ARBEITSGEMEINSCHAFT DER INSTITUTE FÜR BIENENFORSCHUNG E.V.

Landwirtschaftskammer Nordrhein-Westfalen

Tagungsband

71. Jahrestagung der Arbeitsgemeinschaft der Institute für Bienenforschung e.V.

Fürstenberghaus der Universität Münster

19. – 21. März 2024

Inhalt

Vortragsprogramm

ab 11:00	**Anmeldung im Tagungsbüro im Foyer des Fürstenberghauses** Posterbeiträge platzieren – Foyer EG, Vorträge aufspielen – Hörsaal 1. OG		
13:00	**Eröffnung – Begrüßung - Grußworte** Dr. Marina Meixner, Vorsitzende der Arbeitsgemeinschaft Dr. Marika Harz, Landwirtschaftskammer Nordrhein-Westfalen Karl Werring, Präsident der Landwirtschaftskammer Nordrhein-Westfalen		
13:30	**Hauptvortrag** **Genomische Selektion bei der Honigbiene –** **Ein Schritt zur nachhaltigen Absicherung der Imkerei oder akademisches Wunschdenken?** **Gertje Petersen**, LAVES Institut für Bienenkunde, Celle Chair: Marika Harz		
	Session Bestäubung & Bienenprodukte Chair: Saskia Wöhl		
14:30	**Welche Pflanzungen eigenen sich zur Förderung von Bestäubern? Ein Attraktivitätsvergleich von heimischen Wildstauden und nah verwandten Kultursorten** **Michael Glück**, Landesanstalt für Bienenkunde, Stuttgart	**N**	V1
14:45	**Optimized seed mixtures supporting wild bees and honeybees in agricultural landscapes** **André Krahner**, JKI - Institut für Bienenschutz, Braunschweig		V2
15:00	**Image-based multispectral flow cytometry – A new approach for fast and efficient pollen analysis** **Fransiska Walther**, Helmholtz-Zentrum für Umweltforschung, Leipzig	**N**	V3
15:15	**Quantitation of pesticides in pollen and bee bread collected by honey bees and the botanical origin of pesticide-contaminated pollen** **Christina Kast**, Swiss Bee Research Center - Agroscope, Bern		V4
15:30	Kaffeepause im Foyer		
	Session Ökologie Chair: Robert Paxton		
16:00	**Observations on the effects of parasites, nest depredators and landscape context on the winter survival of feral honeybee colonies in German forests** **Patrick L. Kohl,** Universität Würzburg	**N**	V5
16:15	**Population trends of wild-living honeybees (Apis mellifera) in Europe: a call for research and conservation action** **Benjamin Rutschmann,** Universität Würzburg	**N**	V6
16:30	**Bienenwald Hessen – Ein Wald für Bienen / Bienen für den Wald** **Martin Gabel,** LLH- Bieneninstitut Kirchhain		V7
16:45	**Big Data im Honigbienen-Monitoring: Modellierung und Vorhersagen aus umfassenden Datensätzen mittels State-of-the-art Methoden der Zeitreihenanalyse** **Oleg Lewkowski**, JKI - Institut für Bienenschutz, Braunschweig		V8
17:00	**TrachtNet: Long-term recording of food availability for honeybees in space and time** **Christoph Otten**, DLR – Fachzentrum Bienen und Imkerei, Mayen		V9

Fortsetzung: Dienstag, 19.03.2024

17:15	**Can hive weight from monitoring campaigns (TRACHTNET) be predicted by land cover products and weather data?** **Jürgen Groeneveld,** Helmholtz-Zentrum für Umweltforschung, Leipzig		V10
17:30	**The role of host phylogeny, foraging niche and parasites on bee virome dynamics** **Vincent Doublet**, Universität Ulm		V11
17:45	Kaffeepause im Foyer		
	Session Physiologie & Verhalten Chair: Annely Brandt		
18:15	**Acoustic monitoring allows detection of honeybee queen presence and absence** **Martin von Bergen,** Helmholtz-Zentrum für Umweltforschung, Leipzig		V12
18:30	**Effects of Queen Excluders on the Colony Dynamics of Honeybees (Apis mellifera L.) under biodynamic management** **Jana Bundschuh,** Forschungsring e.V., Darmstadt		V13
18:45	**Vitalbiene – Effects of innovative beekeeping on performance and vitality of *Apis mellifera* L.** **Lena Frank**, LLH- Bieneninstitut Kirchhain	**N**	V14
circa 19:00	Ende des ersten Tages		

Mittwoch, 20.03.2024

09:00	**Grußworte** Torsten Ellmann, Präsident des Deutschen Imkerbundes		
	Session Genetik & Zucht Chair: Stefan Berg		
09:15	**Longterm genomic consequences of thelytoky in the Cape Honeybee** *Apis mellifera capensis* **Johanna T. Pieplow**, Stiftung Leibniz-Institut zur Analyse des Biodiversitätswandels, Bonn	N	V15
09:30	**Simulationsstudien zur Optimierung von Besamungsstrategien in der Bienenzucht** **Manuel Du,** Länderinstitut für Bienenkunde, Hohen Neuendorf		V16
09:45	**Reliability of the mating station Erbeskopf and the genetic background of foreign drones** **Richard Bernstein,** Länderinstitut für Bienenkunde, Hohen Neuendorf		V17
	Session Bienenschutz & Pflanzenschutz I Chair: Ricarda Scheiner		
10:00	**What are the transfer routes of fungicide residues from field to the hive?** <u>Karoline Wueppenhorst</u>, JKI - Institut für Bienenschutz, Braunschweig	N	V18
10:15	**Feed laced with biofungicide copper induces decreased food consumption, increased mortality and brood loss and leads to reduced learning ability of honey bees (*Apis mellifera*)** **Elsa Friedrich**, Landesanstalt für Bienenkunde, Stuttgart	N	V19
10:30	**Der Einfluss von Pflanzenschutzmittel-Mischungen auf die Flugaktivität von Honigbienen** **Antonia Schuhmann, Universität Würzburg**	N	V20
10:45	**Untersuchung von Effekten kombinierter Pflanzenschutzmittel während der Larvenentwicklung von *Apis mellifera*** **Sarah Manzer**, Universität Würzburg	N	V21
11:00	Kaffeepause im Foyer		
	Session Bienenschutz und Pflanzenschutz II Chair: Silvio Erler		
11:30	**In-hive behavioural responses of honeybees (*Apis mellifera*) after exposure to different plant protection products** **Cassandra Uthoff**, Helmholtz-Zentrum für Umweltforschung, Leipzig	N	V22
11:45	**Können Pflanzenschutzmittel Flügelasymmetrien bei Honigbienen verursachen?** **Monika Weber,** JKI - Institut für Bienenschutz, Braunschweig	N	V23
12:00	**Radiofrequency electromagnetic fields (RF-EMF): Do they negatively affect honey bees and other pollinators?** **Manuel Treder,** Landesanstalt für Bienenkunde, Stuttgart	N	V24
12:15	Mittagspause im Foyer		

Fortsetzung: Mittwoch, 20.03.2024

13:00–15:00	**Postersession**
ab 15:30	**Rahmenprogramm / Führungen** • Münsteraner KrimiTour: Tatort, Wilsberg und reale Fälle Treffpunkt: Rathausinnenhof/Platz des Westfälischen Friedens (an der Chillida-Skulptur) um <u>15:30</u> • Altstadtführung Treffpunkt: Rathausinnenhof/Platz des Westfälischen Friedens (an der Chillida-Skulptur) um <u>15:30</u> • Zooführung Treffpunkt: Eingang Allwetterzoo, Sentruper Straße 315, 48161 Münster um <u>15:30</u> ÖPNV: Haltestelle Aegidiimarkt B1/LWL-Museum mit Stadtbuslinie 14 bis Haltestelle „Zoo/LWL-Naturkundemuseum"
ab 19:00 bis 23:00	**Rahmenprogramm / gemeinsames Abendessen** Treffpunkt: Hafenkäserei, Am Mittelhafen 20, 48155 Münster um <u>19:00</u> https://hafenkaeserei.de/ Aus der Innenstadt zu Fuß in 25 bis 30 Minuten erreichbar. Danach stehen im Hafenviertel viele Lokalitäten zum späten Einkehren zur Verfügung ☺.

Donnerstag, 21.03.2024

	Session Bienenpathologie Chair: Sebastian Gisder		
09:15	**Auswirkungen der herkömmlichen und der innovativen Bienenhaltung auf die Gesundheit von Honigbienen,** **Lioba Hilsmann**, Universität Würzburg	**N**	V25
09:30	**Die Verbreitungsphase spielt eine entscheidende Rolle für die erfolgreiche Vermehrung junger Varroamilben (*Varroa destructor*)** **Lina Sprau**, Landesanstalt für Bienenkunde, Stuttgart	**N**	V26
09:45	***Varroa destructor* estimation of infestation during the bee season using three different methods** **Leon Reinhold,** Landesanstalt für Bienenkunde, Stuttgart	**N**	V27
10:00	**Evaluating BQCV and DWV-B spillover between honey bees and bumble bees across the flight season** **Matthew Wallace**, Queen's University Belfast	**N**	V28
10:15	**Flagella of *Paenibacillus larvae* – influence on multicellular behaviour and virulence** **Josefine Göbel**, Länderinstitut für Bienenkunde, Hohen Neuendorf	**N**	V29
10:30	Kaffeepause im Foyer		
	Session Bienenpathologie Chair: Hammes Beims		
11:15	**Validation of a newly developed American foulbrood detecting fast test tool with genotype differentiation using field samples** **Sandra Ehrenberg,** Friedrich-Loeffler-Institut Greifswald		V30
11:30	**Selective molecular detection of *Paenibacillus larvae* spores** **Daniela Sint,** Universität Insbruck		V31
11:45	**Is deformed wing virus (DWV) genotype B replacing DWV genotype A across the world** **Robert Paxton**, Martin-Luther Universität Halle-Wittenberg		V32
12:00	**Observing the displacement of *Nosema apis* by *Nosema ceranae* in the *Apis mellifera* population in north-eastern Germany** **Sebastian Gisder,** Länderinstitut für Bienenkunde, Hohen Neuendorf		V33
12:15	**Verleihung der Evenius-Preise für die besten Nachwuchswissenschaftler:innen** **Verabschiedung**		
ab 13:30	Mitgliederversammlung (nicht öffentlich)		

Posterpräsentationen

N: Nachwuchswissenschaftler:in

Abstracts der Vorträge

V1 Welche Pflanzungen eigenen sich zur Förderung von Bestäubern? Ein Attraktivitätsvergleich von heimischen Wildstauden und nah verwandten Kultursorten

What plants are better for promoting pollinators? A comparison of native perennials and their closely related cultivars

Michael Glück[1], Kathrin Scharsich[2], Vera Joedecke[2], Jaspar Lütke[1], Kirsten Traynor[1], Ute Ruttensperger[2], Manuel Treder[1]

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Pollinator-friendly plantings play an important role in promoting pollinators in urban areas by creating a suitable food supply. But must these plants be native to the region to support the endemic pollinator populations? The value of non-autochthonous perennial plantings for various pollinators is still debated, as currently it remains unclear if the attractiveness of closely related cultivated forms and hybrids differ from the unselected, native plant.

