes will be analysed at the molecular level using quantitative Real-Time PCR.

*Keywords* *Osmia bicornis*, plant protection products, pesticides, survival, immune system

## A06: Buzzing toward better risk assessment: advancing bee effect modelling with the ICPPR bee modelling interest group

*Fortschritte der ICPPR-Arbeitsgruppe Bienenmodellierung*

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### ABSTRACT

Mechanistic pesticide exposure and effects models have the potential to improve the efficiency and accuracy of risk assessments for bees and other pollinators. Several models have been introduced or are under development, spanning organism-level effects (e.g., toxicokinetic-toxicodynamic models), colony models, and population models, for a range of taxa including honey bees, bumble bees, and non-*Apis* bees. However, these models are not yet well integrated into the risk assessment process, and a number of challenges remain. In response, the Bee Modelling Interest Group was established within the International Commission for Plant-Pollinator Relationships (ICPPR), with the aim of improving the acceptability and usability of exposure and effects models in bee risk assessments. The interest group provides a platform for exchange and discussion between stakeholders from different groups including regulators, industry, contract research organizations and academia. Within the interest group, three work groups have been created based on a survey of members' perceptions of the urgency and feasibility of various topics: (1) improving characterization of exposure pathways, (2) incorporation of sublethal effects, and (3) establishing a bee model inventory. In this presentation, we will introduce the aims, activities and goals of the ICPPR Bee Modelling Interest Group and its three active work groups. Through these collaborative efforts, we aim to accelerate the adoption of mechanistic models within regulatory frameworks, ultimately enabling more accurate and efficient pollinator risk assessments that better protect bee populations while supporting sustainable agriculture.

*Keywords* Ecological effect models, pesticide risk assessment, stakeholders, interdisciplinary

## A07: Optimum curve of oilseed rape cover for bumble bee colonies

*Optimumkurve von Rapsdeckung für Hummelkolonien*

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### ABSTRACT

Oilseed rape (OSR), as an extremely abundant resource in some areas, can drive bumble bee colony growth in otherwise resource-scarce landscapes. However, this positive effect may be offset by the elevated pesticide exposure that comes with it. While during its flowering period, resources are hyper-abundant, afterwards pollinators often lack alternative flowering resources. If the end of flowering coincides with the onset of sexual reproduction, this might lead to a lower gyne and drone production than would be expected from colony size alone. To test how bumble bee colonies respond to different proportions of OSR cover in their surroundings and to assess the potential for landscape-based mitigation options, we deployed 40 sentinel *Bombus terrestris* colonies on sites covering gradients of low to high OSR cover, low to high cover of semi-natural areas and landscape heterogeneity. We assessed size and fitness after freezing the colonies by counting all eclosed cells or eclosed queen cells respectively. While Westphal et al. (2009, *Journal of Applied Ecology* 46:187–193) did not observe an effect the proportion of colonies that produced gynes or drones in relation to OSR cover, we hypothesise that colony sizes are positively affected but that there is a quantitative, rather than qualitative difference in fitness. Our results seem to show an optimum curve of OSR availability both for colony size and colony fitness. It seems that, as long as OSR is not the predominant or only resource, it can have positive effects on bumble bees. Whether this applies to other pollinators, that may be more prone to stressors, remains a question which we aim to tackle in upcoming experiments.

*Keywords* bumble bee, pesticides, agricultural stressors, landscape heterogeneity, pollination

SB

## A08: Plant protection product exposure affects honey bee worker (*Apis mellifera*) behaviour and functions of gut and brain

*Exposition von Pflanzenschutzmitteln beeinflusst das Verhalten und die Funktionen von Darm und Gehirn bei Honigbienenarbeiterinnen (*Apis mellifera*)*

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### ABSTRACT

Honey bee (*Apis mellifera*) workers harbour a simple yet stable intestinal microbiota. Beyond digestion, the honey bee gut microbiota interacts with host gut and brain through the microbiota-gut-brain axis, influencing cell signalling, learning and other behaviours. Exposure to plant protection products (PPPs) at environmentally relevant concentrations can disrupt this system, but the extent to which functional changes take place on all these levels remains unclear. Here, we show that although brain morphological changes were minimal, acute exposure to three commonly used PPPs (SIVANTO® prime, Cantus®, ClickPro®) induced widespread and persistent functional changes across the microbiota, gut and brain at the molecular level. Specifically, brain energy metabolism pathways were increased in abundance, alongside pathways involved in transcription and translation. ClickPro® exhibited delayed metabolic effects in the gut, in line with a shift toward lipid-based energy utilisation. All PPPs persistently disrupted the microbiota composition, and altered short-chain fatty acid production, consistent with impaired microbe-microbe interactions. Moreover, we documented 16 different behavioural phenotypes, which were grouped into five larger categories (social, individual, brood care, colony maintenance, and foraging behaviour). The insecticide SIVANTO® prime significantly decreased colony maintenance behaviours, but increased the proportion of social grooming in the first days after exposure. The fungicide Cantus® increased resting behaviour, while Click Pro® decreased brood care behaviours, driven mainly by a decrease in the feeding of larvae. Together, these findings demonstrate that environmentally relevant PPP exposure induces coordinated functional disruption across multiple biological levels. Further research is needed to assess the magnitude of observed effects at the population level.

*Keywords* honey bee, sub-lethal effects, plant protection products, metabolomics, meta-proteomics

SB

## A09: Investigation of Bee Poisoning Incidents in Germany

*Untersuchung von Bienenvergiftungen in Deutschland*

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### ABSTRACT

In general, honey bees are potentially put at risk due to the exposure to plant protection products (PPP) in agriculture. Therefore, distinct statutory rules have been implemented on a national level like the German Bee Protection Act. For the authorization of PPP, an intensive risk assessment is conducted, which stipulates compulsory risk mitigation measures for the practical use of PPP. Despite these precautions, honey bee colonies get damaged by the misuse of PPP every year. According to Article 57(2) 11 of the German Plant Protection Act, bee damages suspected to originate from PPP poisoning have to be examined by the Investigation Office for Bee Poisoning Incidents at the Institut for Bee Protection, Julius Kühn Institute. Bee keepers or the plant protection service can send bee samples from damaged colonies and plant material from suspect fields to the office for an investigation free of charge. In a special bioassay using mosquito larvae of *Aedes aegypti* L. as an indicator, appropriate bee and plant samples are tested for unspecific contamination. Additionally, bee samples are tested for *Nosema* spores and for symptoms of other bee diseases. Furthermore, pollen from the bees' hair coat or pollen loads are identified with a light microscope to localize the possible floral source or crop, from which the poisoning may have originated. If the results of the biological tests suggest poisoning of the bees, bee and corresponding plant samples are screened for 300 substances via multi-residue chemical analyses, including 147 bee toxic insecticides, acaricides and nematicides as well as synergistically interacting EBI fungicides and other relevant substances using highly sensitive LC-MS/MS und GC-MS technique. Here, we present the results of these investigations of poisoning incidents in Germany over the last decades.

*Keywords* investigation, honey bee, poisoning incidents

## A10: Support for the investigation of bee poisoning incidents using satellite imagery provided by web services

*Unterstützung der Untersuchung von Bienenvergiftungen mithilfe von Satellitenbildern durch Webdienste*

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### ABSTRACT

Only for a fraction of incidents submitted to the investigation centre for bee poisoning incidents (Untersuchungsstelle für Bienenvergiftungen of the Julius Kühn-Institute) plant samples are sent for analysis; in most cases only bee samples are available. In order to fully investigate the incidents, in addition to analysing dead bees, it is also necessary to analyse plant material from fields and areas that may have been improperly treated with pesticides. The search for fields in the surrounding of the colonies is often difficult; to obtain samples from all potentially relevant fields usually no detailed information on flowering bee attractive crops in the flight range is available. To better support orientation and plant sampling, a web-based framework was developed in the project Sen2Bee for integrating and presenting information of the surrounding field crops and weather conditions to enable support for institutions or persons conducting plant sampling, but also interpretation of the incident and its circumstances. Using true colour images from Sentinel-2 satellites of the Copernicus Programme initial orientation is provided. Flowering of crops can be visualized based on the satellites' spectral bands, spatial information of air temperature and further weather data provided by other web services, which build on data of a DWD climate model. Both actual data, but also retrospective data can be obtained, and thus interpretation of analytical data of residues on plants facilitated. A great advantage of the web application will be that both up-to-date and also firstly unnoticed and later detected potential PPP incidents can be better interpreted. Further, identification of locations for plant sampling is facilitated. The project resulted in two user-oriented applications: a specialist application for experts (UBieV) and a mobile app for staff conducting the plant sampling.

*Keywords* honey bees, plant protection products, Sentinel-2, Copernicus, bee poisoning incidents

## B01: Exploring the migratory behaviour of *Apis dorsata* colonies in a tropical megacity

*Untersuchungen zum Migrationsverhalten von Apis dorsata Kolonien in einer tropischen Millionenstadt*

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### ABSTRACT

The giant honey bee, *Apis dorsata*, is a major pollinator across India and South East Asia. Despite its ecological importance, very little is known about its biology. *A. dorsata* colonies prefers to nest on large trees and rock cliffs, and in cities on high-rise buildings and other human-made structures like water towers. These large, exposed colonies are easy to spot and observe in the urban landscape providing a unique opportunity to study their annual life cycle and migratory behaviour. Here, we report a first study on the distribution of *A. dorsata* nesting sites and seasonal changes in colony abundance across the metropolitan area of Bangalore (Karnataka, India). Using a random grid survey, we estimated the density and nesting site preferences across the city. We recorded a density of 1.81 ( $\pm 1.83$ ) colonies/km<sup>2</sup>, with tall buildings and trees as the most preferred nesting sites. Although colony aggregations were observed at several locations, most colonies were solitary. Longterm monthly monitoring at one aggregation revealed a very dynamic migratory behaviour of the colonies. Number of resident colonies varied with season, peaking during flowering periods and declining during the monsoon. Duration of nesting varied from 1-14 months, but most of the colonies (76.7%) stayed not more than 3 months. Our study identifies the presence of two types of migration: (i) food resource induced nest relocations and (ii) an innate seasonal migratory behaviour in response to the monsoon. Close inspection of the nesting sites suggests that these are marked with small persistent wax blobs that are likely used by colonies as signals indicating good nesting conditions. Furthermore, the marked nesting sites could function as a matrix to guide colony movements. Based on our findings we propose that colony migratory behaviour of *A. dorsata* resembles more closely the migrations of elephants within a large home range than the seasonal long-distance migrations of butterflies and birds.