We investigated the attractiveness of 11 different native plant species and their closely related cultivated forms in Heidelberg, Germany over two years. For each plant species, four different perennial variants were examined during our pollinator observations, performed every two weeks: I) the autochthonous (regional) perennial, II) the native perennial, III) a cultivar, and IV) a hybrid variant. On a total of 120 plant pots, each planted with three identical plants, we were able to perform 1,107 two-minute observations, recording over 2,100 pollinators in total. In addition to those quantitative observations, we also regularly documented wild bee species on the individual perennial variants by catching and identifying them to the species level.

Our preliminary results showed specific differences in the attractiveness of individual plant variants for different pollinator groups, whereas the number of honey bee visits did not differ between the individual plant variants. In addition, the overall pollinator visitation rates showed major differences between the respective months and years. The yet to be completed bee species analyses and the continuing pollinator observations will show whether cultivated forms of perennials are also visited by specialized wild bee species and will further improve our dataset about the attractiveness of different perennial variants over a longer trial period. This work is funded by the Ministry of Food, Rural Affairs and Consumer Protection Baden-Württemberg, Germany.

Keywords: pollinator-friendly perennials, wild bees, flower visitation rates, pollinators

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V2 Optimized seed mixtures supporting wild bees and honeybees in agricultural landscapes

Optimierte Blühmischungen zur Förderung von Wild- und Honigbienen in der Agrarlandschaft

André Krahner, Felix Klaus, Anke C. Dietzsch

Julius Kühn-Institut (JKI) – Bundesforschungsinstitut für Kulturpflanzen, Institut für Bienenschutz

Keywords: flower strips, honeybees, wild bees, agriculture

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V3 Image-based multispectral flow cytometry – A new approach for fast and efficient pollen analysis

Bildbasierte multispektrale Durchflusszytometrie - ein neuer Ansatz für die schnelle und effiziente Pollenanalyse

<u>Franziska Walther</u>, Carolin Plos, Till J. Deilmann, Annalena K. Lenk, Christine Römermann, Elsa Friedrich, Annette Schroeder, Selina Campbell, Martina Janke, Demetra Rakosy, Stan Harpole, Martin Hofmann, Thomas Hornick, Susanne Dunker

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Manual microscopic analyses are traditionally the gold standard for various palynological applications. But the trend is towards automated, database-driven pollen analyses that are expected to be cheaper, less time-consuming and allow better reproducibility than the traditional microscope-based methods. Such a new automated method is multispectral imaging flow cytometry in combination with machine learning. It enables microscopic brightfield and fluorescence images and a variety of pollen traits (e.g. diameter, fluorescence or shape) of pollen to be recorded quickly. Based on this data, a convolutional neural network classifier can be trained, which then allows pollen identification based on pollen pictures. This method was tested for pollen identification in various (honey)bee-relevant matrices such as honey or pollen baskets. In addition, intraspecific pollen trait variation was studied to better understand the amount of variation needed to robustly identify pollen with this method. In this presentation, I would like to introduce this novel method with a focus on the identification of insect-pollinated plant pollen. Pollen analysis in honey and in pollen baskets will be presented as application examples. Moreover, I will summarize a pollen trait variation study, in which we found significant spatial as well as temporal variation for at least one pollen trait of four plant species (*Achillea millefolium*, *Lamium album*, *Lathyrus vernus*, *Lotus corniculatus*). All in all, pollen analysis using image-based multispectral flow cytometry is a promising application for Palynology.

Keywords: flow cytometry, pollen analysis, machine learning, honey, intraspecific variation

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V4 Quantitation of pesticides in pollen and bee bread collected by honey bees and the botanical origin of pesticide-contaminated pollen

Quantifizierung von Pestiziden in Pollen und Bienenbrot von Honigbienen und die Bestimmung der botanischen Herkunft von pestizidbelastetem Pollen

Christina Kast, Marion Fracheboud, Emmanuel Schaad, Benoît Droz

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Honey bees can introduce pesticides into their colonies while foraging in an agricultural environment. To investigate pesticide contamination, pollen and bee bread samples were taken every fortnight from April to August 2022 from five bee colonies in an agricultural region of Switzerland. The samples were analysed individually. Ultra-high performance liquid chromatography and mass spectroscopy allowed the quantitation of 50 pesticides. The individual pollen pellets of some pollen samples that showed high pesticide levels were separated into different fractions according to their colours. The pesticide concentrations were then determined again for each fraction. The botanical origin of the pollen pellets was determined by microscopic analysis to identify the type of pollen related to pesticide contamination.

Twenty-three pesticides were quantified in pollen and 26 in bee bread. The highest insecticide concentrations in the individual samples were measured for thiacloprid (70 µg/kg in pollen and 37 µg/kg in bee bread) and acetamiprid (48 µg/kg in pollen and 16 µg/kg in bee bread). The levels for fungicides ranged up to 2213 and 1964 µg/kg (cyprodinil) in the analysed pollen and bee bread samples and the levels for herbicides up to 72 and 38 µg/kg (prosulfocarb). Thiacloprid could be assigned to oilseed rape pollen collected by bees during the flowering period of the oilseed rape crops (5th April to 15th May 2022) near the beehives, while several other pesticides originated from wild plants, such as for example plantain and clover. These results show the risk of pesticide exposure of honey bees from non-cultivated, wild plants growing near cultivated area.

Keywords: honey bees, pollen, bee bread, pesticides, oilseed rape

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Ökologie
Dienstag 19.03.2024 von 16:00 – 17:45

V5 Observations on the effects of parasites, nest depredators and landscape context on the winter survival of feral honeybee colonies in German forests

Beobachtungen zu den Effekten von Parasiten, Nestplünderern und des Landschaftskontexts auf das Winterüberleben verwilderter Honigbienenvölker in deutschen Wäldern

Patrick L. Kohl[1,5], Benjamin Rutschmann[1], Luis G. Sikora[2], Norbert Wimmer[3], Volker Zahner[4], Paul D'Alvise[5,6], Martin Hasselmann[5], Ingolf Steffan-Dewenter[1]

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Keywords: wild honeybees, survival rates, tree cavities, landscape composition, bee conservation

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V6 Population trends of wild-living honeybees (Apis mellifera) in Europe: a call for research and conservation action

Populationstrends wild lebender Honigbienen (Apis mellifera) in Europa: ein Appell für Forschung und Schutzmaßnahmen

Benjamin Rutschmann[1] & Patrick L. Kohl [1, 2]

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Keywords: wild honeybees, survival rates, bee conservation, limiting factors

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V7 Bienenwald Hessen – Ein Wald für Bienen / Bienen für den Wald

Bienenwald Hessen – Trees for Bees / Bees for Trees

Martin Gabel[1], Alix Roosen[2], Katharina Kröcker[2], Oliver Diehl[3], Jörg Obergfell[4], Hannes Schulz[5], Tim Treis[6] & Judith Treis[2]

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Tremendous negative effects of climate change and diversity loss are threatening our society. Fragile forest ecosystems and pollinator communities are particularly jeopardised. Food and timber production are thus gaining increasing attention. However, differing primary interests often lead to land-use conflicts between the production of food and raw materials, as well as the conservation of pollinator driven ecosystem functions. We therefore elaborate approaches of multipurpose forest use to bridge land-use interests and belay ecosystem services. Many private forest owners recently lost their spruce plantations due to drought and bark beetle infestation. Three of such forest plots were partly sown with perennials and restocked with trees adapted to semi-arid conditions in 2022. Besides their potential for log production, most of this tree species offer rich forage for pollinators. In addition, they open up the potential of non-timber forest products as additional income (e.g., honey). We compare this so-called "Bienenwald" sites to young and old grown reference plots managed in common forestry practice. Wild bee communities and honeybee colonies are monitored regarding their development and resource use to assess the respective habitats. In 2023, the number of wild bees catched by netting was significantly affected by plot type ($F(2, 2) = 8.57$, $p = 0.02$) with the highest abundance ($n = 309$) on Bienenwald plots compared to the old reference ($n = 111$, Tukey: $p < 0.05$) and young reference ($n = 180$, n.s.). Adult honeybee population was affected by an interaction of plot type and time of season (lmm: $\chi2 = 29.35$, $p = 0.02$, $df = 16$). At the end of June, it proved to be highest on Bienenwald plots compared to both reference types (Tukey $p < 0.05$, respectively). In addition, commercial beekeeping operations gather honey harvest data in full-grown forests of the respective tree species (e.g., acacia: 49.2/51.3, sweet chestnut: 20.6/20.3 kg/colony in 2022/2023, respectively).

Keywords: pollinators, non-timber forest products, reforestation, bee diversity, floral resources

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V8 Big Data im Honigbienen-Monitoring: Modellierung und Vorhersagen aus umfassenden Datensätzen mittels State-of-the-art Methoden der Zeitreihenanalyse

Big data in honeybee monitoring: Modeling and prediction from extensive datasets with state-of the-art time series analysis methods

Oleg Lewkowski, Wiebke Kämper, Abdulrahim Alkassab, Henri Greil, André Krahner, Jens Pistorius

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Keywords: Trendmonitoring, MonViA, Zeitreihenanalyse, Honigbienenvitalität

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V9 TrachtNet: long-term recording of food availability for honeybees in space and time

Das TrachtNet: Langzeiterfassung der Nahrungsverfügbarkeit für Honigbienen in Raum und Zeit

Christoph Otten und Jes Johannesen

DLR Fachzentrum für Bienen und Imkerei, Im Bannen 38, D-56727 Mayen

The availability of food influences the vitality of all living organisms. Corresponding information for honeybees can contribute to a better understanding of their condition and behaviour.
TrachtNet is a network of automated, high-resolution electronic hive-scales. *TrachtNet* hive-scales record food input and thus food availability for honeybees, but they also gather information on food consumption in times without nectar flow. With the help of short 5min measuring intervals, beekeeping interventions are detected and data corrections can be made to give estimates of bee-related weight-changes of colonies. Summarized as daily weight changes, *TrachtNet* offers the possibility to calculate average weight changes for clusters of hive-scales. In this way, *TrachtNet* allows for a comparison of food intake and consumption between single hive-scales, geographic regions and years. Today, almost 700 *TrachtNet* hive-scales located in diverse landscapes are collecting data in Germany and neighbouring countries.
By recording the daily weight changes throughout the year, it is possible to document foraging and collecting phases, including the beginning and end of honey flow, absolute honey flow values and to relate them to site parameters and climate impacts. For example, the magnitude of the summer harvest has a significant influence on the winter mortality of honeybee colonies, whereby good harvests have a positive effect.

Keywords: Apis mellifera, recording food availability

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V 10 Can hive weight from monitoring campaigns (TRACHTNET) be predicted by land cover products and weather data?

Können Bienenstockgewichte aus Beobachtungskampagnen (TRACHTNET) durch Landbedeckungsprodukte und Wetterdaten vorhergesagt werden?