*Keywords* *Apis dorsata*, urban landscape, nest relocation, migratory behaviour, elephants

## B02: Non-destructive monitoring of honey bee brood using a flatbed scanner: results from a three-month field study

*Nicht-destruktives Monitoring der Honigbienenbrut mit einem Flachbettscanner: Ergebnisse einer dreimonatigen Feldstudie*

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### ABSTRACT

Honey bee colonies face significant threats from pathogens and pests, including chalkbrood disease caused by *Ascosphaera apis* and *Varroa destructor* mites. Traditional monitoring methods for these issues are often destructive, hindering continuous and detailed observations. This study introduces a novel, non-destructive monitoring technique using a modified flatbed scanner integrated into a honey bee brood frame. The scanner, housed within a Dadant frame and connected to a Raspberry Pi, captures high-resolution images of the brood cells at regular intervals. This method enables continuous observation of the brood life cycle, including egg laying, larval development, and the presence of pathogens and mites. Over a three-month pilot study, the scanner successfully monitored 419 cells, capturing 2,819 images of each cell and documenting critical events such as *Varroa* infestations and chalkbrood development. The method demonstrated high-resolution imaging capabilities, enabling detailed analysis of pathogen dynamics and hygienic behaviours like *Varroa*-sensitive hygiene (VSH) without apparent disturbance of the colony. The results revealed a high frequency of brood removal and pathogen detection, providing insights into the natural behaviours of honey bees and their interactions with pests.

*Keywords* brood monitoring, *Varroa destructor*, automated phenotyping, research instruments

## B03: Bumble bees remove their larvae after exposure to a bacterium-based biopesticide

*Hummeln entfernen ihre Larven nach Exposition mit einem bakterienbasierten Biopestizid*

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### ABSTRACT

The behavioural defence mechanisms to actively remove sick or diseased individuals from colonies are well described for most social insects. This strategy as part of the colonies' social immunity prevents them from transmission of pathogens and parasites, and consequently disease outbreaks. However, there is only limited information about corpse removal in bumble bees. Here, we investigated the active brood removal of *Bombus terrestris* larvae treated with a bacterial biopesticide. Therefore, we exposed full-size bumble bee colonies to a product containing *Bacillus thuringiensis* ssp. *aizawai* (strain: ABTS-1857). A daily larval removal was recorded in comparison to mechanically wounded and sugar treated controls using a newly developed trapping system. Over a period of 24 days, the bacteria-exposed colonies removed more larvae than control groups. In general, the majority of removed larvae were of white colour and of light weight (< 100 mg) independent of treatment. None of the treatments impacted colony development or the production of new sexuals. Bumble bee colonies might ensure successful colony growth by the regulation of corps removal behaviour. However, underlying mechanisms need further investigation.

*Keywords* bumble bees, corps removal, larval ejection, *Bacillus thuringiensis*, social immunity

## B04: Multiple sensor application in sentinel bumble bee colonies to disentangle multiple pressures on bee health

*Einsatz mehrerer Sensoren in Hummelkolonien zur Auseinanderhaltung von Belastungen für die Bienengesundheit*

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### ABSTRACT

Pollination is essential to both natural and agricultural ecosystems. However, wild bees, as important pollinators, are declining worldwide with severe implications for biodiversity and food security. Traditional methods to assess potential pressures can be very labour intensive, subject to observer bias, and unevenly implemented across regions. Moreover, these methods make it difficult to disentangle the many pressures acting simultaneously and to react in time when ecosystems begin to degrade. Autonomous monitoring methods offer a promising way forward to fill these gaps with a higher temporal and spatial resolution. Bumble bees are essential pollinators that respond strongly to pressures such as floral resource availability, climate change and pesticide exposure. As part of the EU-project PHENET (<https://www.phenet.eu/en>), I am working exploring the potential of bumble bee colonies as automated bioindicators. I equipped commercially available bumble bee hives with multiple automated monitoring devices – a scale for continuous weighing of the colony, a microphone for recording internal sound activity, cameras for measuring forage and within the colony activity, and temperature loggers within and outside the colony for temperature responses. Based on a semi-field experiment controlling dietary, temperature, and pesticide exposure condition, AI-driven time-series methods (audio and video) are now developed to combine the information from the different sensors to identify stress signatures and to ultimately predict colony performance and health using multimodal model approaches. First results based on machine learning algorithms indicate high classification accuracy for the identification of temperature stress using acoustic data.

*Keywords* automatic monitoring, bumble bees, *Bombus terrestris*, environmental pressures, AI-driven methods

SB

## B05: Safeguarding pollinators facing multiple stressors in multifunctional landscapes (SafePol)

*Schutz von Bestäubern, die in multifunktionalen Landschaften mehreren Stressfaktoren ausgesetzt sind (SafePol)*

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### ABSTRACT

Pollination is a key ecosystem function of direct relevance to the human economy and well-being. However, dramatic declines in the abundance and diversity of pollinators have been reported across Europe and globally. This is due to the increase in toxicological stress, climate change induced heat stress, the loss of suitable habitats, and the alteration of landscape structures, which, if intact, might mitigate these stressors. Because these factors often interact, it is important to consider them together when designing sustainable and climate-resilient future ecosystems and multifunctional landscapes and for improving the risk assessment of plant protection products. Through the integration of various disciplines, we aim to draw a holistic picture of pollinator health in modern landscapes. To understand pesticide and other chemical exposure to bumble bees, an analytical method is being developed using advanced chromatographic mass-spectrometry techniques. This will be used to link chemical loads in bees to external exposure. Through controlled exposure to heat and pesticides, as well as the combination of both stress factors, we aim to better understand the effects on the behaviour and health of bumble bees using multi-omics approaches. We will deploy sentinel bumble bee colonies in landscapes spanning the gradient from semi-natural to intensively used agricultural areas to assess the influence of landscape structure, pesticide exposure, as well as resource abundance and diversity on multiple performance metrics of the colonies. We also examine the relative importance of habitat structure and pesticide regimes for bumble bee population vitality using an individual- and process-based, spatially explicit model. With our PhD cohort "SafePol" we want to connect different methodologies from mechanistic modelling, analytics, field observations under real world conditions and experiments under controlled conditions.

*Keywords* bumble bee, pesticides, pollination, multiple stressors, climate change

## C01: Morphometric measurements of the Asian hornet (*Vespa velutina*)

*Morphometrische Größenmessungen an der Asiatischen Hornisse (Vespa velutina)*

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### ABSTRACT

The Asian hornet (*Vespa velutina*) is spreading across Central Europe. This alien species preys on bee colonies. Beekeepers generate extensive practical knowledge on this topic, which can be tapped into through AKIS and citizen science. In the context of a citizen science project, morphometric data on *V. velutina* was collected in order to quantitatively describe the body parameters and to test whether an easily identifiable characteristic allows individual specimens to be assigned to a caste. In southern Hesse, ten nests were secured in May (1 nest; 2025), July (2; 2025), August (2; 2025) and November (2 from 2024, 3 from 2025). The mesoscutum width (MW), number of tergites, fresh mass (FM), body width (B), body length (L) and wingspan (FS) were determined for 670 individuals from these nests using a precision balance and a digital calliper. Drones appeared in May, accounting for 5% of the animals examined, and reached a proportion of 60% in November. Female individuals with an MW > 4.5 mm were classified as queens. Young queens were observed from July (9%) onwards, with a maximum in November (16%). Workers had an average FM of 305 mg (204–492 mg), a B of 5.6 mm (5.0–6.9 mm), an L of 19.6 mm (13.6–25 mm) and an FS of 38.9 mm (32.5–42.8 mm). The respective values for queens were 601 mg (464–1115 mg); 6.7 mm (6.0–7.7 mm); 24.7 mm (21.2 mm – 28.6 mm) and 43.6 mm (40.6 mm – 49 mm); Drones reached 477 mg (164–730 mg), 6.6 mm (5.3–7.3 mm), 23.2 mm (17.3–28.2 mm) and 41.7 mm (32.7–45.2 mm). A Gaussian mixture model was applied to the characteristics of the November samples to identify worker bees and young queens as separable subpopulations. It was not possible to identify a characteristic that allowed all animals across all colonies to be assigned to a caste, as there were some areas of very strong overlap. The factors of time and colony had a significant effect on the parameters.

*Keywords* Asian hornet, citizen science, body measurements

## C02: Does activated charcoal make an effective control agent for the invasive Asian Hornet (*Vespa velutina*): Results from field and laboratory trials

*Ist Aktivkohle ein wirksames Bekämpfungsmittel gegen die invasive Asiatische Hornisse (Vespa velutina)? Ergebnisse aus Feld- und Laborversuchen*

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### ABSTRACT

Lorem The invasive Asian hornet (*Vespa velutina nigrithorax*) threatens biodiversity and beekeeping through its predatory behaviour on insects, especially honey bees. This has made nest removal to dampen their impact increasingly necessary. Because secondary nests are often high in treetops and difficult to reach, activated charcoal applied via telescopic lance offers a practical and environmentally friendly alternative to insecticides or costly mechanical removal. Its effectiveness, however, has not yet been scientifically evaluated. In our field study, 23 secondary nests were treated with activated charcoal using a telescopic lance and reevaluated for hornet survival after one week. In the laboratory trial, 250 adult hornets and 250 larvae were exposed to five different charcoal concentrations (0 mg, 3mg, 30mg, 300mg, 600mg), and mortality was recorded at six time points within 48 hours. In the field, 63.2 % of the charcoal treated nests showed no continued activity one week later, indicating successful treatment. Higher amounts of charcoal (>0,5kg/nest) increased efficacy to 85.7 %. In the laboratory, adult hornets showed a clear, concentration dependent increase in mortality ( $p = 6.283 \times 10^{-7}$ , Type II Wald chi square tests). While only 1 out of 50 individuals died in the control group, all adult hornets exposed to 300 mg and 600 mg succumbed within 48 h. In contrast, larvae remained unaffected across all concentrations ( $p = 0.59$ , Type II Wald chi square tests). A higher dose of charcoal likely improves nest inactivation, potentially because the newly emerging adults continue to be exposed to the active charcoal and perish within the treated combs. Nevertheless, mechanical destruction of the combs post immediately treatment remains advisable to prevent potential reactivation. The absence of an effect on larvae may be related to differences in respiratory structures compared to adults.

*Keywords* *Vespa velutina*, invasive species control, activated charcoal

## C03: Aktionsplan *Vespa velutina* in Bavaria

*Aktionsplan Vespa velutina in Bayern*

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### ABSTRACT

Lorem In July 2025 Bavaria launched the "Aktionsplan *Vespa velutina*" to limit establishment and impacts of the invasive Asian hornet (*Vespa velutina*). A central element is the official reporting platform beewarned.de, intended to collect observations across the state and channel verified reports to response teams. Observations submitted to beewarned.de are screened by the Koordinierungsstelle *Vespa velutina* and released for follow up. Verified nests are targeted for prompt removal. Volunteer personnel in Bavaria receive standardized training, personal protective equipment kits (including protective suits), and financial support to perform nest removal. A targeted morphological assessment measured sting (stinger) lengths from 180 specimens sampled from three nests to inform protective equipment recommendations. Rapid reporting through the centralized platform and decentralized, trained volunteer removal teams form the operational backbone of the action plan. The stinger length survey yielded a mean length of 3.4 mm with maximum observed lengths of 4.5 mm, contradicting common assertions of lengths up to 7 mm. Existing hornet specific suits featuring >6 mm padding or high puncture resistance are therefore considered adequate protection; standard beekeeper clothing is not recommended. The Bavarian action plan combines centralized citizen reporting, verification, and locally empowered removal capacity to curb *Vespa velutina* spread. Morphological data support the use of hornet rated protective clothing.

*Keywords Vespa velutina, Asian hornet, nest removal, yellow legged hornet*

## C04: MLVA-based epidemiology of American foulbrood

*MLVA-basierte Epidemiologie der Amerikanischen Faulbrut*

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### ABSTRACT

American foulbrood (AFB) is a bee disease that occurs worldwide and is fatal to honey bee brood. It is caused by the bacterium *Paenibacillus larvae*. This bacterium can be genotyped in various ways. One possible method is repPCR (repetitive element PCR) with ERIC primers (Enterobacterial Repetitive Intergenic Consensus), which has been used to identify five different genotypes of *P. larvae* to date. However, a significantly higher resolution of the genetic variability within the species *P. larvae* is provided by MLVA (Multiple-Locus VNTR Analysis), when 11 tandem repeat sequence regions in the genome of *P. larvae* are analysed. Based on the VNTRs (variable number of tandem repeats) codes determined in this way, more than 400 MLVA types for *P. larvae* have been derived. This makes MLVA an excellent method for conducting epidemiological analyses of AFB. Our research into the epidemiology of *P. larvae* has so far focused primarily on the analysis of isolates originating from Germany. However, investigations of *P. larvae* strains from honey and brood comb honey samples collected worldwide will now complement the MLV analyses and provide a more comprehensive picture of the epidemiology of AFB, allowing potential regional differences to be characterized.

*Keywords Paenibacillus larvae, MLVA, epidemiology*

## C05: Characterization of interspecific competition between *P. larvae* and potential bacterial competitors

*Charakterisierung von interspezifischer Konkurrenz zwischen *P. larvae* und möglichen bakteriellen Konkurrenten*

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### ABSTRACT

The spore-forming bacterium *Paenibacillus larvae* (*P. larvae*) is the causative agent of American Foulbrood (AFB), a worldwide occurring, lethal disease of the honey bee brood. The life cycle of *P. larvae* within the bee larvae comprises three phases (commensal phase, invasive phase and necrotrophic phase) during which a pure culture of *P. larvae* has to be established in order to secure an efficient transmission within the bee colony. We recently demonstrated that the *P. larvae* antibacterial secondary metabolites paenilamicin (Pam) and sevadicin (Sev) are involved in suppressing competing bacteria during pathogenesis. This led to the hypothesis that the transmission and virulence evolution of the bee pathogen is influenced by the competition of *P. larvae* with concomitant bacteria. To test this hypothesis, we first identified several potential bacterial competitors that *P. larvae* might encounter during pathogenesis. We performed interbacterial antagonism assays and competitive swarming experiments to analyse the interspecific interactions between *P. larvae* and potentially competing bacteria in vitro. The results obtained show that *P. larvae* inhibits the growth of many, but not all, bacteria. Using gene inactivation mutants for Pam and Sev, we show that the outcome of interspecific interactions depended on the resistance or sensitivity of competitors to the above-mentioned secondary metabolites of *P. larvae*.

*Keywords* *Paenibacillus larvae*, American Foulbrood, interspecific competition

## C06: Effects of *Bacillus thuringiensis* strains from different insecticides on honey bee larval survival

*Auswirkungen von Bacillus thuringiensis-Stämmen aus unterschiedlichen Insektiziden auf das Überleben von Honigbienenlarven*

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### ABSTRACT

*Bacillus thuringiensis* (Bt) is widely used as a biological insecticide for specific insect pests and has generally been considered safe for non-target organisms, including honey bees. In apiculture, Bt preparations containing Bt spores and Bt toxins are sprayed onto wax combs in order to kill the larvae of the greater wax moth, *Galleria mellonella*, thus preventing destruction of stored wax combs or infestations of colonies by *G. mellonella*. Recently, we showed that *B. thuringiensis* var. *aizawai*, isolated from the wax moth control product B401®, reduces honey bee larval survival in bioexposure assays and can complete a full infection cycle within larvae. In addition to direct application in hives, honey bee larvae may also be exposed to Bt indirectly via Bt spore contaminated food originating from foraging bees that collect Bt spore-contaminated nectar or pollen from crops treated with Bt-based insecticides. In this study, we used bioexposure assays to compare the effects of bacteria from B401® (*B. thuringiensis* subsp. *aizawai*) with those from two crop-applied Bt insecticides, DiPel® DF (*B. thuringiensis* subsp. *kurstaki*) and FlorBac® (*B. thuringiensis* subsp. *aizawai*), kindly provided by the Julius Kühn-Institut (JKI). We observed that spores from B401® and both crop-applied products caused a significant reduction in larval survival. This lethal effect however was dependent on the timing of infection, with younger larvae being more susceptible than older larvae. Using fluorescence in situ hybridization, we confirmed that Bt spores from all tested insecticides can germinate and proliferate in both living and dead larvae. These results show that bacteria from crop-applied Bt products can affect honey bee larval survival under laboratory conditions, similar to B401®. The findings highlight the need to carefully consider potential risks to honey bee larvae when applying Bt based insecticides in agricultural and apicultural settings.

*Keywords Bacillus thuringiensis, fluorescence in situ hybridization, honey bee larvae, pathogen*

SB

## C07: Characterization of *Paenibacillus larvae* bacteriocins

*Charakterisierung der Bakteriozine von Paenibacillus larvae*

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### ABSTRACT

American Foulbrood (AFB), caused by the Gram-positive, spore-forming bacterium *Paenibacillus larvae*, is a lethal brood disease of honey bee larvae. *P. larvae* is classified into different genotypes (ERIC I–V), of which ERIC I and ERIC II account for current AFB outbreaks worldwide. Recent in silico genome sequence analyses indicated that both *P. larvae* ERIC I and ERIC II harbour gene clusters involved in bacteriocin production. Bacteriocins belong to the group of antibiotics, which exhibit antimicrobial activity between closely related bacterial strains. This is called spiteful behaviour and may help *P. larvae* eliminating bacterial competitors during pathogenesis. Bacteriocins are ribosomally synthesized and undergo a two-step posttranslational modification, converting the precursor peptide into its active form. The identified gene clusters encode different posttranslational modification enzymes in ERIC I and ERIC II, yet the putative *P. larvae* bacteriocin precursor peptide shares an identical core peptide in both genotypes. This suggests that the bacteriocins produced by the two genotypes slightly differ. As a first step for investigating whether *P. larvae* ERIC I and ERIC II exhibit spiteful behaviour and for determining the role of *P. larvae* bacteriocins in this process, gene inactivation mutants for these bacteriocins were generated in both genotypes and tested using in vitro plate inhibition assays.

*Keywords Paenibacillus larvae, American Foulbrood, bacteriocin, spiteful behaviour*

## C08: Comparison of hybridoma- and diatom-derived antibodies for a sustainable production of Immunoassays for American foulbrood detection

*Vergleich von Antikörpern aus Hybridoma- und Kieselalgen für eine nachhaltige Produktion von Immunoassays zum Nachweis der Amerikanischen Faulbrut*

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### ABSTRACT

American foulbrood (AFB) is the most devastating bacterial brood disease of honey bees. AFB causes colony and economic losses worldwide and is a notifiable disease in many countries. *Paenibacillus larvae*, the causative agent of AFB, can be distinguished into ERIC-genotypes. The two mainly occurring ERIC-genotypes ERIC I & ERIC II show different levels in virulence and thus containment strategies could differ accordingly. Disease diagnosis is usually conducted via visual inspection. If a colony is suspicious, the causative agent has to be confirmed in the laboratory, which often is very time-consuming. For fast AFB diagnostic tools like ELISAs and lateral flow assays (LFAs) specific antibodies are needed. While antibody production is usually hybridoma based and often needs animal-derived products like FCS, we are using diatoms for the production of monoclonal antibodies (mAb). Diatoms can serve as cheap and sustainable protein factories, needing only low amounts of nutrition and a light source for photosynthesis. We sequenced the variable regions of the previously developed hybridoma-derived mAbs, introduced them into diatoms, and subsequently cultivated and selected mAb-producing diatom strains. Furthermore, diatom-derived mAbs were compared to hybridoma-derived mAbs. We conducted SDS-Page, Western Blot and ELISAs for comparison of hybridoma and diatom-derived mAbs. So far, four diatom-derived mAbs have been transferred and tested. Three of these diatom mAbs show similar reactivity compared to hybridoma-derived mAbs and will be used in an LFA. Here, we present a sustainable and cost-effective approach for antibody production that achieves functionality comparable to conventional hybridoma-derived mAbs. In addition, mAb production using diatoms represents an inexpensive and reliable platform that can make ELISAs and LFAs more affordable for diverse stakeholders, broaden their applicability, and will thereby help to prevent the spread of AFB.