Jürgen Groeneveld, Anna Wendt, Volker Grimm

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Honey bee colony performance depends among many other factors crucially on spatial and temporal availability of nectar and pollen resources in the landscape and weather conditions. To test this dependency, we investigate here whether we can predict hive weights as measured by the TRACHTNET campaign with land cover and weather data. For the land cover data, we use a land cover classification map by Preidl et al. (2020, Remote Sensing of Environment 240) that is based on Sentinel-2A data. The map has a resolution of 20 m, is mapping 19 land cover classes (e.g. oilseed rape, maize, forest) and is covering all of Germany. We will present two types of analysis: 1) using a random forest (machine learning) we model daily changes in the hive weights (as a proxy for changes in honey reserves) depending on land cover and weather. 2) We use general linear models to model indicators of time series of cumulated daily changes in the weight of the hive depending on land cover and weather. In the first study using machine learning techniques we can show that daily changes in hive weight were mainly driven by temperature and daily sun shine hours. For the second study we identified several useful indicators such as the day of the year when hive weight starts to increase and the day of the year when the maximum cumulated hive weight has been reached. In the second analysis weather was less important and pairwise interactions of land cover types became more important. However, some hypothesis, e.g. that oilseed rape cover will predict the day of the year when hive weight starts to increase, could not be confirmed by our study. This clearly highlights that additional factors such as colony size and colony health play an important role.

Keywords: TRACHTNET, land cover, weather, random forests, honey flow

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V 11 Der Einfluss der Phylogenie des Wirts, der Nahrungsnische und der Parasiten auf die Dynamik des Bienenviroms

The role of host phylogeny, foraging niche and parasites on bee virome dynamics

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Keywords: Honeybees / Bumblebees / Viruses / Transmission / Networks

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V 12 Acoustic monitoring allows detection of honeybee queen presence and absence

Akustisches Monitoring kann die An- und Abwesenheit der Honigbienenkönigin detektieren

Cassandra Uthoff[1], Masun Nabhan Homsi[1], Victor Jose Garcia Martinez[2], Jacek Nowak[2], Michel Rennert[2], Nico Jehmlich[1], Michael Beckmann[3], Paul Remmler[4], Jan Bumberger [4,9], Michael Hardt [5,6], Jens Pistorius[7], Sylvo Jäger [2#], Martin von Bergen [1,8,9#]

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During the honeybee season, queen presence is vital to ensure the functionality of the colony, and thus, a high rate of honey production. Manual control of a colony results in a high workload for beekeepers and can cause harm and stress to workers and queens. Thus, non-invasive technical solutions that detect presence of the queen without disturbing the beehive can potentially prevent issues resulting from visual inspection. In this study, we established an acoustic monitoring system inside beehives to classify queen absence after removal. An AudioMoth© microphone was installed in each hive and programmed to record 15 seconds of data every 15 minutes in the range of 20-16,000 Hz. In total, 3528 signals from three hives were initially segmented into fixed sliding windows. Subsequently, 383 features are extracted from each window. Finally, a Random Forest algorithm was trained and several experiments were conducted to detect the presence of the queen during various time periods throughout the day. The best proposed model achieved an F-score of 85% for detecting the absence of the queen and 83% for detecting her presence during the signals recorded in the morning (1 am to 5 am). In addition, we mounted accelerometer sensors (TELID®780, Micro-Sensys Gmb, Germany) to one frame per hive, which recorded data for 30 seconds every 15 minutes with a frequency range of 2 – 1,600 Hz. Data analysis was performed by extracting 94 features from each file and passing them through an optimised random forest machine learning algorithm. Using only data from 12 am to 5 am and the top ten features we achieved an F-score of 91% for queen absence and 96% for queen presence classification. Overall, the results show that acoustic and vibration signals can provide reliable information about queen presence. Larger sample numbers and ensemble methods that incorporate signal data from either accelerometers or microphones are required to integrate these approaches into precision beekeeping successfully.

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V 13 Effects of Queen Excluders on the Colony Dynamics of Honeybees (*Apis mellifera* L.) under biodynamic management

Effekte des Absperrgitters auf die Volksdynamik von Honigbienenvölkern in der biodynamischen Imkerei

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The evaluation of beekeeping management practices (BMPs) is important for beekeepers worldwide because their choice affects health and survival of managed honeybee (*A. mellifera* L.) colonies and touches ethical and economic questions. This study focusses on queen excluders, a common hive addition in contemporary beekeeping. Its impacts are controversially discussed but have not been studied scientifically yet. Within a four-year participatory on-farm experiment, we assessed effects on colony dynamics in 64 hives in 8 apiaries during one season in Germany using the Liebefeld estimation method. We found no significant deviation for parameters of colony dynamics (number of adult bees, brood cells, food and pollen storage) between hives managed with and without queen excluders. A qualitative decision-making tool (Pugh decision matrix) facilitated concept selection only for specific beekeepers. Despite these robust results queen excluders may influence other important areas like honey quality and work organization.

Keywords: organic beekeeping, beekeeping management practices, colony dynamics, honeybees, queen excluder

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V 14 Vitalbiene – Effects of innovative beekeeping on performance and vitality of *Apis mellifera* L.

Vitalbiene – Auswirkungen innovativer Bienenhaltung auf die Leistung und Vitalität von *Apis mellifera* L.

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Keywords: *Varroa destructor* ; summer brood interruption ; honey bee health

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V 15 Longterm genomic consequences of thelytoky in the Cape Honeybee *Apis mellifera capensis*

Genetische Langzeitfolgen thelytoker Parthenogenese in der Kap-Honigbiene *Apis mellifera capensis*

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The Cape Honeybee *Apis mellifera capensis* is the southernmost subspecies of the Western Honeybee, native to the fynbos biome in the very south of South Africa. In contrast to all other *A. m.* lineages most Cape Honeybee workers possess the ability to produce female offspring from unfertilized eggs via thelytoky with central fusion, a form of asexual reproduction where

diploidy is restored by the fusion of meiotic products.

This mode of reproduction has numerous implications for worker behaviour and colony fitness such as the ability to re-queen the colony from worker-laid eggs but also the potential of thelytokous workers to parasitise on foreign colonies. On a genetic level thelytoky with central fusion is predicted to result in a loss of heterozygosity (LOH) over time, and therefore in a reduction of genetic variation and fitness. Despite this detrimental effect a permanently thelytokous parasitic lineage of Cape bees, called the "clones", is persisting since more than 30 years, while large fractions of its genome preserved heterozygosity.

Using whole genome sequence data from individuals collected over a period of 16 years between 2006 and 2022, we aim to assess the extent and progression of LOH over time in the clones and map genomic regions that retained heterozygosity. They may act as a barrier against the progression of LOH, e.g. due to selection against homozygotes, and may be indicative of genetic variants that are crucial for the manifestation of the unique clone phenotype.

Keywords: Cape Honeybee, thelytoky, genetic diversity, heterozygosity, social parasitism

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V16 Simulationsstudien zur Optimierung von Besamungsstrategien in der Bienenzucht

Simulation studies to optimize insemination strategies in honeybee breeding

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Honeybee breeding relies on selecting genetically superior individuals for reproduction. New queens must be chosen from good colonies, and have to mate fine drones. The latter can be ensured by instrumental insemination. The control gained by instrumental insemination raises questions of optimization potential. Here, we examine how many drones should be used per insemination and how to distribute drones to virgin queens.

We compared different insemination strategies in computer simulations. First, we compared single colony insemination (SCI) and pooled semen insemination (PSI) as two extreme ends in the strategy spectrum. In both cases, we chose the same number of colonies as drone producers. But while in SCI all drones for a queen came from the same colony, in PSI drone semen from all selected colonies was mixed and queens were inseminated from the resulting sperm pool. After 70 years of breeding, SCI schemes led to up to 44% higher genetic gain than PSI schemes - alongside higher inbreeding rates. Differences were small for phenotype selection but large when selecting for estimated breeding values. By mixing semen, much pedigree information was lost and breeding value estimations were heavily biased. Thus, for current pedigree-based genetic evaluation methods, PSI is not a compatible strategy.

We then focused on SCI, varying the number of drones per insemination. We saw clear differences between single drone insemination (SDI) and multi drone insemination (MDI). SDI led to up to 14% higher genetic gain at up to 30% higher inbreeding rates. Comparing MDI with different drone numbers yielded only small, mostly insignificant differences. For general breeding purposes, we thus recommend a sufficient drone number to fill the queen's spermatheca. In specialized settings, SDI can be an interesting alternative.

Keywords: instrumental insemination, inbreeding, genetic gain, pooled semen

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V 17 Reliability of the mating station Erbeskopf and the genetic background of foreign drones

Sicherheit der Belegstelle Erbeskopf und der genetische Hintergrung der Fremddrohnen

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Mating stations are a proven way to ensure adequate mating control in Germany. To determine the proportion of foreign drones genomic analyses are necessary. Genotyping with a SNP chip can additionally inform us about the origin of the foreign drones and their genetic background.

At mating station Erbeskopf in 2023, 100 workers from 20 colonies and all 19 drone producing queens (DPQs) were genotyped on a SNP chip comprising 70'814 markers. To estimate the proportion of foreign drones at the mating site required several steps. The first step was to determine which workers descend from which DPQ, or whether they descend from a foreign drone, based on the number of opposing homozygotes between the genotypes of the worker and the DPQs. In the second step, the super siblings were then identified among each group of workers sampled from the same hive, to determine the number of patrilines. With a probability of 95%, the reliability of the mating station is at least 58% and at most 77%. The genomic relationships among the workers across different colonies were evaluated. The workers sired by the DPQs separated from workers sired by foreign drones. The worker genotypes were compared compared with 568 samples of various subspecies from 15 European countries, but the closest relatives were German bees of mixed origin. For the genomic breeding value estimation, the pedigree and performance data on 214'429 colonies of *Apis mellifera carnica* was used, combined with 2'499 genotypes of queens from phenotyped colonies. High differences between the workers sired by the DPQs and the workers sired by foreign drones were observed for two Varroa resistance traits.

Genotyping with a SNP chip provides information more information than the mating station reliability. In combination with a comprehensive data set, the subspecies of foreign drones can be determined, relatives within the data set can be found, and genomic breeding value estimation is possible.

Keywords: Mating station reliability, SNP chip, Genetic diversity, Breeding value estimation

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V 18 What are the transfer routes of fungicide residues from field to the hive?

Wie sieht der Transfer von Fungizidrückständen vom Feld in das Volk aus?

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V 19 Feed laced with biofungicide copper induces decreased food consumption, increased mortality and brood loss and leads to reduced learning ability of honey bees (*Apis mellifera*)

Wenn das als biologisch verwendete Fungizid Kupfer dem Futter von Honigbienen (Apis mellifera) beigemischt wird, führt dies zu einer verringerten Nahrungsaufnahme, erhöhter Sterblichkeit, Brutverlust und verminderter Lernfähigkeit.

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Honey bees (Apis mellifera) encounter environmental pollutants, such as pesticides and heavy metals while foraging. Copper-based products are commonly used as fungicides in organic pest management. To date they have been poorly investigated for their potential negative impacts on honey bees, though studies on stingless bees demonstrate sublethal negative impacts. We investigated the potential negative effects of copper on bee health using commercially available copper fungicides. To document changes in copper concentration due to spray application, we took apple and dandelion blossom samples before and directly after orchard application. A significant increase in copper concentration was measurable after spraying in both apple and dandelion anthers. In a food choice assay cage trial, we measured food consumption and mortality (n = 1,600). For all three copper doses, there was less consumption of copper laced feed and a concomitant reduction in sugar syrup consumption at the highest dose. Bee mortality increased with copper concentrations. In field trials, we fed copper mixed into candy to Miniplus colonies (n = 6) and examined the emergence rate of new brood, emergence weight, and longevity in cage trials post emergence. In a subsequent trial, we looked at the sucrose sensitivity (n = 467) and absolute olfactory learning of adult bees (n = 263). Increased brood loss was observed in the colonies treated with copper in both trials, while there were no significant differences in emergence weight. The copper treated group was less sensitive to low sucrose concentrations and showed reduced learning ability. Healthy offspring and intact learning performance, as well as the ability to perceive sucrose to locate appropriate nectar sources are vital for colony health. The results of this study indicate that the risks of heavy metal pollution in the environment should not be underestimated and need further investigations.

V 20 Untersuchung von Effekten kombinierter Pflanzenschutzmittel während der Larvenentwicklung von *Apis mellifera*.

Investigation of effects of combined plant protection products during the larval development of Apis mellifera.

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Plant protection products (PPP) are widely used in agriculture and known as prominent stressors for honeybees. PPPs have been abundantly found in beehives, especially in pollen. This could have an impact on developing bees, since their food is produced with pollen.

To analyse potential effects, we raised honey bee larvae (*Apis mellifera*) *in vitro* with larval food containing low and high concentrations of the neonicotinoid acetamiprid, the fungicides boscalid and dimoxystrobin as well as their mixture. We used concentrations derived from residues found in pollen.

Size and weight of newly emerged bees seemed to be unaffected, except in the low fungicide treatment: the bees were lighter in comparison to the control (Dunn's test, $p < 0.001$). Larval survival was reduced by the high insecticide treatment only (chi square test, $p < 0.05$). The bees emerging from this group also lived shorter ($p < 0.001$). Interesting effects occurred in the mixture: while the low concentrations of insecticide and fungicide did not have an influence on survival by themselves, their combination affected survival negatively ($p < 0.05$). Conversely, the negative effect of the insecticide on larval and adult survival was eliminated in the high concentration when combined with fungicides ($p > 0.05$).

Recent studies show that honey bees may be less susceptible to insecticides due to "priming" processes of naturally occurring toxins in diverse pollen. This includes the upregulation of genes involved in metabolic processes, which could help to detoxify insecticides. Other studies have discussed a similar mechanism, when honey bees were pretreated with low doses of SBI fungicides prior to insecticide application.

A similar process may have occurred in our PPP mixture as well. However, the results in our experiment appeared to be dose dependent. Our results highlight the complexity of PPP research and the need for further investigation especially in realistic contamination scenarios.

Keywords: in vitro larval rearing, insecticide, fungicide, synergistic effect

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V21 Der Einfluss von Pflanzenschutzmittel-Mischungen auf die Flugaktivität von Honigbienen

The effect of plant protection product mixtures on the flight activity of honey bees

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There has been a significant decline in pollinating insects in recent decades. In addition to factors such as changes in land use, climate change and various diseases, the use of plant protection products (PPPs) is regarded as a major factor in this decline. The effects of PPP mixtures, in particular, are difficult to predict. However, mixtures occur naturally in the field, and this is why bees are exposed to multiple PPPs at the same time. The consumption of mixtures can lead to unexpected harmful effects. In this study, the flight activity of honey bees was investigated after chronic treatment with two PPP mixtures. RFID technology was used, in which individual bees can be precisely identified by a chip and their flight activity can be accurately recorded by scanners at the hive entrance. While the mixture of neonicotinoid (Mospilan®, active ingredient (a.i.) acetamiprid) and non-SBI (sterol biosynthesis inhibiting) fungicide (Cantus® Gold, a.i. boscalid and dimoxystrobin) had no negative effects on bees, the mixture of neonicotinoid (Mospilan®, a.i. acetamiprid) and SBI fungicide (Difcor®, a.i. difenoconazole) had a negative effect on the number of foraging trips. Bees that consumed the mixture performed significantly fewer foraging trips (GLMM, $p < 0.05$). Such an effect could be due to the interaction of the SBI fungicide with the detoxification mechanism which leads to an inhibition of crucial detoxification enzymes. The study shows that more detailed investigations into the effect of PPP mixtures are needed in order to be able to make a suitable risk assessment.

V 22 In-hive behavioural responses of honeybees (*Apis mellifera*) after exposure to different plant protection products

Die Auswirkungen von drei Pflanzenschutzmitteln auf das Verhalten der Arbeiterinnen im Bienenstock von *Apis mellifera*

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Honeybee colonies function as superorganisms, depending on effective communication and coordination. Exposure to pesticides can disrupt tasks such as brood care and individual and social behaviours. In-hive behaviour recordings of workers after exposure can reveal the extent of these changes and thus provide an indication of colony health.

In this study, we conducted an in-hive feeding experiment using SIVANTO® Prime (Flupyradifurone), Cantus® (Boscalid) and Syngenta Click Pro® (Terbuthylazine and Mesotrione).

Pesticide-spiked sucrose solutions with environmentally relevant concentrations were offered to hives for one day. Mortality (n=100 per hive) and in-hive behaviour (n=20 per hive) of age-matched workers were monitored for eight consecutive days. The experimental setup was replicated three times over the honeybee season. In total, we documented 5,891 worker behaviours, consisting of 16 different behavioural phenotypes, which can be grouped into five larger categories (social, individual, brood care, colony maintenance, and foraging behaviour).

We did not observe any noteworthy impact on mortality within any of the groups. However, the in-hive behaviours exhibited variations based on the mode of action of each pesticide. Among the tested pesticides, the insecticide SIVANTO® prime had the most pronounced effect on behavioural phenotypes. We observed an increase in both social and individual behaviours, while colony maintenance behaviours were decreased. The fungicide Cantus® also showed increases in individual behaviour while Click Pro® showed a decrease in brood care and individual behaviours.

While alterations in foraging behaviour were observed as a result of pesticides exposure, we identified several significant effects on in-hive behaviour. Further studies with full size colonies under field realistic conditions are required to evaluate magnitude of observed in-hive behavioural responses on colony performance and developments.

Keywords: Plant protection products, honeybee, behaviour, sociality

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V23 Können Pflanzenschutzmittel Flügelasymmetrien bei Honigbienen verursachen?

Can plant protection products cause wing asymmetries in honey bees?

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Morphological asymmetries in insects are often associated with stress during development such as environmental pollution. Asymmetries can lead to reduced mating success and asymmetrical wings in flying insects might affect their flight capacity. Effects of different substances on insect development can be studied for a few species only, as not every species can be reared under controlled laboratory conditions. This study investigates whether the exposure of female honey bee larvae to plant protection products during individual development might cause wing asymmetry in imagines. For this purpose, honey bee larvae were reared in the laboratory until hatching and fed with diets spiked with field-realistic concentrations of various plant protection products. Insecticides, herbicides and fungicides with varying modes of action and potential risks to bees were used, including chemical and microbial based products. The dataset was expanded by honey bees of other laboratory and field studies, which were compared with their respective control. Various distances and angles between branches in wing venation were measured and analysed. Preliminary results showed that bees showed a higher proportion of crippled wings or wings with vein deviations than control bees taken from colonies. Bees reared with food spiked with plant protection products rarely showed higher proportions of transformed wings or wing asymmetry compared with their respective water or solvent control. The potential effects of most tested insecticides are still being analysed.

Keywords: Morphometrics, wing asymmetry, bee fitness, ecotoxicology

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V 24 Radiofrequency electromagnetic fields (RF-EMF): Do they negatively affect honey bees and other pollinators?

Hochfrequente elektromagnetische Felder (RF-EMF): Haben sie negative Effekte auf Honigbienen und andere Bestäuber?

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Urbanization and the increasing use of wireless technologies contribute to elevated emission rates of radiofrequency electromagnetic fields (RF-EMF) within populated areas. This anthropogenic electromagnetic radiation represents a form of environmental pollution and poses a potential stressor for bees and other flying insects. Cities often have a high density of wireless devices operating on microwave frequencies, which generate electromagnetic frequencies, e.g. in the 2.4 and 5.8 GHz bands commonly used by wireless technologies, but the effects of this non-ionizing radiation on the vitality and behavior of insects are poorly understood.

Our aim was to investigate the effects of these frequencies on pollinators while meeting the challenge of a defined and realistic radiation exposure required for such experiments. In order to generate this radiation in a defined way, we used a novel and high-quality technical setup that generates a consistent and realistic electromagnetic radiation, developed for these experiments by the Communications Engineering Lab (CEL) at the Karlsruhe Institute of Technology.

We tested the effects of 2.4 and 5.8 GHz on I) honey bee brood development, longevity and homing ability, II) gene expression in honey bees, and III) flower visitation rates of different pollinators.

Our results show significant effects of long-term exposure on homing ability of foraging honey bees and gene expression (preliminary), but no effects on brood development and adult worker longevity. In addition, we see reduced flower visitation rates for individual pollinator groups.

This interdisciplinary work with a controlled RF-EMF exposure enabled studying the effects of these widely used frequencies on important fitness parameters of free-flying honey bees and the foraging behavior of pollinators.

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V 25 Auswirkungen der herkömmlichen und der innovativen Bienenhaltung auf die Gesundheit von Honigbienen

Effects of conventional and innovative beekeeping on honeybee health

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Varroa destructor is a major threat to honeybee colonies. It is known that varroa mites can act as a vector for honeybee diseases and can lead to colony collapse. Therefore, beekeepers treat their hives against the mite. Under conventional methods, chemical treatments with organic acids are used to reduce the mite load. In addition, drone brood is removed in spring. A possible alternative to this method is a more natural method of beekeeping with (1) leaving the drone brood in the hive, thereby supporting natural selection of drones. (2) During an induced brood interruption by caging the queen in summer, which resembles the situation of natural swarming, the mites cannot reproduce. Also, (3) one chemical treatment with oxalic acid when the hives are brood free should reduce the infestation rate.

To observe differences in mite loads, we compared varroa infestation during the year using sticky bottom boards. To evaluate the changes in DWV-B virus loads we investigated honeybees of both methods using quantitative real-time PCR. We sampled newly emerged honeybees and foragers at three different time points. We did not find any differences in virus load after overwintering between both methods. In summer, shortly before treatment, innovatively maintained honeybees had significantly higher virus loads compared to conventionally kept honeybees. Nevertheless, we found that DWV-B load was reduced at the third time point before overwintering, so there were no differences between both beekeeping methods.

In conclusion, varroa has a high impact on DWV-B virus load in summer when mite loads are high in the innovatively kept honeybees. However, a highly efficient biotechnical varroa treatment can reduce mite loads as well as virus loads to ensure that honeybees are healthy in the critical phase of winter bee production.