*Keywords* American foulbrood, monoclonal antibodies production, ERIC-genotyping

## C09: Effective short-term application of formic acid for varroa mite control in honey bee colonies using sponge cloths

*Effektive Kurzzeit-Applikation der Ameisensäure zur Varroa-Bekämpfung in Honigbienen-Völkern mittels Schwammtuch*

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### ABSTRACT

Formic acid (FA) has been used successfully since 1979 to combat the ectoparasite *Varroa destructor*, which was first detected in Germany in 1977. In 1985, FA application was initially approved in the form of the Illertisser mite plate. In contrast, the standard approval of 60% FA ad us. vet. granted in 2000, focused on using long-term evaporators (e.g. Nassenheider evaporator) for FA treatment against the *Varroa* mite. Nevertheless, short-term application using household sponge cloths based on the principle of the Illertisser mite plate remained widespread because the application via sponge cloths could be better adapted to the conditions of use (microclimate) and the degree of infestation of the bee colonies with a lower amount of 60% FA. Regulation (EU) 2019/6 of December 11, 2018, on veterinary medicinal products (Article 5(4)) made individual approvals mandatory. To obtain data for such an individual approval, common methods of applying 60% FA were compared with each other. Starting on August 8, 2022, 32 colonies from an apiary were treated with 60% FA ad us. vet. for two weeks, as described below, at daytime temperatures of up to 34 °C, sitting on two frames in a transverse construction in Segeberger Styrofoam magazine hives. The volume of the space, including the high floor, was 96 l. For treatment with Nassenheider Professional evaporator, the volume of these colonies was increased to 130 l: a) 2 Nassenheider Professional with 560 ml FA, b) 3 x 1 sponge cloth with 66 ml FA each, once a week = 198 ml FA, c) 4 x 1 sponge cloth with 66 ml FA each 2x/week = 264 ml FA, d) Positive control with FormicPro, e) Negative control without treatment. Follow-up treatment was carried out from September 5 to October 17 with Bayvarol. Considering the continued reproduction of *Varroa* mites surviving the FA treatment during the post-treatment period, treatment variants a and b achieved efficacies > 90%, variant c 78%, while the positive control achieved only 64%.

*Keywords* varroa, formic acid, sponge cloth, Nassenheider, FormicPro

## C10: Experimental infection of larvae with SBV: The viral load influences the outcome of the infection.

*Experimentelle Infektion von Larven mit SBV: Der Virustiter beeinflusst den Verlauf der Infektion*

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### ABSTRACT

Honey bee viruses have attracted considerable interest over the last two decades and it is becoming increasingly clear that viral infections play an important role in the deterioration of bee health. Among the rather neglected viruses in Europe is sacbrood virus (SBV). This neglect could be due to the fact that, although SBV can be quite frequently detected in adult bees in apparently healthy colonies, it rarely causes symptoms and cannot be linked to colony losses. However, the virus can cause significant damage to honey bee larvae, resulting in the appearance of a watery bladder and, in severe cases, larval mortality and colony decline. Recently, we successfully established a laboratory infection assay for SBV, in which larvae were orally infected with SBV-spiked larval diet. To analyse SBV tissue tropism in experimentally infected larvae, we detected viral RNA and virions using fluorescence in situ-hybridization (FISH) and immunofluorescence (IF), respectively. We show that various concentrations of SBV resulted in different infection outcomes in larvae. To enhance the efficiency of laboratory infection experiments, we used RT-TaqMan-qPCR to determine SBV concentrations in infected larvae, compared the infection rates of larvae across different SBV concentrations, and can now provide reference for future laboratory infection experiments.

*Keywords* honey bee viruses, molecular diagnostic, TaqMan-qPCR

## C11: Rapid tests for detecting pathogens in honey bees

*Schnelltests zum Nachweis von Krankheitserregern der Honigbiene*

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+equal contribution

### ABSTRACT

The Western honey bee (*Apis mellifera*) is an important pollinator that contributes to the preservation of biodiversity in natural and agricultural ecosystems. The economic value of honey bees is based not only on honey production but rather on pollination services for various agricultural crops and the resulting higher crop yields. Infectious diseases caused by viruses, bacteria, and fungi pose a major threat to the health of honey bees and the survival of bee colonies. Rapid and easy diagnosis of diseases is essential to enable quick intervention and prevent their further spread. Conventional laboratory methods, such as bacterial cultivation, microscopy or RT-PCR are time consuming and require specialised equipment and trained technicians. To achieve fast, low-cost and easy pathogen diagnostics, we developed three rapid diagnostic assays: (I) A lateral flow assay (LFA) for the detection of black queen cell virus (BQCV), one of the most prevalent honey bee viruses, which can cause larval and pupal mortality during development. (II) A duplex-LFA for the detection and differentiation of the *Paenibacillus larvae* genotypes ERIC I and II, which cause American foulbrood (AFB), a highly contagious, notifiable disease of honey bee larvae. (III) A loop-mediated isothermal amplification (LAMP) for the detection and differentiation of the microsporidian pathogens *Nosema apis* and *Nosema ceranae*, both of which cause nosemosis, a widespread, contagious disease of adult bees that can lead to the weakening or even collapse of the affected colony. Overall, all three assays show excellent performance and will greatly simplify the detection of pathogens in honey bees. They therefore provide a valuable addition to existing diagnostic methods, particularly in settings where rapid, on-site testing is required.

*Keywords* diagnostics, BQCV, American foulbrood, *Nosema apis*, *Nosema ceranae*

## C12: The Red Mason Bee is not a host for the honey bee pathogen *Nosema ceranae*

*Die Rote Mauerbiene ist kein Wirt für das Honigbienenpathogen *Nosema ceranae**

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### ABSTRACT

Honey bees and wild bees are equally important for pollinating cultivated and wild plants that depend on pollination by insects. Therefore, not only the health of honey bees is of great importance, but also that of wild bees. Past studies have shown that wild bees, which share floral sources with managed honey bees (*Apis mellifera*), may be increasingly exposed to infectious pathogens, such as *Nosema ceranae*, through interspecific pathogen transmission. In several field studies the presence of *N. ceranae* has been detected in various wild bee species, including the most common solitary red mason bee (*Osmia bicornis*). However, the actual impact of this obligate intracellular microsporidian parasite of the honey bee on the solitary bee health remained uncertain. In order to investigate the infectivity, virulence and pathogenesis of *N. ceranae* infections in *Osmia bicornis*, we performed controlled laboratory bioassays involving the oral inoculation of infectious *N. ceranae* spores to adult red mason bees, as we have done previously with bumblebees (*Bombus terrestris*). We analysed the infection status of the bees using microscopic analysis of squash preparations, PCR-based detection of *N. ceranae* DNA, histology of Giemsa-stained tissue sections and species-specific fluorescence in situ hybridisation. By repeating the experiments, we ensured that the infectivity of the spores, the experimental procedure, or the origin of the red mason bees did not influence the outcome. Our results clearly show that oral ingestion of infectious *N. ceranae* spores did not lead to infection of mason bees and that there was no proliferation of microsporidia with the formation of new spores. Our findings highlight the need for studies on the transmission of pathogens between honey bees and wild bees, as even if typical honey bee pathogens are ingested by wild bees, they may not cause infection because wild bees are not true hosts for them.

*Keywords* honey bee, wild bee, pathogen spillover, *Nosema ceranae*

## C13: Bee viruses beyond *Apis mellifera*: A case study on the violet carpenter bee (*Xylocopa violacea*)

*Bienenviren außerhalb von Apis mellifera: Eine Fallstudie zur violetten Holzbiene (Xylocopa violacea)*

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### ABSTRACT

The western honey bee (*Apis mellifera*) is one of the most extensively studied insect pollinator species, and viral diseases have been identified as a major cause of honey bee colony losses worldwide. At the same time, an increasing number of viruses that were originally considered honey bee-specific have been detected in a wide variety of other pollinating insects. Despite these observations, the modes, directionality and mechanisms of virus transmission within pollinator communities remain poorly understood. In particular, it is often unclear which species are true hosts and whether viral pathogens are primarily transmitted from managed honey bees to wild pollinators, or if wild species act as reservoirs that facilitate transmission to honey bees. Recent surveillance studies suggest that pollinator management practices and also the commercialization of pollinators may facilitate viral transmission across species boundaries. However, the ecological consequences of such infections in alternative hosts are not well understood. In this context, studying virus infections in non-*Apis* pollinators will help shed light on the epidemiology, pathogenicity, and transmission routes of these viruses. Here, we present the results of a molecular pathogen analysis of a crippled violet carpenter bee (*Xylocopa violacea*) which was collected alive in front of a nest tunnel. DWV was not detected at all, but a BQCV-infection was identified in both abdominal and wing tissues. Sequence analysis confirmed that the detected virus belonged to the BQCV clade. These findings highlight the complexity of viral circulation within pollinator communities and emphasize the need for a more comprehensive understanding of the dynamics of interspecies virus transmission between managed and wild pollinators.

*Keywords* bee virus, BQCV, *Apis mellifera*, *Xylocopa violacea*

## C14: Multiple key hosts and network structure shape viral prevalence across multispecies communities of bees

*Mehrere Schlüsselwirte und die Netzwerkstruktur prägen die Virusprävalenz in multispezies Bienen-Gemeinschaften*

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### ABSTRACT

Survival of wild bees is threatened by many factors, of which diseases have received increasing attention. Many pathogens are shared between managed and wild bee species, with flowers as the most likely route of interspecific transmission. An increased density in the landscape of managed honey bees, the assumed reservoir hosts of many viruses, may therefore aggravate pathogen spillover among bee communities. To explore this possibility, we manipulated the density of honey bee colonies across 32 agricultural landscapes differing in floral abundance, recorded plant-pollinator interactions, screened managed and wild bee species for common pollinator viruses and estimated the contribution of each bee species to viral  $R_0$ . We found that the density of virus-positive honey bees, network connectance and network niche overlap were important predictors of viral presence in wild bees. Our study provides insights into the viral transmission dynamics in bee communities which can inform management decisions to reduce disease threat to wild bees.

*Keywords* DWV, BQCV, ABPV, *Bombus lapidarius*, *Apis mellifera*

## C15: Tackling Chronic Bee Paralysis: a citizen science approach to test effective countermeasures against an emerging disease

*Chronische Bienenparalyse im Fokus: Ein Citizen-Science-Ansatz zur Erprobung wirksamer Gegenmaßnahmen gegen eine zunehmend auftretende Bienenkrankheit*

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### ABSTRACT

Chronic Bee Paralysis (CBP), caused by the Chronic Bee Paralysis Virus (CBPV), has increasingly affected European - and specifically Austrian honey bee colonies - in recent years. Bee colonies have been infected with increased frequency and severity, leading to high numbers of weakened or dead beehives. Economic losses for beekeepers arise mainly because infected colonies are unable to sufficiently provide themselves with honey and/or pollen. Current treatment recommendations rely largely on anecdotal evidence, and so far, validated countermeasures are lacking. The project CS-DeChrEase aims to address critical knowledge gaps by integrating practical experience from beekeepers with scientific expertise in bee health and viral genomics. Together, beekeeping Citizen Scientists, beekeeping advisors and researchers will test and evaluate two promising CBP-countermeasures: 1) formic acid short-term treatment and 2) Brutling/Flugling-treatment. Additionally, the project will assess minimally invasive diagnostic sampling methods and generate a comprehensive dataset on CBPV genetic diversity in Austria. Furthermore, the project aims to establish a regional knowledge exchange network and promote interdisciplinary collaboration (e.g. beekeepers, researchers, advisors, veterinarians, media specialists). Existing communication pathways will be strengthened, and freely accessible dissemination material – such as high-quality educational videos and a practice oriented CBP-management guideline - will be produced. By combining applied beekeeping expertise, viral genomics and participation of Citizen Scientists, this project will deliver applied, well-tested recommendations to support beekeepers in managing CBP. Ultimately, CS-DeChrEase will contribute to improving honey bee health and resilience in the face of emerging diseases.