Keywords: *Varroa destructor*, beekeeping, brood interruption, Varroa treatment, DWV

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V 26 Die Verbreitungsphase spielt eine entscheidende Rolle für die erfolgreiche Vermehrung junger Varroamilben (*Varroa destructor*)

The dispersal phase plays a crucial role in the successful reproduction of young varroa mites *(Varroa destructor).*

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It has been postulated that *Varroa destructor* needs a dispersal phase to activate her ovaries. To investigate the significance of the dispersal phase in varroa reproduction, we conducted experiments inserting marked mother mites directly into freshly capped cells using the direct infestation method. This allowed us to isolate both the marked mother and her unmarked eldest daughter mite just prior to bee emergence. These mites were then divided into two groups: one group was immediately reinserted into freshly capped cells without experiencing a dispersal phase, while the other group was placed onto adult nurse bees for three days before being reintroduced into freshly capped cells. Eight to ten days after insertion, we assessed mite fecundity. Results revealed that directly inserted daughter mites, lacking a dispersal phase, exhibited only about 7% of normal reproduction. A staggering 93% of these mites either failed to produce offspring (42%) or showed delayed reproduction (51%). Similarly, for mother mites directly inserted into cells, 59% failed to reproduce, with 19% producing no offspring and 40% displaying delayed reproduction. In contrast, mites allowed a three-day dispersal phase on worker bees exhibited a reproduction rate of around 70%. This indicates the critical role of the dispersal phase in ensuring normal reproduction, particularly for young daughter mites. Our findings also highlight the risks associated with using the powder sugar shake method for harvesting mites in the direct infestation method, as it may lead to reduced reproduction by collecting young daughters and newly emerged mother mites, who have not had their dispersal phase. Consequently, mite reproduction data should be interpreted cautiously when the dispersal phase duration of mites is unknown. Further studies are needed to explain if a nutritional benefit obtained from feeding on hosts during the dispersal phase or the passage of time are the primary factors responsible for a normal reproduction.

Keywords: *Varroa destructor*, dispersal phase, varroa reproduction, varroa biology

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V 27 *Varroa destructor* estimation of infestation during the bee season using three different methods

Varroa destructor Befallsschätzung während der Bienensaison mit drei verschiedenen Methoden

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Varroa destructor remains the most significant threat to *Apis mellifera* and their populations must be controlled via treatments before the population crosses an economic damage threshold. In our study, we compared three diagnostic methods — natural mite fall (NMF), adult bee infestation (percentage of nurse bees infested) (BI), and cell infestation score (percentage of worker brood cells infested) (ZI) — to determine appropriate treatment times based on economic thresholds of 10 mites per day NMF, 3% BI, and 10% ZI.

Our results indicate that NMF serves as an effective early warning system. A higher mite population is detected approximately 14 days earlier than the other two methods. If the NMF suggests treatment, confirmation with the BI is recommended. Before the late summer treatment with a 60% formic acid solution, significant differences were observed between the results of the NMF and the two other diagnostic measures through a binomial comparison of colonies that exceeded damage. The ZI rate with *V. destructor* varied across the frames in the colony. Unlike other studies, we found no significant difference in BI on bees located on the outermost, honey, and brood frames and thus advocate that similar economic treatment thresholds are applied throughout the colony.

We also investigated *V. destructor* populations in 6 complete colonies and found an equal distribution between mites in the dispersal phase on adult bees and the reproductive phase in brood cells from June through September. This higher-than-expected rate of mites in the dispersal phase has implications for the effectiveness of different treatment methods. Elevated *V. destructor* populations can occur during early summer honey production, necessitating earlier monitoring, as numerous colonies surpassed economic treatment thresholds by June 15. While strong summer colonies need not be immediately treated upon exceeding the threshold, beekeepers should plan to treat them as soon as feasible.

Keywords: Treatment timing; comparison of methods; distribution of mite phases

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V 28 Evaluating BQCV and DWV-B spillover between honey bees and bumble bees across the flight season

Bewertung der Übertragung von BQCV und DWV zwischen Honigbienen und Hummeln während der Flugsaison

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Pollinator biodiversity is falling, especially within the clade Anthophila (the bees). Honey bees alongside wild bees carry out the majority of insect pollination, which is an essential component of the production of many crops. Both managed and wild bees face many threats, one of which is RNA viruses such as black queen cell virus (BQCV) and deformed wing virus (DWV). These viruses are highly mutable and appear capable of inter-species spillover, allowing them to spread through bee communities. The factors promoting spillover are currently a matter of debate, and it is unknown if spillover varies across the flight season. This investigation attempted to fill this knowledge gap by quantifying spillover at four locations in Great Britain across three consecutive months by comparing viral prevalence and sequence composition of BQCV and DWV B from *Apis mellifera*, *Bombus terrestris*, and *Bombus pascuorum*. For all sites, viral prevalence was highest in *A. mellifera* and lowest in *B. pascuorum*, suggesting *A. mellifera* is the reservoir host of both viruses. All bee species tended to exhibit consistently high or consistently low relative viral prevalence at a site across all three months of sampling. This suggests that spillover is an ongoing phenomenon across the year. Moreover, for BQCV, viral sequences varied across sampling sites but did not vary across host species or time points sampled within a site. This suggests that spillover was occurring within a site throughout the flight season. DWV-B sequences exhibited slight haplotype clustering by site, but the evidence to support whether spillover was happening across host species was not robust enough for inference of spillover. This study informs on spillover dynamics of BQCV and DWV-B between honey bees and wild bees and provides insights into the threat they pose to bee biodiversity.

Keywords: Honeybee, Bumblebee, Spillover, BQCV, DWV-B

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V 29 Flagella of *Paenibacillus larvae* – influence on multicellular behaviour and virulence

Die Flagellen von *Paenibacillus larvae* – Einfluss auf das multizelluläre Verhalten und die Virulenz

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American Foulbrood (AFB) is one of the most devastating diseases of the honey bee brood, posing a threat to the health of bee colonies worldwide. The causative agent of AFB is *Paenibacillus larvae*, a Gram-positive, spore-forming bacterium that is classified into different genotypes (ERIC I-V). Only *P. larvae* ERIC I and ERIC II are responsible for current AFB outbreaks among these genotypes. AFB infection begins when the ingested spores of *P. larvae* germinate in the midgut lumen of young honey bee larvae. Following a massive proliferation of vegetative bacteria in the midgut, *P. larvae* invades the midgut epithelium, subsequently infiltrates the haemocoel resulting in the death of the larva. The bacteria decompose the larval carcass into a ropy mass that dries into a tightly adhering scale, consisting of billions of spores. During the infection cycle various genotype specific virulence factors as well as multicellular behaviour like swarming and biofilm formation help the bacteria to colonize it´s host. Further, *P. larvae* synthesises peritrichously arranged flagella on its cell surface. These bacterial appendages are known not only to mediate motility of individual planktonic cells, but also to play an important role in swarming and biofilm formation. To enhance our understanding of AFB pathogenesis, we investigated whether the flagella of *P. larvae* ERIC I and ERIC II influence multicellular behaviour and virulence of the bacteria. We discovered mutations in two flagellar biosynthesis genes of *P. larvae* ERIC I presumably causing the non-swarming phenotype previously described for this *P. larvae* genotype. Furthermore, we discovered that the flagella of both genotypes are essential for biofilm formation and full virulence, thus identifying the flagella of *P. larvae* as virulence factor.

Keywords: *Paenibacillus larvae*, flagella, virulence, swarming, biofilm

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V 30 Validation of a newly developed American foulbrood detecting fast test tool with genotype differentiation using field samples

Validierung eines neu entwickelten Schnelltests zur Detektion der Amerikanischen Faulbrut mit Genotyp-Unterscheidung mit Feldproben

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American foulbrood (AFB) is the most devastating bacterial brood disease of honey bees (*Apis mellifera*). AFB causes colony and economic losses worldwide and is a notifiable disease in many countries. The causative agent of AFB, *Paenibacillus larvae*, can be distinguished into two mainly occurring genotypes ERIC I & ERIC II that show variability in virulence and could be treated differentially. Disease diagnosis is usually conducted via visual inspection. If a colony is suspicious, the disease has to be confirmed in the laboratory, which often is very time-consuming. We developed a sensitive and fast diagnostic tool (lateral flow device = LFD) to diagnose AFB and distinguish between the two main genotypes (ERIC I and ERIC II) of *P. larvae* and are now validating it.

The newly developed LFDs are validated in two steps. In a first step we validate the performance of the LFD in a laboratory setting using field samples of larvae and adult bees, comparing the results to results obtained through conventional PCR and through microbial cultivation of the same samples. In a second step we send out the LFDs to our collaborators in the field to validate their performance under field conditions.

The validation under laboratory condition shows, that while the LFDs are not as sensitive as the microbial cultivation method, the LFDs do show a sensitivity comparable to that of PCR.

Furthermore, the laboratory tests suggest that adult honey bees are also suitable test material for AFB detection and contain enough vegetative *P. larvae* cells for a successful AFB detection using the LFDs. Here we present the results of the validation of the LFD under laboratory conditions and the initial results of the validation under field conditions.

Keywords: Amerikanische Faulbrut, Schnelltest, ERIC-Genotypisierung

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V31 Selective molecular detection of *Paenibacillus larvae* spores

Selektiver molekularbiologischer Nachweis von *Paenibacillus larvae* Sporen

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American foulbrood is a noticeable and severe disease of bee larvae, caused by the spore forming bacteria *Paenibacillus larvae*. Freshly hatched larvae get infected via spore contaminated food, making it essential to determine and quantify the presence of *P. larvae* spores in honey to assess if a bee colony is infected. A big disadvantage of the current microbiological detection of CFUs is the long timespan needed for germination and colony formation. Therefore, attempts were made to detect *P. larvae* molecularly to speed the diagnostics up. Unfortunately, no reliable information on the presence of *P. larvae* spores could be obtained with the so far applied methods due to several reasons. Besides the presence of vegetative cells in samples, problems to detect and quantify spores are rooted in the fact, that the mother cells secrete extracellular DNA together with the spores and that spores have very thick cell walls, resistant to many standard DNA extraction methods. We describe a new approach, allowing to exclusively detect the DNA from bacterial endospores, but not from vegetative cells or extracellular DNA. To do so, we modified a method for molecular differentiation between dead and living microbes by applying a DNA binding stain, that blocks DNA from PCR-amplification, but cannot enter intact cells. Heating made the DNA of vegetative cells in our samples accessible to the stain and thus excluded it together with free DNA from subsequent molecular detection. In addition, spores were mechanically disrupted with a dedicated spore DNA extraction kit. This combination allowed us to selectively detect *P. larvae* spore DNA from lab cultures and honey samples. An ongoing evaluation of this new method tests the ability to quantify spore numbers in honey samples in correlation to the classical determination of CFUs to significantly decrease the time from sampling to result for suspicious foulbrood samples.

Keywords: American foulbrood, spore detection, viability PCR

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V 32 Is deformed wing virus (DWV) genotype B replacing DWV genotype A across the world?

Verdrängt der Genotyp B des Deformed Wing Virus (DWV) weltweit den Genotyp A?

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Parasitism of honey bees (*Apis mellifera*) by the ectoparasitic mite *Varroa destructor* has led to a profound rise in prevalence of deformed wing virus (DWV) in host honey bees that, if unchecked, eventually results in colony death. The mite is known to be an extremely efficient vector of DWV, which is nowadays found as two widespread variants, genotypes A (DWV-A) and B (DWV-B). DWV-A has long been known to have a worldwide distribution whilst DWV-B was first described in 2001 in Dutch honey bees and mites. Over the past two decades, DWV-B has expanded its distribution across most of the globe, most likely due to its enhanced transmission. Somewhat surprisingly, DWV-B has effectively replaced DWV-A in parts of Europe including Germany. Our epidemiological modelling suggests that replacement is only possible when the two variants (DWV-A and DWV-B) inhibit one-another e.g. through superinfection exclusion. DWV's pattern of evolution is reminiscent of that of SARS-CoV-2, in which one variant is displaced over time by another. We now pose the question: is DWV-B replacing DWV-A across the globe? Own data from the Yucatan Peninsula of Mexico and others' published data from the USA suggest the answer is no, at least not yet; after >10 years presence in Mexico and USA, DWV-A remains dominant. The high prevalence of DWV-A may help it block take-over by DWV-B, possibly through the mechanism of recombinational meltdown. We discuss the ramifications of these results for the future outlook of colony health.