*Keywords* honey bee health, honey bee viruses, disease management, chronic bee paralysis virus (CBPV), whole genome sequencing (WGS)

## C16: Effects of direct and indirect antibiotic-induced gut dysbiosis on bumble bee health

*Toxizität und Dysbiose - direkte und indirekte Effekte von Antibiotika in Hummeln*

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### ABSTRACT

Bees host a highly conserved, coevolved gut microbiome that is socially transmitted and provides essential protection against pathogens. Disruption of this microbiome, such as through antibiotic exposure, has been linked to reduced survival and increased pathogen susceptibility. However, the specific mechanisms underlying these negative effects remain unclear; they could stem from direct antibiotic toxicity or, alternatively, from the disruption of the gut microbial community. To disentangle these effects, naive bumble bees (*Bombus terrestris*) were extracted from cocoons and inoculated with either a healthy microbiome or a dysbiotic microbiome (sourced from oxytetracycline-exposed bees), allowing bees to acquire an altered microbiome without direct antibiotic exposure. A separate group received a healthy microbiome followed by direct antibiotic treatment. Bees were subsequently challenged with Slow Bee Paralysis Virus (SBPV). Our results demonstrate that both direct antibiotic exposure and the transmission of a pre-disrupted microbiome significantly affect host health and viral defence. qPCR analysis revealed elevated SBPV titres in both treatment groups compared to controls. In addition, 16S rRNA sequencing showed that these treatments significantly altered gut microbiota composition, specifically reducing alpha diversity. These findings suggest that loss of a diverse, stable microbiome—rather than antibiotic toxicity alone—is a key driver of increased viral susceptibility in bumble bees, highlighting the critical role of the gut microbiome in mediating bee health.

*Keywords* bumble bees (*Bombus terrestris*), gut microbiome, antibiotic exposure, dysbiosis, viral susceptibility

SB

## C17: Interspecific pathogen transmission and its impact on wild and managed bees

*Intraspezifische Übertragung von Krankheitserregern und ihre Auswirkungen auf wilde und bewirtschaftete Bienen*

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### ABSTRACT

Wild and managed bees are essential pollinators, supporting natural ecosystems and agricultural productivity. Growing wild bee declines have highlighted the need to better understand the impact of pathogens shared between managed honey bees and wild pollinators. Previous research has shown that pathogens can be shared among bee species, but the extent of transmission, the consequences for wild bee reproduction, and the role of bee management remain unclear. The BEENERGIA project aims to better understand the impact of shared pathogens on wild bee reproduction and long-term population dynamics. Focusing on five wild and four managed species, we use genomic tools to 1) explore which pathogens are shared and to what extent shared pathogens affect their hosts; 2) investigate the effect of interspecific transmission on virus evolution and virulence; 3) compare pathogens infecting historical and contemporary bee specimens to explore the long term impact of bee management on pathogen transmission and evolution; and 4) study the effect of bee management on pathogen transmission. Altogether, the findings of BEENERGIA will inform conservation policies and promote best practices in beekeeping and pollinator management, thereby contributing to a more sustainable coexistence of managed and wild bees.

*Keywords* bee pathogens, pollinator health, pathogen evolution, host-pathogen interactions

## D01: Sex, size and parasites: a multifactorial assessment of the population fitness in *Andrena vaga*

*Geschlecht, Größe und Parasiten: Eine multifaktorielle Analyse der Populationsfitness bei Andrena vaga*

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### ABSTRACT

Many wild bee species are threatened. Although the majority of them is ground-nesting, most research on stressors and their effects on bee population fitness has focused on cavity-nesting bees. Therefore, in our study, we focused on a representative of this important functional group of ground-nesting bees, *Andrena vaga*. In an urban setting, we analysed the species' body size, sex ratio, and parasitism rate, which are traits associated with the population fitness of bees. For our study, we used emergence traps, a rarely applied method that enables reliable links between sampled individuals and nesting site characteristics. Using this approach, we observed a consistently female-biased sex ratio. High nest densities were associated with a less female-biased sex ratio and a higher body size variability. The body size variability further increased with a higher degree of urbanization, while the intra-specific body size decreased. Parasitism rates were lower in comparison to previous studies, although parasitism by *Stylops ater* reached up to 9%, affecting host phenology and sex ratio. The presence of *Bombylius major* appeared to act as a stressor for the host, leading to increased intra-specific variations in body size in *A. vaga*. In turn, environmental factors such as bare ground cover and temperature influenced parasite prevalence. Food availability, both in terms of pollen and nectar resources, showed no effect. Our study shows that despite the negative impact of urbanization on bee body size, low parasitism and stable foraging conditions suggest that cities can provide suitable habitats for ground-nesting bees.

*Keywords* parasitism, body size, sex ratio, phenology, solitary wild bee

## D02: More than just flowers: the latest edition of the Baden-Württemberg forage catalogue as a tool for effective pollinator support

*Mehr als Blühflächen: Der neue Bienenweidekatalog Baden-Württemberg als Werkzeug für wirksamen Bestäuberschutz*

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### ABSTRACT

The decline of pollinators is driven by habitat loss and the widespread reduction of floral resources and nesting habitats. To address these challenges, the Pollinator Plant Catalogue (Bienenweidekatalog) of Baden-Württemberg was comprehensively revised to promote biodiversity and pollination services. The catalogue supports species diversity and pollination services in agriculture and urban environments by offering evidence-based, target-group-specific plant recommendations for beekeepers, municipalities, and private gardeners. The revision integrates current scientific literature, regional monitoring data and close collaboration with practitioners, including beekeepers, farmers, gardeners and scientists. In 2025, expert interviews with professional beekeepers, farmers and a wild bee specialist provided applied knowledge that is integrated into the catalogue through concise information boxes. The core element of the revised catalogue is an extensively updated botanical database comprising over 900 plant species, featuring a newly developed search and filter system and detailed plant profiles on flowering period, nectar and pollen value, habitat requirements and use by honey bees and wild bees. By linking floral resources with nesting structures, the catalogue promotes continuous forage availability throughout the growing season, enhances pollination of wild and crop plants through improved wild bee diversity and supports honey bee colony development and honey yield. The catalogue serves as a practical decision-support tool for diverse stakeholders and contributes to effective, locally adapted pollinator conservation.

*Keywords* pollinators, biodiversity, plants, conservation, database

## D03: Pollen diversity in honeys from Northeastern Germany: influence of forage origin, mass flowering crops, and seasonality

*Pollenvielfalt in Honigen aus Nordostdeutschland: Einfluss der Herkunft der Futterpflanzen, massenblühender Kulturpflanzen und der Jahreszeit*

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### ABSTRACT

Microscopic pollen analysis of honey offers valuable insights into the floral resources exploited by honey bees and reflects the biodiversity of plants within their foraging landscapes. This study investigates how forage origin, particularly mass flowering crops, influences pollen diversity in honeys from northeastern Germany, while also considering seasonal variation. A total of 2,379 honey samples collected between 2023 and 2025 were analysed using standardized light microscopic pollen analysis. Pollen taxa were identified and their relative abundances quantified. Samples were classified according to honey type (monofloral vs. polyfloral), harvesting period, and dominant forage sources, with special emphasis on mass flowering crops. The results demonstrate clear differences in pollen biodiversity associated with forage origin. Monofloral honeys are characterized by the dominance of a single leading taxon but still contain a diverse spectrum of accompanying pollen types. Polyfloral honeys show higher taxon richness and diversity indices. Mass flowering crops are associated with a reduction in relative pollen diversity, however pollen spectra remain heterogeneous and retain signals of surrounding floral resources. Seasonal patterns further structure pollen composition across the sampling period. Overall, the findings underline the suitability of honey pollen analysis for evaluating the effects of forage origin and mass flowering events on floral biodiversity. The influence of site-specific factors will be addressed in future studies.

*Keywords* honey, biodiversity, botanical origin, mass flowering crops

## D04: Mason bees' nesting success in apple orchards depends on landscape diversity, management and nest position

*Der Bruterfolg von Mauerbienen in Apfelplantagen in Abhängigkeit der Landschaftsvielfalt, der Bewirtschaftung und der Nestposition*

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### ABSTRACT

Organic farming practices can promote the abundance and diversity of bee pollinators that provide essential pollination services to wild plants and crops. However, the benefits of organic farming for biodiversity depend largely on the landscape context. The underlying mechanisms by which bee populations benefit from organic farming or increased landscape diversity are not yet well understood. Our project #2beefit aims to investigate the health status of solitary bees in apple orchards in middle Saxony, Germany. As a model system, we focus on wild cavity-nesting solitary bee species of the genus *Osmia* which are important pollinators in apple orchards in central Europe. We analyse direct and indirect effects of landscape diversity and farming practices on different indicators of bee health. Bees were recorded in nesting aids placed within and near the edges of 15 conventionally and 15 organically managed apple orchards located along a landscape diversity gradient. Preliminary results suggest that landscape diversity and management promote *Osmia* reproduction in apple orchards depending on the nest position. We observed that in both conventionally and organically managed orchards more brood cells were built at the edge of the orchard as 100 m within. The same results were found with an increasing landscape diversity, where significantly less brood cells appeared in the inner position than at the edge. This indicates that conventionally managed apple orchards benefit from diverse landscapes.