Keywords: epidemiology, virulence, competition, honey bee

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V 33 Observing the displacement of *Nosema apis* by *Nosema ceranae* in the *Apis mellifera* population in north-eastern Germany

Beobachtung der Verdrängung von *Nosema apis* durch *Nosema ceranae* in der *Apis mellifera*-Population in Nordostdeutschland

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Nosema apis and *Nosema ceranae* are obligate intracellular, fungal pathogens belonging to the phylum Microsporidia. They infect the midgut epithelium of adult bees and can cause nosemosis. In 1906, *N. apis* was described as a microsporidian pathogen that specifically infects *A. mellifera*. In 1996, a new microsporidium was detected as pathogen in the Eastern honey bee (*Apis cerana*) and consequently named *N. ceranae*. Experimental infections at that time had already shown that *N. ceranae* has the potential to also infect *A. mellifera*, but natural *N. ceranae* infections in *A. mellifera* were not found until ten years later. Further investigations of historical samples then revealed that *N. ceranae* had already extended its host range decades earlier. Since then, there have been multiple reports on the detection of *N. ceranae* in *A. mellifera* populations, showing a worldwide distribution of this pathogen and even a displacement of *N. apis* through *N. ceranae* in some regions. In Europe, the displacement of *N. apis* is mainly reported from the south, while in northern Europe *N. apis* can still be detected, suggesting a climatic effect on the spread and assertiveness of *N. ceranae*. In our twelve-year cohort study published in 2017, for example, we showed that no significant decline in *N. apis* infections was observed in north-eastern Germany over more than a decade, although the prevalence of *N. ceranae* infections increased significantly over the same period. However, the continuation of this unique long-term longitudinal cohort study on the epidemiology of *Nosema* spp. and the reanalysis of the data set, which has now been collected over more than two decades, has shown that we have indeed observed and are still observing the gradual displacement of *N. apis* by *N. ceranae* in north-eastern Germany. The results of our study impressively underline that long-term phenomena such as epidemiological processes can only be observed and analyzed by long-term studies.

Keywords: *Nosema apis, Nosema ceranae*, epidemiology

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Abstracts der Posterpräsentationen

N: Nachwuchswissenschaftler:in

Bestäubung

P 1 Untersuchung der Populationsentwicklung von *Apis mellifera carnica*- Völkern an landwirtschaftlichen Nutzflächen mit *Silphium perfoliatum* L. (N)

Population development of *Apis mellifera carnica* colonies on agricultural land with *Silphium perfoliatum* L.

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Previous studies on agricultural fields with *Silphium perfoliatum* L. often describe an intensive visitation of the flowers by honeybees. Other studies show that honeybees do not necessarily use this plant as a main source of nectar or pollen and therefore has little added nutritional value for the *Apis* colonies. To clarify this question, we compared the population development of *Apis mellifera carnica* colonies at two *S. perfoliatum* locations located in different landscape structures in the Eifel region to a control site without *S. perfoliatum*.

We used the Liebefelder estimation method to examine the population development. Between July and September (2023), the stages of eggs, larvae, capped brood and adult individuals of *A. m. carnica* were estimated (Zander comb format). In addition, data on honey and pollen yields were collected.

The development of *A. m. carnica* was statistically analysed as a function of both the time of estimation and the location. Regardless of the time of estimation, there was a significant difference in the mean number of estimated eggs and capped brood between the *S. perfoliatum* sites and the control site. However, there was no significant difference in the mean number of adult *A. m. carnica* individuals. Increased collection performance and more intensive brood care at the sites with *S. perfoliatum* compared to the control could be a reason for increased mortality of adult *A. m. carnica* individuals.

Keywords: Agricultural structure, flowering period, honeybee, brood rearing, *Silphium perfoliatum* L.

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P 2 The importance of the cultivation of medicinal and aromatic plants for maintaining and promoting bee health

Die Bedeutung des Arznei- und Gewürzpflanzenanbaus für den Erhalt und die Förderung der Bienengesundheit

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In agricultural production there are often trade-offs between food, feed and energy production on the one hand and the conservation and promotion of biodiversity as well as landscape and cultural care on the other. To reduce these trade-offs and to become more multifunctional, farming systems need to take all of these aspects into account more equally.

One way to reconcile these goals is to cultivate medicinal and aromatic plants. The project "AMOBILA – medicinal plant cultivation as an instrument of modern, yield-oriented and at the same time biodiversity-promoting agriculture" examines what contribution the cultivation of poppies, coneflowers, anise, chamomile and fennel can make to the preservation and promotion of biodiversity and what role flower-visiting insects may play in securing income. Cultivation is carried out in the open field and in insect flight tunnels in order to quantify the pollination performance of different groups of insects.

In addition to recording flower visitors - especially bees - another focus of the project is on quantifying the floral resources of pollen and nectar. By combining the results of determining the origin of the pollen collected from honey bee colonies and the pollen from the collecting apparatus of wild bees, conclusions can then be drawn about what importance the cultivation of these special crops can have for bee health in agricultural landscapes.

Comprehensive communication strategies are being developed via the project partner South Westphalia University of Applied Sciences in order to adequately pass on the findings to all target groups. In addition, key findings will be communicated to political decision-makers.

Keywords: Medicinal plants, Spice plants, Bee health, Pollination, Biodiversity

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P 3 Observation of visiting insects on various agricultural flowering mixtures over a period of three years

Beobachtung des Insektenflugs auf verschiedenen landwirtschaftlichen Blühmischungen über einen Erfassungszeitraum von drei Jahren

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In an agricultural landscape, flower strips are a good opportunity to support and promote pollinator insects. As part of this study, four different flower mixtures were observed for their function as a habitat or source of food for honey bees (*Apis mellifera*) and various wild pollinators, such as wild bees, hoverflies and moths, at a site in the Soester Börde over a three-year period (2020-2022). For this purpose, the insect flight on each mixture was recorded on three times per year, within one square meter, for one hour using Go-Pro cameras. The plants on the areas were assessed with regard to the degree of flowering and cover. The evaluation of the flight observations was carried out using "Mangold Interact" evaluation program. The aim was to determine which flowering strips were most attractive to pollinators and which mixture developed well over the course of the study years and proved to be a reliable source of food for the insects in the long term. The focus of the study was on the number of visits by the insect groups: honeybees, bumblebees, hoverflies and moths; other insects were summarized. The statistical evaluation was carried out using an univariate analysis of variance in SPSS ($p \leq 0.05$). The total number of insects observed on the different mixtures did not differ significantly over the three years of the study.

Between the individual years, there were some significant differences ($p \leq 0.05$) between the mixtures in the number of visits by the individual insect groups.

Across all years, the annual mixture 02 showed the highest attractiveness over the years. Followed by the perennial mixture 03 and the annual mixture 01 with similarly high visitation figures.

Keywords: flowering strips, pollinators, insect observation

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P 4 The sunflower diet: Pollen and nectar nutrition and impacts on pollinator development and health (N)

Die Sonnenblumendiät: Pollen- bzw. Nektarernährung und deren Auswirkungen auf die Entwicklung und Gesundheit von Bestäubern.

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Sunflower, *Helianthus annuus*, is a prominent global oilseed crop gaining renewed attention for its potential to enrich ecosystem services by providing nutritional resources for pollinators. With the rise of sunflower cultivation in Europe as a bee-friendly crop, combined with the current threat of pollinator decline, it is important to review the current knowledge regarding sunflower nutrition for bees. This would contribute a combined benefit for farmers to make informed decisions regarding sunflower cultivation and for future breeding efforts to make pollinator attractive cultivars. The aim of this scope review was to summarize the reported nutritional components in pollen and nectar of Helianthus annuus and the impact of sunflower pollen diets on bees' development and health. Overall, the nutritional quality of sunflower pollen was often questioned due to reported lower protein levels and poor developmental parameters in Bombus and Apis species. Conversely, studies quantified a positive impact on pollinator health due to the frequently reported reduction of the gut parasite Crithidia bombi in Bombus species. These findings probe the question on how to precisely define the quality of floral resources, emphasizing the need for caution when categorizing sunflower as a low quality nutritional resource. This review also brings into light a prominent gap in scientific knowledge regarding nectar quality on bee nutrition and health, thereby warranting further research to gain a more comprehensive view of sunflower nutritional resources for pollinators.

Keywords: *Helianthus annuus*, floral rewards, pollinator nutrition, pollinator health, plant-pollinator interaction

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Bienenprodukte

P 5 Honig als Spiegelbild der Landschaft

Honey as a reflection of the landscape

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Honey is not only food for *Apis mellifera* or for human consumption, it also stores valuable information from space and time. As *Apis mellifera* collects nectar, the corresponding pollen is stored in the honey. Honeydew as a further food source also includes various sediment components as well as minerals. The sediment components and pollen can ultimately provide information about different types of honey. Pollen analysis and other physical characteristics combined with various site-specific and beekeeping data can help to answer various questions about the landscape structures.

In the state-funded project „REGIO-Honig Rheinland-Pfalz", more than 500 honeys of the years 2021-2023 from Rhineland-Palatinate were examined. The location assignment in combination with the pollen analysis made it possible to create regional honey maps and kind of food availability for honeybees. In the future, these honey maps could help beekeepers to use locations for migration their beehives to harvest varietal honey.

However, pollen analysis can do even more: the influence of agricultural crops on honeybees and thus on honey can also be shown, provided that a nectar input is associated with this. Furthermore, the detection and possible spread of neophytes can also be monitored.

Finally, a long-term monitoring with a consistent scope of investigation can also provide conclusions about the influence of climate change on honeybee foraging conditions and food availability - both in terms of nectar availability from flowers and the occurrence of honeydew caused by aphids.

Keywords: *Apis mellifera*, honey, pollen, landscape

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P 6 Frühtrachthonig mit Ahornhonig – eine besondere Frühjahrsernte in 2023

Spring honey with maple honey – a special spring harvest in 2023

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During the analysis of spring honeys 2023 at the LAVES Institut für Bienenkunde Celle 29 honeys were classified as spring honeys with maple honey (Frühtrachthonig mit Ahornhonig) based on their organoleptic, phyico-chemical and microscopic characteristics. The characteristics determined are presented here:

Color: golden yellow, dark yellow, amber-coloured; consitency: clear liquid, liquid cloudy; aroma: floral-heady, caramel-like, aromatic, medium intensity; water content: 16,2 ± 0,9 %; electrical conductivity: 0,73 ± 0,14 mS/cm; invertase: 285,6 ± 95,2 U/Kg; Fructose: 36,7 ± 1,23 g/100g; Glucose: 30,7 ± 2,05 g/100g; F/G: 1,20 ± 0,08; relative frequency of Acer (Mavel) Pollen: 23 ± 16 %.

To specify compositional limits for unifloral maple honeys (Ahornhonig) several additional data sets are needed.

Keywords: Spring honey, Maple, Acer, Frühtrachthonig mit Ahornhonig

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P 7 Comparison of microscopic pollen analysis and metabarcoding to determine the botanical diversity in honey

Vergleich der mikroskopischen Pollenanalyse und Metabarcoding zur Bestimmung der botanischen Vielfalt in Honigen

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Melissopalynology is a well-established Method for determination of the botanical and geographical origin of honey. The conventionally used microscopic pollen analysis is time consuming and needs a high degree of expertise. Metabarcoding is an alternative technique which allows to identify pollen by their plant-specific genetic information, the so-called barcode-region. The both methods are compared and the pros and cons exhibited.

Microscopic pollen analysis followed a standardized protocol (DIN 10760). The pollen grain isolated from honey were identified under the microscope according to their external shape and quantified. For Metabarcoding, the DNA contained in the pollen sediment was isolated. To establish the method, the enrichment of the pollen and its digestion process were first optimized. Next Generation Sequencing was used for detection of the suitable barcode regions. These sequences of pollen DNA were identified by matching to specific reference libraries.

Using microscopic pollen analysis, pollen from 18,2 ± 3,4 plant families per honey (n=14) were detected. For metabarcoding, different single barcodes and their combinations were tested. By combining barcode regions (trnL/ITS2), pollen of maximum 14,4 ± 4,2 plant families per honey (n=7) were identified. By contrast, metabarcoding led to a higher differentiation of the species in a plant family.

Both methods complement each other in determining the botanical origin of pollen in honey. Since additional information is obtained using barcoding and also quantification is possible using microscopic pollen analysis, these methods can form the basis for estimating biodiversity at the locations of bee colonies.

Keywords: Metabarcoding, pollen analysis, botanical origin, honey analysis,

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P 8 Elektrische Leitfähigkeit von Honig. Ist eine Änderung der deutschen Honigverordnung (HonigV) erforderlich?

Electrical Conductivity of Honey. Should the German Honey Regulation (HonigV) be revised?

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In the last four years (2020-2023), honey quality analyses were conducted on 3,400 honey samples from the state of Baden-Württemberg at the laboratory of the State Institute of Bee Research at Hohenheim University. The analyses included water content, electrical conductivity, invertase activity, and microscopy including pollen spectrum identification to characterize the different honey sources. We noticed a trend of increasing values in electrical conductivity. We would like to shed additional light on this issue. The honey samples can be divided into 3 categories (floral honeys, floral-honeydew mixed honeys, and honeydew honeys). According to the German Honey Regulation, the electrical conductivity of honeydew honey, chestnut honey and mixtures of these types of honey should be at least 0.8 mS/cm (Appendix 2 from § 2 & 4, section II – specific requirements, 4. Electrical conductivity).

During the last four years, we found only 2.9 % of honeydew and chestnut honey samples with an electrical conductivity lower than 0.9 mS/cm, whereas 65.6% of the floral-honeydew mixed honeys reached an electrical conductivity of 0.8 mS/cm and higher. However, 97.1 % of the honeydew and chestnut honey samples showed a minimum electrical conductivity of 0.90 mS/cm and 89.2 % were at 1.0 mS/cm. Therefore, we suggest the German Honey regulation be modified by shifting the limit of electrical conductivity of honeydew and chestnut honeys from at least 0.8 mS/cm to at least 0.9 mS/cm.

Keywords: honey, electrical conductivity, guidelines of the German Honey Regulation (HonigV)

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P 9 Wie zuverlässig ist die organoleptische Verkostung zur Sortenbestimmung von Honigtauhonigen? (N)

How reliable is organoleptic tasting for determining honeydew honey varieties?

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Current methods of honey variety identification for honeydew honeys are essentially based on organoleptic tasting. Based on subjective perceptions, these results can be difficult to reproduce, which is why the development of supplementary laboratory methods has long been called for. However, as the current sensory taste testing methodology is the only reference for their validation, we have attempted to assess the reliability of variety identification by means of a blinded tasting.

In a tasting trial, six tasters classified 36 honeydew honeys into the honey varieties fir, spruce, linden and the more generalized categories of conifer, leaf and "mixed honeydew". Before the start of the trial, all honeys were categorized as honeydew honeys of different varieties. The tasters were also asked to state how confident they were in their assessment of the individual honeys.

For one of the 32 honeys analyzed, all tasters were unanimous; for another, five of the six tasters made identical classifications. In both cases it was classified as linden-honey. In the case of the samples categorized as linden or conifer honey, the tasters who rated the honey as this category stated on average that they were "very certain" in their self-assessment, while they were on average "certain" for the fir, spruce, mixed and leaf categories. In the case of eight honeys, at least one taster assessed that it was not a honeydew honey.

Three honeys were each included twice. For one of them, three tasters reassessed the honey identically during the second tasting. For the other two honeys, only two tasters were consistent in their own assessment. The fact that the results rarely matched, even though the tasters were experienced in honey sensorics, shows on the one hand the need to develop additional methods, but also the difficulties in validating new methods. On the other hand, it demonstrates how important good training of the tasters is.

Keywords: honeydew, varietal determination, taste test, sensory analysis

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P 10 Rückstandsstudie nach Verabreichung von APITRAZ bei Honigbienen über 6 und 10 Wochen

Residue depletion study after administration of APITRAZ in honeybees during 6 and 10 weeks

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Amitraz is a formamide insecticide and acaricide, and it is the active substance of the veterinary medicinal product APITRAZ which is used as a sustained-release strip containing 500 mg of Amitraz. The product APITRAZ is use in-hive, hanging up two strips per hive and maintaining the strips in the hive per 6 weeks. In these conditions, the withdrawal period for APITRAZ has been demonstrated previously to be 0 days. The aim of the present study is to confirm that the withdrawal period is also 0 days if the strips are maintained in the hive for 10 weeks.

Amitraz is included in Table 1 of the Annex of Commission Regulation (EU) No 37/2010 regarding maximum residue limits in foodstuffs of animal origin, and a maximum residue limit of 200 µg/kg for the sum of Amitraz its metabolites is established for honey.

A residue study was performed in the Beekeeping and Agri-environmental Research Centre (CIAPA) (Guadalajara, Spain). 22 beehives of *Apis mellifera iberiensis* were used in the study. The hives were Langstroth type with only a brood box (10 frames per box). Hives were uniform in adult honeybee population and box size.

All hives were treated with APITRAZ. APITRAZ strips were maintained at the recommended dosage (2 strips/hive, 500 g Amitraz per strip) for 6 weeks in 11 out of the 22 hives and for 10 weeks in the other 11 hives.

Approximately 100 grams of honey from each hive were harvested some 6 months after treatment, when at least 75% of honey cells were filled and capped. Samples were filtered, homogenized, and analysed by HPLC-MS/MS.

All 22 samples analysed in the study showed concentrations of Amitraz below the limit of quantification of the analytical method, established at 100 µg/kg, which is far below the maximum residue limit (200 µg/kg) established in the Annex mentioned above. Consequently, a withdrawal period of 0 days was confirmed for a treatment duration of either 6 or 10 weeks.

Keywords: Residues, Amitraz, Apitraz, Honey

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P 11 Untersuchung von Kontaminanten und Rückständen in Bienenwachsproben nach Überflutung: Eine umfassende Analyse (N)

Analysis of contaminants and residues in beeswax samples after flooding: a comprehensive study

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Keywords: Contaminants, residues, heavy metals, PAHs, flood

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Wildbienen

P 12 Morphological adaptation in a solitary bee (*Andrena vaga*)-endoparasite (*Stylops ater*) system

Morphologische Anpassungen in einem Solitärbiene (*Andrena vaga*)-Endoparasit (*Stylops ater*)-System

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The grey-backed mining bee *Andrena vaga* is one of the hosts for the Strepsipteran endoparasite *Stylops ater*, which is known for extreme sexual dimorphism and hypermetamorphosis. For most regions in Europe, were both are occurring, the population structure, genetic diversity and morphological adaptations are unknown. Here, we sampled hosts and parasites of both sexes at several nest aggregations in and around Braunschweig (Germany) to study their biology and distribution. Genetic analysis revealed the absence of local variation within *Stylops*. Host bees emerged earlier than non-parasitized bees. Individual male and female bees hosted up to four parasites in their bodies. A trend was detected in the *Stylops*' preference for hosts of their own sex and the position of extrusion from the host abdomen. Morphological adaptations upon parasitation include: ovary reduction and reduced head width for bees infested by male *Stylops*, host masculinization (indicated by the shape of the metabasitarsus), and intensified tergal hairiness (most strongly near the point of parasite extrusion). Parasites responded to the hosts' sex and multiple infestation with reduced size of cephalothoraxes. Future studies are needed to understand the mechanisms behind parasite-induced host manipulation.

Keywords: host-parasite interaction, size variation, ecology, urban environment, population

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P 13 Pollination behaviour of Bombus terrestris - influences of drought stressed plants along an altitudinal gradient in the Taunus Mountains (N)

Bestäubungsverhalten von Bombus terrestris – Einflüsse von trockengestressten Pflanzen entlang eines Höhengradienten im Taunus

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Pollinating insects such as honey bees, Apis mellifera, and bumble bees, Bombus terrestris, are affected by a variety of environmental stressors such as climate change, which is pushing wild bees in particular to their ecological tolerance limits due to prolonged periods of drought and heat. Lack of water can lead to changes in floral cues (e.g. flower scent, flower size) and floral rewards (e.g. nectar concentration) in flowering plants, which in turn can reduce reproductive success. The extent of these changes and their impact on plant-pollinator interactions is still relatively unexplored. It is therefore important to find out how drought stress in forage plants affects the pollination behaviour of bumblebees, and to what extent altitude plays a role.

The institute is located in the low mountain range of the Taunus, which is ideal for a study along an altitudinal gradient. The chosen elevation gradient is 25 km long and includes five sites ranging from 122-823 m above sea level, from the Science Garden of the Goethe University Frankfurt am Main to the Kleiner Feldberg. In the summer of 2023, behavioural experiments were conducted in observation tents with commercially bred bumblebee colonies, buckwheat (Fagopyrum esculentum) and white clover (Trifolium repens) at each site. The foraging behaviour of the bumblebees was recorded individually for 10 minutes at a time. A total of 148 trials of plant-pollinator interactions were documented. These can be quantified in terms of the number of times a bumblebee visited a flower in a given time (visit rate) and the duration of the visit. Preliminary analyses of the data show differences in behaviour towards drought-stressed plants and the control group. A detailed analysis is not yet available. Our study combines behavioural experiments with a field study and provides an experimental and qualitative contribution to the discussion on rising temperatures and their effects on pollinators.