*Keywords* solitary bees, apple orchards, landscape diversity, reproduction

## D05: A large-scale and long-term monitoring of bee diversity in German agricultural landscapes

*Bundesweites Langzeitmonitoring der Bienenvielfalt in deutschen Agrarlandschaften*

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### ABSTRACT

As part of a nationwide monitoring of biological diversity on agricultural land in Germany (MonViA), we have been working on a monitoring scheme for bees and other flower visiting insects. In spring 2023, we piloted this scheme at a large scale, covering the north-eastern quarter of Germany, i.e. 5 out of 16 federal states. Sampling with pan-trap triplets (UV fluorescent blue, white and yellow) at 54 sites from the High Nature Value farmland monitoring, we counted 6,956 Anthophila individuals in total. Following DNA-metabarcoding, the BLAST search generated 1,288 matches for Anthophila, the consensus resulting in 88 taxon matches at family, 82 at genera and 48 at species level. At 22 sites, we assessed the effects of exposure time (24h, 48h, 72h) and ambient temperature on pan-trap samples. Based on our results, we advocate for a pan trap exposure time of 48h in order to maximize trap efficacy in terms of number of sampled bee individuals and sampled bee taxa, while limiting unnecessary bycatch. Accordingly, we have been piloting the monitoring scheme since 2024 at a smaller scale, but using 4-5 sampling rounds per year in order to account for seasonal species turnover. To this end, we sampled 16 agricultural sites in two study areas in the German federal states of Lower Saxony and Saxony-Anhalt. In order to ensure comparability of community data across sites and years, sampling rounds targeted phenological events spread over the bee season. Our pilot study demonstrates the feasibility of standardized, phenologically fixed monitoring events over large areas for establishing long-term trends of the diversity of bees and other pollinators.

*Keywords* phenology-based sampling, long-term pollinator monitoring, standardized biodiversity assessment

## D06: Monitoring bees in agricultural landscapes: perspectives on sampling conditions

*Bienenmonitoring in Agrarlandschaften: Beprobungsgegebenheiten im Blickpunkt*

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### ABSTRACT

In the face of declining bee populations, pollinator monitoring schemes are being initiated, e.g. the EU Pollinator Monitoring Scheme (EUPOMS). We piloted a large-scale monitoring scheme that aims at estimating long-term trends in bee communities within agricultural landscapes in Germany. To this end, we combined pan trap sampling of bees and other flower-visiting insects and DNA metabarcoding (three sets of UV-fluorescent blue, white & yellow traps along a 100m transect, one sampling event per site between late April and early May 2023). Our 54 sampling sites cover the northeastern quarter of Germany and are part of the German Ecosystem Monitoring (ÖSM) and the Monitoring of High Nature Value Farmland (HNVF). Overall, we sampled 2652 bee individuals from 67 taxa (BOLD barcode identification numbers). Combining habitat data sampled on the ground and with remote sensing data, we present preliminary results regarding correlations between landscape and local factors (e.g., agricultural land use, Shannon landscape diversity, edge density, flowering woody features, floral diversity) with bee community metrics (abundance, taxon richness, community composition). We demonstrate the feasibility of our monitoring approach, i.e., using pan traps for sampling meaningful data at a large spatial scale. Our findings also provide an example of leveraging synergies between monitoring schemes with matching sampling design.

*Keywords* monitoring, pan traps, DNA metabarcoding, agricultural landscapes

## D07: Attractiveness and development of two flowering mixtures for honey bees and different insect groups

*Attraktivität und Entwicklung zweier Blümmischungen für Honigbienen und weitere Insektengruppen*

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### ABSTRACT

In this study, two different commercially available flower mixtures (referred to as M1, annual, and M2, perennial) were compared in terms of their attractiveness to flower-seeking insects and vegetative development in the first year of cultivation. After seedbed preparation, two plots were sown with one of the two flower mixtures, each with three replicates, on the approximately 1 ha trial area. On the three assessment dates (18 July, 26 July and 9 August 2023) the degree of flowering and coverage according to Braun-Blanquet were measured and the insect flight was recorded using GoPro cameras in 2 x 1 m<sup>2</sup> areas over a period of 1 hour, without disturbing the insects. The reproducible analysis of the recordings was performed visually and manually using the video analysis software Mangold-Interact® (Lab Suite version 2016). The statistics were compiled using the R programme. The number and dwell time of the following insect groups were recorded: honey bees, bumble bees, hoverflies, butterflies and other insects. Observations were made during the main flight period of the insects. The insects showed a quantitative preference for the perennial flower mixture M2, which was more weeded and therefore had a higher degree of flowering from the second date onwards. Although this is beneficial for the insects, it can increase weed pressure in neighbouring arable crops. If the perennial representatives become more dominant from the second year onwards, they could also suppress undesirable species. In the case of high weed pressure, it is advisable to use annual species and good seedbed preparation, even if the perennial mixtures have a more positive effect on the insect population. Both mixtures can improve the nectar and pollen supply for various insect groups and extend the bee plants - forage conveyor belt. Flower mixtures, but also undesirable plant species, offer a valuable food source for many insect groups in any case.

*Keywords* flower mixtures, insect counting, nectar, pollen

## D08: Honey bees as biosensors

*Honigbienen als Biosensoren*

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### ABSTRACT

Can honey bees serve as biosensors for the early detection of local severe weather events and for determining the degree of biodiversity of pollen and nectar plants within the flight radius of a bee colony? Prof. Dr. Martin Ziron and Felix Karger (South Westphalia University of Applied Sciences, Department of Agricultural Economics) are attempting to answer this question in the project “Smart City – Bees as a Data Source” in cooperation with the city of Mönchengladbach. To carry out the experiments, four bee colonies will be set up in the city of Mönchengladbach from July 2025 to September 2027. The prediction of heavy rain, for example, will be made by measuring the volume and frequency of the bees' buzzing. For this purpose, the volume/frequency sensor will be mounted on the inside of the hive above the flight hole. These two parameters will be compared with weather data for frequency and volume patterns that may repeat themselves before heavy rain. The weather data is collected using the ApiWeather-RF6 weather station, which is mounted next to the beehive. The degree of biodiversity of pollen and nectar sources is to be determined using pollen and nectar samples. At the same time, representative flowering areas within the flight radius of the experimental bee colony will be assessed according to the Braun-Blanquet scheme. The assessment data will serve as reference values and show what percentage of flowering plant species are covered by the pollen and nectar samples. In order to generate as many reference values as possible, the assessments will be expanded to include a citizen science project component. This will enable interested citizens to use an identification app to identify flowering plants, e.g., in their own gardens, and feed the data obtained into the project. As the project was only launched six months ago, no meaningful results can be presented at this stage. It's a presentation of the project idea.

*Keywords* biosensors, biodiversity, weather forecast

SB

## D09: Smart hives as a comprehensive data source for various applications for multivariate data analysis

*Intelligente Bienenstöcke als umfangreiche Datenquelle für verschiedene Anwendungsgebiete der multivariablen Datenanalyse*

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### ABSTRACT

Technological advances now make it possible to use inexpensive sensors in any industry. This allows large amounts of data to be collected quickly and easily. Combined with subsequent machine evaluation of this vast amount of data, there is the prospect of identifying and describing previously undiscovered correlations and patterns. For example, there are still many unanswered questions about honey bees, particularly their communication. The Smart Hive project series aims to contribute to a more comprehensive understanding of the honey bee's way of life by equipping bee colonies with multi-sensory devices. Among other things, vibration, temperature, infrared, force, pressure, pollutant, and image-generating sensors will be installed to collect various data. This data pool can be supplemented with further measurement results from laboratory tests, such as honey analyses, bacteriological and genetic tests. In addition, individual bees can be equipped with sensors to obtain data on flight behaviour and flight distance. This extensive amount of data will be evaluated using machine learning. Furthermore, the aim is to uncover profound interactions between the local environment and the honey bee colonies living in it. The variety of data also allows it to be used in other areas of application. Assistance systems can be developed for the early detection of swarming behaviour and diseases. The data can also be used in meteorology. The Smart Hive project series requires interdisciplinary collaboration and is carried out through the completion of graduation theses.

*Keywords* smart hive, data source, interdisciplinarity, data, beehive

## D10: Do sunflower hybrids nourish pollinators differently?

*Bieten Sonnenblumenhybride Bestäubern unterschiedliche Nahrung?*

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### ABSTRACT

Sunflower, *Helianthus annuus* L., is often considered a “low-quality” pollen resource for pollinators. Such claims are tied to low crude protein findings, yet this is not always the case. Not much is known regarding its’ nutritional potential for pollinators. Laboratory studies report inconsistent developmental parameters after bee consumption of sunflower pollen. Field realistic conditions and the incorporation of nectar as an important nutritional resource are lacking. We conducted a semi-field study in which *Bombus terrestris* colonies exclusively foraged on different IFVCNS sunflower hybrids (Duško, NS Konstantin, NS Romeo, and NS Kruna) with variable pollinator favourable traits. The nutritional potential of pollen and nectar were investigated quantitatively and hybrids were screened for pollen related genes. We found that the colonies that foraged on sunflower hybrids selected based on their nectar characteristics (Duško and NS Romeo), were significantly heavier two to three weeks after sunflower exposure. All hybrids had monosaccharide dominant nectar but NS Konstantin had significantly lower sugar mass per floret after 48 hours compared to 24 hours of undisrupted nectar accumulation, suggesting quicker nectar reabsorption. NS Kruna had significantly higher concentrations of free amino acids and fatty acids suggesting a potentially elevated availability for pollinators, that could be correlated to its increased drought resilience due to the presence of DYP12 gene. Between the hybrids, proteomic analysis revealed 4,365 differentially expressed proteins, of which 19 had differences greater than 16-fold responsible for metabolic processes and stress responses. These findings offer new insights that crop selection can improve pollinator colony development and reproduction. However, the difficult question remains on how the identified differences in floral resource quality between the hybrids realistically impacts pollinator health.

*Keywords Helianthus annuus, nectar, pollen, pollinator health, pollinator nutrition*

SB

## D11: What role does sunflower and cup plant pollen play for bumble bees?

*Welche Rolle spielen Sonnenblumen- und Silphiepollen für Hummeln?*

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### ABSTRACT

Species-specific differences in pollen foraging are increasingly recognised as a key factor shaping pollinator nutrition and health. Laboratory studies suggest that sunflower (*Helianthus annuus*) pollen may reduce pathogen loads in bumble bees, but such effects are only ecologically relevant if sunflower pollen is actually collected under field conditions. Field-based data on realised pollen intake remain scarce. Here, we quantified the pollen spectra of *Bombus terrestris* and honey bees (*Apis mellifera*) in agricultural landscapes within the FInAL project, focusing on sunflower (*H. annuus*) and cup plant (*Silphium perfoliatum*). Field investigations were conducted in Lower Saxony, Germany, during the flowering periods of sunflower (2024) and cup plant (2025). Pollen intake was assessed using species-specific pollen traps, including a newly developed, non-lethal 3D-printed trap optimised for *B. terrestris*. Trap-collected pollen was pooled per species and sampling date, identified to genus or family level, aggregated into functional pollen groups, and expressed as relative proportions. Honey bees consistently collected only small proportions of sunflower and cup plant pollen (generally <5%). In contrast, *B. terrestris* did not collect sunflower pollen despite extensive crop availability, while cup plant pollen contributed moderately to pollen intake in 2025 (approximately 3–8%). Bumble bee pollen spectra were strongly dominated by Solanaceae pollen, frequently exceeding 65–90% of total pollen loads. Our results show that laboratory-based hypotheses on health effects of sunflower pollen must be interpreted in the context of realised field exposure. Species-specific pollen intake data provide a necessary basis for evaluating the ecological relevance of crop pollen for bumble bee health. As the present study focused on a single sunflower cultivar, cultivar-specific differences in pollen attractiveness and utilisation cannot be excluded.

*Keywords* pollen intake, *Bombus terrestris*, *Apis mellifera*, sunflower and cup plant pollen, pollen traps

## D12: Investigations into the invertase activity of honeys with a low natural enzyme activity

*Untersuchungen zur Invertase Aktivität von Honigen mit einer geringen natürlichen Enzymaktivität*

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### ABSTRACT

The low natural enzyme activity of honeys of certain botanical origins is taken into account in the EU Honey Directive and other directives (e.g., D.I.B. Warenzeichensatzung, Bioland Richtlinie) with specific limits for diastase or invertase activity. This does not apply to blossom honeys with a significant proportion of nectar from sources with low natural enzyme activity. In a series of experiments (N = 46), we measured the invertase activity (DIN 10759; U/kg) of mixtures of black locust honeys (50.2 U/kg; DZ 17.1), feed samples (0 U/kg; DZ = 0, 7.3 U/kg; DZ = 7.0 and 38.6 U/kg; DZ = 8.3) and honeys with high enzyme activity (201.6 U/kg; DZ = 32.7). Diastase activity (Phadeba's method; DZ) was determined from the raw materials. The results show a dilution effect but provide no evidence of inhibition, inactivation, or other negative effects on invertase activity. We will continue to investigate effects on enzyme activity in further mixing/storage experiments.

*Keywords* invertase activity, natural low honey enzyme activity

## D13: Investigations of the honey pollen spectrum at a location in Hannover in spring 2025

*Untersuchungen des Honig-Pollenspektrums eines Standortes in Hannover im Frühjahr 2025*

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### ABSTRACT

The pollen spectrum of honey can be used to identify the nectar sources at a location that are relevant for honey bees. In the present study, the pollen spectrum of the early harvest in 2025 (N = 23, partial harvests from 10 May to 31 May 2025) of a group of colonies at a location in Hannover (Calenberger Neustadt) was analysed using light microscopic pollen analysis (DIN 10760). In addition, the electrical conductivity (DIN 10753) was determined for the partial harvests. Between 23 and 51 different pollen types were found in the partial harvests. Maple, forget-me-not, rapeseed, horse chestnut, pomaceous and stone fruit and willow characterised the partial harvests as mass forage sources. The respective attractiveness and yield could be mapped over the period examined. The electrical conductivities of the partial harvest quantities ranged between 0.31 and 0.59 mS/cm. The designation 'spring blossom honey' was recommended for all partial harvest quantities.

*Keywords* honey pollen spectrum, early harvested honey

## D14: A machine learning-derived surrogate model of BEEHAVE predicts how honey yield depends on weather and region across Germany

*Ein aus maschinellem Lernen abgeleitetes Surrogatmodell von BEEHAVE sagt voraus, wie der Honigertrag von Wetter und Region in ganz Deutschland abhängt*

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### ABSTRACT

Complex simulation models such as BEEHAVE help to investigate the effects of multiple on honey bees, such as weather, land use, and parasites. However, they usually run too slowly to be used for the whole of Germany, for example. To solve this problem, we ran BEEHAVE for a large number of weather scenarios and fed the results into machine learning models, which ultimately led to a so-called surrogate or meta-models that closely imitates BEEHAVE but runs much faster. We ran the BEEHAVE simulations with a new, faster implementation in the programming language GO and generated millions of synthetic weather scenarios using a newly developed weather generator called SynHr. We trained two metamodels using this data. When applied to historical weather data from all over Germany, both metamodels accurately reproduced BEEHAVE's annual honey yield forecasts. Our spatial and temporal simulations confirmed a positive linear relationship between total foraging time and total honey yield, which reaches its saturation limit at high foraging times. The worker bee population peaked at medium foraging times and then declined. Our work shows how weather affects the performance of bee colonies and demonstrates that surrogate modelling can effectively complement mechanistic models, enabling scalable digital twin applications for environmental research.

*Keywords* honey bees, BEEHAVE model, machine learning, honey production

## D15: From learning to action: enhancing motivation, knowledge, and engagement through a solitary bee monitoring with students as citizen scientists

*Vom Lernen zum Handeln: Motivation, Wissen und Engagement durch ein Wildbienenmonitoring mit Schülerinnen und Schülern als Citizen Scientists stärken*

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### ABSTRACT

Citizen science is considered a promising approach to bridging the gap between environmental awareness and behaviour (Bonney et al., 2009; BioScience). In this multi-year project, a teach-the-teacher format was implemented, in which teachers from all school types were trained as multipliers to engage students as citizen scientists in an international solitary bee monitoring program. The aim was to promote motivation, knowledge, and engagement (cf. Phillips et al., 2018; Citizen Science: Theory and Practice). Project data from 2024 and 2025 were analysed. Motivation was measured by long-term participation, knowledge by the accuracy of nest identification using a specially developed identification app that guides laypeople through questions, and engagement by self-initiated activities in solitary bee conservation. Each group received a trap nest providing insight into the nest and monitored the nests twice per year, supplemented by photo documentation. Of 38 participating schools, 74% took part in both monitorings. Of the 5,483 nesting tubes processed by the citizen scientists, 45% contained nests, while 55% remained empty. Species diversity varied by sites from one to eleven species, with an average of six species in 2025. Identification performance was high: nest contents were correctly determined in 77% of cases, bees and wasps were correctly distinguished in 69%, and assignment to species or genus was correct in 72%. The results indicate that hybrid training formats, individual feedback, and the social networking of multipliers through a virtual course and a messenger group supported high data quality, long-term participation, and engagement of students in conservation and research activities. These findings highlight the importance of scientific and didactic guidance.

*Keywords* citizen science, solitary bee monitoring, trap nests identification, wild bee identification app, intention–behaviour gap

## D16: Sustainable beekeeping – development of a resource-efficient beekeeping practice

*Nachhaltige Imkerei- Entwicklung einer ressourcenschonenden und effizienten Betriebsweise*

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### ABSTRACT

Rising operating and feed costs, climate change-induced changes in beekeeping conditions as well as diseases and parasites, in particular Varroa destructor, are confronting beekeepers with growing economic and ecological challenges. Against this background, the EIP-AGRI project 'Sustainable beekeeping - resource-conserving and efficient beekeeping for a sustainable future' aims to develop and optimise a time- and resource-efficient management practice that is adapted to the conditions of Hessian beekeeping. The innovative approach of the project lies in the combination of several beekeeping practices and their accompanying scientific investigation. These include early split colony formation with capped brood combs, omission of drone brood removal and reduced winter treatment against V. destructor. As part of the project, the novel EIP-management approach will be compared with existing individual operating methods of the participating beekeepers. Material, time and energy expenditure as well as honey quality and yield are recorded and then analysed from an ecological and economical business perspective. We create an individual climate footprint for each beekeeping operation. In addition, we prepare an economic analysis of the previous beekeeping practices in comparison to the novel EIP-Project management approach. The central objectives are to record and analyse economic key figures to increase the efficiency of resource use and to promote the exchange of experience and knowledge between the participating beekeepers and the beekeeping community. An intensive exchange within the seven EIP-project beekeeping operations and with the beekeeping community will strengthen a shared culture of learning and innovation. The results are disseminated via lectures, training courses and events and supplemented by citizen science approaches.

*Keywords* climate change, beekeeping management, climate footprint, business management analysis

## D17: Widespread neonicotinoid residues in commercial honey from Thailand

*Weitverbreitete Neonicotinoid-Rückstände in kommerziellem Honig aus Thailand*

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### ABSTRACT

Environmental contamination by pesticides, including neonicotinoid insecticides, is a major driver of biodiversity loss and poses risks to pollinators and human health. Honey integrates environmental exposure across large foraging areas and therefore represents a valuable sentinel matrix for monitoring pesticide contamination; however, systematic datasets from tropical regions remain scarce. Here, we report that neonicotinoid residues are widespread in commercial honey from Thailand, although occurring at concentrations associated with low acute risk to humans and bees. Residues of five neonicotinoid insecticides were quantified in 31 commercial honey samples produced by native (e.g., genus *Apis dorsata* and *Tetragonula laeviceps*) and introduced (*A. mellifera*) bee species using ultra-high-performance liquid chromatography coupled with tandem mass spectrometry (UHPLC-MS/MS). Neonicotinoids were detected in more than 60% of samples, frequently as mixtures, with concentrations reaching up to 3.11 ng g<sup>-1</sup>. Detection frequencies and residue levels did not differ significantly among bee species or sampling locations (all P's > 0.2). Detected residue levels were negligible with respect to human consumption. Although exposure assessments indicated low immediate risk for bees, concentrations overlapped with levels reported to cause sublethal effects under chronic exposure. To our knowledge, this is the first broad survey of neonicotinoid contamination in Thai honey, which reveals pervasive low-level exposure in a tropical agroecosystem and highlights the need for harmonized pesticide monitoring frameworks beyond temperate regions. Integrating honey-based surveillance into regulatory risk assessment could strengthen global evaluation of pesticide exposure and support more sustainable pest management and pollinator protection strategies.

*Keywords* biodiversity, pesticides, pollinators, pollution, sustainability

## D18: Automated hive scales for monitoring bee health in the German Bee Monitoring Programme (DeBiMo)

*Automatisierte Bienenstockwaagen zur Überwachung der Bienengesundheit im Deutschen Bienenmonitoringprogramm (DeBiMo)*

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### ABSTRACT

The German Bee Monitoring Programme (DeBiMo) commenced in 2004 with the primary focus of understanding drivers of winter colony losses. The programme monitors parameters relevant to honey bee health, such as pathogen prevalence in colonies and apiaries, pesticide exposure in bee bread as well as resource availability in the form of nectar and pollen sources found in honey and pollen diversity of bee bread. Up until now, foraging success has only been quantified as honey harvests reported by the participating beekeepers. To better understand how honey flow interacts with bee health, DeBiMo is being expanded in 2026 to include monitoring of honey flow using automated hive scales connected to weather stations. Each of the 120 participating apiaries, situated throughout Germany, will operate one hive scale. All hive scales are integrated into the existing nationwide hive-scale network TrachtNet (Otten and Berg, *Bienen & Natur*, 2018, 4:18-19). Hive scales in TrachtNet measure colony weight in 5-minute intervals with a resolution of 5-10 grams. Based on the 5 min weights, cumulative weights, i.e. the running total of weight gains (+) and losses (-) every 5 minutes, are calculated. Weight measurements are corrected for external weight increments, e.g. beekeeper-related actions. Thus, gains or losses based on corrected weights can be considered measures of bee activity. These new hive scales will enable DeBiMo to relate honey flow and weather parameters to pathogen prevalence and pollen diversity with the aim of gaining new insights into factors governing bee health.

*Keywords* hive scales, honey flow, climate, colony losses, monitoring

D19: Pollinator-friendly farming practices between implementation and incentive design: Conceptual insights based on empirical data from 12 countries.

*Bestäuberfreundliche Praktiken in der Landwirtschaft zwischen Umsetzung und Anreizsteuerung: Eine Konzeptualisierung auf Basis qualitativer empirischer Daten aus 12 Ländern.*

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## ABSTRACT

Specific agricultural practices beneficial for pollinators need to be implemented on a higher spatial scale and much more frequently if agricultural practices shall contribute to the halt of insect loss in western Europe. To investigate the mechanisms why the necessary change in practices has not yet been a result of such a huge incentive system as the EU common agricultural policy, we researched the expectations of the farming community, their motivation for, attitudes towards and experience with pollinator-friendly farming practices. Based on empirical qualitative data from two surveys among and 24 group discussions with members of a Thematic Network on Biodiversity-friendly farming in 11 EU countries and Switzerland (471 members, FarmBioNet 2022-2026, EU Horizon) we investigated, which practices were most important under which circumstances. We find that pesticide reduction, tree planting, planting and maintenance of hedgerows were widely known and perceived to have a positive impact on both biodiversity and the long-term farm economy, whereas flowering strips, bee scrapes and bee hotels were perceived to have a rather negative economic impact on the farm, while still being widely known for having positive effects on pollinator communities. We further evaluated i) the timing of practice implementation (which is in many cases the first step before participation in schemes), ii) perceived availability of incentives (in many contexts, practitioners are not aware of the range of available schemes, and advisors tend to have an only slightly higher overview, across Europe) and iii) the general understanding of the incentive system (34% of farmers reported to not understand the system). A text analysis of the group discussions maps knowledge gaps and needs. The results are used to conceptualise the relationship between practice implementation and incentive use.

*Keywords* biodiversity, pollinator-friendly farming, incentive design, agri-environmental schemes

## D20: Honey bees and wild bees – competitions and carrying capacity (BeeCom)

*Honigbienen vs. Wildbienen: Konkurrenzen und Carrying Capacity*

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### ABSTRACT

In recent years, there has been increasing discussion about the possibility of competition for food between honey bees and wild bees. Although primarily conducted in nature reserve areas, the discussion has now also reached the forestry sector. However, discussions there are almost always conducted without a reliable scientific data basis, as there is a complete lack of data on competition between these two groups in the forest. The BeeCom project is attempting to close this knowledge gap. In nine pairs of forest areas in Bavaria, each with a radius of 1 km (3.14 km<sup>2</sup>), the entire flowering flora and wild bee fauna was quantitatively recorded. Six strong honey bee colonies were then set up in one of the two forests in each pair from April to September. The aim is to determine the impact on the natural wild bee population. This will make it possible to determine the carrying capacity of the different forest types and to develop guidelines for the stocking density of bee colonies. The wild bee mapping for the current year (2026) is expected to provide crucial information on possible competition between these two pollinator groups. In April 2025, there are between 2 and 11 wild bee species (average 6.9 +/- 1.9) in the test areas, in July there are between 4 and 17 (12 +/- 3.4) and in August the number of species ranges between 1 and 14 (7.4 +/- 3.4). Across all locations, a total of 39 wild bee species were found in April, 49 in July and 38 in August. No clear pattern can be found regarding the dependence of wild bees on tree species composition in the 17 sample circles. There is only a slight tendency towards a higher wild bee species density and a slightly higher individual density in deciduous forests. Similarly, the evaluations to date have not revealed any clear correlation between the number of flowering plant species mapped and the wild bee species or wild bee densities.

*Keywords* wild bees, competition, carrying capacity

## E01: Stable equilibria of thelytoky and arrhenotoky in the Cape honey bee. A new model based on balancing selection.

*Gleichgewichte zwischen Thelytokie und Arrhenotokie in der Kapbiene. Ein neues Model, gestützt auf ausgleichende Selektion.*

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### ABSTRACT

Some workers of the Cape honey bee (*Apis mellifera capensis* Escholtz 1822) are able to produce diploid female offspring from unfertilized eggs via thelytokous parthenogenesis (thelytoky). This is in contrast to all other Honey bee subspecies, where workers usually can only produce haploid male offspring via arrhenotokous parthenogenesis (arrhenotoky). Thelytoky presents an evolutionary advantage on both the individual and the colony level. It enables workers to requeen the colony from worker laid eggs as well as to become social parasites and take over foreign colonies. Nonetheless, worker reproduction is polymorphic in workers of the Cape honey bee either thelytokous or arrhenotokous. Moreover, thelytoky has not been found to spread into populations of neighbouring subspecies other than through parasitic *A. m. capensis* workers. Previous population genetic models based on a single recessive allele causing thelytoky predicted either fixation or loss of the trait among workers, which stands in conflict with current evidence. I here present an alternative approach assuming that thelytoky is caused by a dominant allele, which reduces the fitness of homozygote females and hemizygous males. It shows that stable equilibria between thelytoky and arrhenotoky can exist over a vast range of the fitness parameter space. The model's predictions are in line with a wide range of empirical data on honey bee population genetics and provide a plausible explanation for the polymorphism within *A. m. capensis*.

*Keywords* Cape honey bee, thelytoky, balancing selection, model

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## E02: GMSP (Gentle Monitoring for Species Protection)

*SMART (Schonendes Monitoring für den ARTenschutz)*

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### ABSTRACT

Insects, especially pollinators, are absolutely crucial to maintaining natural biodiversity and human nutrition. For the first time in the history of the earth, wild insects are in massive decline. Evidence-based protective measures are therefore now appropriate, which require reliable monitoring data. Unfortunately, monitoring of wild insects is currently based on captures, which: 1) kills animals worthy of protection, 2) does not allow reliable statements, especially for social insects, since 10 animals can come from one or 10 colonies. Population genetics is therefore particularly essential for social insects to improve their protection. We are therefore proposing a paradigm shift for insect monitoring: collecting genetic data without killing animals or damaging exhibits, to lay new foundations for the protection of wild insects. The method will be established in the laboratory in Bern using bred bumble bees and exhibits from the museum. The first field applications will then be carried out on endangered bumble bee species in Switzerland. After adaptation, the established method can be applied to other species to support species protection for pollinators worldwide with careful monitoring.

*Keywords* bumble bee ecology, eDNA, monitoring, population genetics

## E03: ZUFI - sustainable future of the Bavarian beekeeping sector – survey among Bavarian beekeepers on queen rearing and breeding practices

*ZUFI - Zukunftsfähige Imkerei Bayern – Umfrage zur Arbeitsweise in der Königinnenvermehrung und -zucht in Imkereibetrieben*

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### ABSTRACT

German beekeeping sectors are characterized by over 96 percent small scale, non-professional apiarists, with an average of only seven colonies per beekeeper (EU average: 27). An anonymized online survey (39 open and closed questions sent to over 200 registered participants) of mainly Bavarian beekeepers was designed, carried out, and statistically analysed. It focused on the process of queen breeding and rearing in order to identify the distribution of business sizes (number of queens reared per beekeeper) and the breeding objectives pursued, including their weighting and prioritization. Following the entire rearing and breeding process, questions were asked about methods applied in practice in order to identify deviations between actual breeding practice and the generally accepted standards of good professional practice. Final questions addressed the acquisition and sources of breeding know how during the participants' careers. Results showed that, as in beekeeping in general, queen breeding and rearing are dominated by small scale operations, often part time. Participating queen breeders mainly pursue breeding goals closely aligned with the index weights defined in the beebreed.eu database. Operational methods vary widely in rearing techniques, mating sites and methods, approaches to performance testing, and channels for selling and distributing mated queens. In practice, some methods balance scientifically recommended animal welfare aspects with economic optimization (e.g., number of series per starter colony). With increasing experience over their careers, queen breeders benefit more from contacts with seasoned colleagues and less from formal training. Furthermore, experienced beekeepers are able to leverage statistical data and tools far more than their less experienced counterparts. Results can be used to further improve training programs for beginners and professionals in practical queen breeding.

*Keywords* beekeeping processes and practices, bee breeding, citizen science

## E04: Ciao Varroa – Genome-wide association studies in honey bees (*Apis mellifera* spp.) with regard to Varroa resistance breeding

*Ciao Varroa – Genomweite Assoziationsstudien bei Honigbienen (Apis mellifera spp.) in Hinblick auf die Varroaresistenzzucht*

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### ABSTRACT

The Varroa mite (*Varroa destructor*) poses one of the greatest threats to the health of the western honey bee (*Apis mellifera*) and, if left untreated, often leads to the collapse of entire bee colonies (Traynor et al. (2020), Trends Parasitol. 36: 592–606). While some populations show increased tolerance to the parasite, the underlying genetic mechanisms are still not fully understood (Mondet et al. (2020), Int. J. Parasitol. 50: 433–447). Genetic markers identified to date can only be transferred to other populations or subspecies to a limited extent (Lefebvre et al. (2024), Insects 15: 419), suggesting that similar resistance traits are likely driven by different polygenic architectures (Eynard et al. (2025), Mol. Ecol. 34, e17637). The aim of this project is to identify and validate genetic markers associated with Varroa resistance in order to better characterise the genetic basis of resistance-conferring behaviours in a Buckfast bee population in Saxony. Initial screening using established markers resulted in low predictive power, highlighting the need for a genome-wide approach to discover novel resistance-associated loci. The study focuses on the traits suppressed mite reproduction (SMR) and recapping. The samples, pooled worker pupae, and phenotype data originate from infestation analyses conducted by the Saxony Association for Varroa Resistance Breeding (Landesverband Sachsen für Varroaresistenzzucht e.V.). Sample selection is based on pedigree information and detailed infestation assessments, to ensure a well-characterised and balanced dataset. The genome-wide association analysis aims to identify both known and novel genetic markers for Varroa resistance. The results may provide new insights into the genetic architecture of social immunity mechanisms in honey bees and lay the foundation for the development of genetic tests to support sustainable and accelerated Varroa resistance breeding.

*Keywords* *Apis mellifera*, varroa, genomics, breeding

SB

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