Keywords: bumblebee, plant-pollinator interactions, drought-stressed plants

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Ökologie

P 14 Enhancing the reliable and effective long-term monitoring of bee diversity in agricultural landscapes through DNA-Metabarcoding

Verbesserung der zuverlässigen und effektiven Langzeitüberwachung der Bienenvielfalt in Agrarlandschaften durch DNA-Metabarcodierung

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P 15 ZUFI - Zukunftsfähige Imkerei Bayern – Professionalisierung des Imkereisektors durch betriebswirtschaftliche Entscheidungshilfen für wachstumswillige Betriebe

ZUFI - Sustainable Future of Bavarian Beekeeping Sector – Support and improve economic efficiency and investment-decision-making of beekeepers with growth perspective

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German and bavarian beekeeping sector are characterized by over 96 percent small non-professional apiarists with an overall average of 7 colonies per beekeeper only (EU average is at approx. 21). During the last decade, beekeeping has taken a considerable 30 percent upswing, adding many newcomers to this sector. After gaining first years experience, some of them are interested in expanding their operations in order to gain family income from beekeeping. The Bavarian State Ministry for Food, Agriculture, Forestry and Tourism strongly supports investing and expanding beekeepers by granting subsidies. Project ZUFI has been setup by the Ministry in order to support decision-making of beekeepers when trying to identify the proper size and specification of required equipment or space or production process for their growing operations. By combining information on the specifics of an existing beekeeping operation and its growth ambition with the specification of available beekeeping equipment, a database has been setup. Using a search algorithm, the database will select recommended equipment and space characteristics for defined production steps, including advantages and disadvantages of certain equipment, safety aspects and required power supply besides the required acqusition cost and depreciation in relation to the expected production output.
Finally the Bavarian State Beekeeping Consultants will be able to use and to update this database in order to standardize their recommendations and to facilitate and accelerate their response to the beekeepers in the field when these are requesting recommendations for their upcoming investment decisions.

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P 16 Comparison of four hive systems along an intervention options gradient: Implications on colony health, energy balance, labor input and honey properties

Vergleich von vier Bienenwohnungen/Beutensystemen entlang eines Gradienten an Eingriffsmöglichkeiten - Einfluss auf Gesundheitsparameter, Energiebilanz, Arbeitsaufwand und Honigeigenschaften

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Honeybees and farming remain inextricably interconnected although specialization and diverse challenges have disentangled both economic subsectors. The project "BienenHaltenHof" (BÖLN) studies whether active beekeeping impacts the biodiversity management of 12 farms, which participate in 'bee-schools' (cp. stable school concept) and establish their own hives. Additionally, we explore which hive systems are practical for which types of farms. Implications on colony health, energy balance, labor input and honey are recorded in a systematic comparison of four hive systems along an intervention options gradient (i) managed nesting cavity (=MNC), ii) stable comb hive, iii) mobile frame horizontal hive and iv) mobile frame vertical magazine hive) in two regions (n=32).

We present preliminary results from two project years (2022 and 2023). Our findings implicate that positive emotional connections to the insect world are vital for the implementation of biodiversity-friendly management options and that active beekeeping can be an instrument to achieve this. Success depends on various factors characterizing the individual farms (e.g. farm focus or involvement of family members). The comparison of hive systems did not yield significant differences regarding health parameters (except survival) or honey properties. In order to investigate correlations between managed hive types and parameters of interest, the experiment needs to be extended to additional years. Survival, working time and total weight gain per hive were significantly lower for tree cavity simulations (=MNCs). We conclude, that under the premise of keeping healthy colonies on farms, MNCs are not achieving desired results, although they might act as swarm sources on the population level. We will analyze, whether MNCs contribute to the emotional relationship of our project farmers to the needs of the insect world to the same extent as other managed hive systems while requiring much less labor input.

Keywords: beekeeping, honeybees, biodiversity, farming

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P 17 *Vespa velutina* **in bavaria – recording the occurrence and locating the nests**

Vespa velutina in Bayern – Feststellung der Verbreitung und Lokalisierung der Nester

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In 2022, a single drone of *Vespa velutina* was detected for the first time in northern Bavaria. In 2023, a *Vespa velutina* task force was formed across three districts with the aim of recording the occurrence of *Vespa velutina* and locating the relevant nests by involvement of beekeepers. Participating beekeepers were given live traps that were checked twice a day and used with the authorisation of the lower nature conservation authorities. In addition to those traps, several sightings of *Vespa velutina* were recorded by direct observations at apiaries sites. By using triangulation and telemetry, it was possible to locate and remove the corresponding nests wherever animals were observed. A total of five nests were identified. In terms of the method used to identify *Vespa velutina*, the observations at the apiaries were much more effective than the live traps. The triangulation method proved to be much more efficient than telemetry in identifying the nest locations. Flying with thermal imaging cameras did not lead to good results; only when the nest location was already known could flyingbe confirmed with thermal imaging cameras. Our results indicate that multiple observations at the apiaries and bait pots appear to be most effective for the initial detection. Marking captured animals, observing the direction of departure and measuring the time until return are good tools for locating nests. The nest location can be gradually narrowed down by moving bait pots in the flight direction of the departing *Vespa velutina*.

Keywords: *Vespa velutina*, asiatische Hornisse

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P 18 Verbreitung und Bedeutung der asiatischen Hornisse in Hessen –Statusbericht aus dem Jahr 2023 (N)

Distribution and relevance of the Asian hornet (*Vespa velutina* L.) in Hesse – status report for the year 2023

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The invasive Asian hornet *Vespa velutina* is rapidly spreading in Europe and reached the state of Hesse in 2019. The present study aims to determine its actual distribution and its relevance for the predation pressure on honey bee colonies. The beekeeping community was asked via the internet-based 'Infobrief' to report sightings. Nest sites were derived from the official database in Hesse (www.HLNUG.de). Starting mid-October 23, we observed hunting behavior in 10 bee yards in the municipality of Bensheim for seven weeks, by counting the number of Vespa (*V. velutina*, *V. crabro*) once per week for 30' per yard. Three apiaries in central Hesse, where *V. velutina* is still absent, served as controls. In addition, 51 nests from southern Hesse were recovered and dissected.

V. velutina occurred mainly in the Rhine valley (district Darmstadt: 52 sightings vs. 181 reported absences) against 6 sightings in the middle of the State (district Giessen, 109 absences) and 3 sightings reported from northern part (district Kassel, 91 absences). Approx. 150 nests were detected in 2023, mainly in the district Bergstraße (118 nests). The northernmost site was near Wetzlar. The highest nest density was observed in Viernheim (11 nests per km²). The nests grew continuously from August (mean 2.9 storeys) to December (8.3 storeys). However, the number of sealed brood cells reached a maximum at the end of September, before dropping to several hundreds at the beginning of December. No predation was recorded in the control yards. The Bensheim yards were visited by a total of up to 55 hunting *V. velutina* per week and up to 24 honey bees were collected. The flight activity of *V. velutina* was significantly dependent on temperature and time ($p < 0.05$, LR). The kill rate was 0.5 bees per hornet attack.

V. velutina is present in the Hessian Rhine valley with partially high nest densities. *V. velutina* increases the predation pressure on bee colonies in late autumn compared to the predation in a *V. velutina*-free area.

Keywords: invasive, predation, Vespa spp., Apis mellifera, flight activity

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P 19 *Vespa velutina* **– Eine neue Bedrohung für Bienenvölker in Baden-Württemberg (N)**

Vespa velutina – a new threat to honey bee colonies in Baden-Württemberg

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The Asian hornet (*Vespa velutina nigrithorax*), a wasp species originally native to Asia, was accidentally introduced to Europe in 2004 and is an invasive threat that voraciously feeds on various insect species including honey bees. Currently classified as an invasive alien species of concern, it falls under EU regulation 143/2014. Assigned to Article 16 of the regulation through the Federal Agency for Nature Conservation in Germany, states must take immediate eradication measures.

While worker hornets feed primarily on carbohydrate-rich sources such as nectar and fruit, larval development requires protein-rich sources, often obtained from flying insects, including honey bees. This predation weakens honey bee colonies and jeopardizes their winter survival. Beekeepers, already concerned about the parasitic mite *Varroa destructor*, are further alarmed by the spread of this new predator, which in other countries has led to colony losses, reduced pollination efficiency and negative impacts on agricultural production.

Initially rare, its sightings have increased dramatically since 2023, signaling a rapid expansion in Germany, especially along waterways. To curb further spread within Baden-Württemberg, a central coordination station will be established at the State Institute of Bee Research (LAB) at the University of Hohenheim, Stuttgart. We will validate sightings and coordinate nest removal with local specialists. We will also provide educational programs and training sessions for beekeepers and other stakeholders. Close collaboration with the university will allow us to address unanswered research questions regarding this new invasive species, improve our understanding of its biology, and develop practical methods for its control and containment.

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Physiologie & Verhalten

P 20 Unraveling the non-neuronal cholinergic system of the honeybee (N)

Aufklärung des nicht-neuronalen cholinergen Systems der Honigbiene

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The cholinergic system is vital for the development of various insect species. Honeybee nurses feed their larvae with brood food, secreted from the hypopharyngeal glands (HPG) and mandibular glands, containing Acetylcholine (ACh) in with peak concentrations of up to 8 mMol in L2 larvae - an order of magnitude higher than in the brain. Previous research from our lab has shown that the size of the HPG is affected by neonicotinoids. However, it is currently unknown what the mode of action of ACh in brood food is and where the receptors are located in the larva. Here, we present preliminary data on ACh concentrations in brood food from colonies exposed to neonicotinoids and on identifying anticipated receptors in the alimentary canal.

We employed small colonies (3000 bees) in Mini-Plus hives, situated under semi-field conditions, receiving sugar solution with varying concentrations of clothianidin (50 or 100 ppb), thiacloprid (8800 ppb), or a solvent control. Pollen was available and renewed twice per day over the 3-week treatment. Brood food was collected from cells with larvae at different developmental stages (L1-L5) for measuring the ACh concentration using fluorometric analysis.

Furthermore, we present two approaches to localize the nicotinic ACh receptor (nAChR) in the larva: Preliminary stainings of honeybee larvae with α-Bungarotoxin conjugated with a fluorophore revealed little to no signal in the alimentary canal. Additionally, a honeybee line was generated using CRISPR/Cas9 induced transgene insertion to label the α1-subunit of the nAChR, allowing us to detect specific nAChR subgroups in different developmental stages.

Unraveling the non-neuronal cholinergic system in honeybees is crucial for a comprehensive understanding of the diverse effects of insecticides, including potential impacts on development and in-hive communication.

Keywords: Acetylcholine, CRISPR/Cas9, nicotinic Acetylcholine receptor

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P 21 Einfluss von Pollenfallen auf das Pollensammelverhalten von Honigbienen

Effect of pollen traps on pollen foraging behavior of honeybees

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Pollen traps are used to harvest and market hive pollen from bee colonies. The pollen trap is placed in front of the entrance or at the bottom of the hive. The bees pass through a grid and lose their pollen pellets, which are collected and removed. We investigated the influence of pollen traps and the removal of pollen from bee colonies on colony development, chronic bee paralysis virus (CBPV) load and honey yield of 18 bee colonies during the 2023 winter rape bloom. Six of the 18 colonies received a pollen trap over the entire observation period. Six colonies received a pollen trap every three days for an interval of three days and six colonies did not receive any trap (control group).

No significant differences were found between the groups with respect to colony development or CBPV load. At the end of the observation period, the weight of newly hatched workers was determined. Here, too, there were no differences between the groups, nor were there any differences in pollen stocks. However, the groups differed in the weight of the collected pollen pellets. The collected pollen pellets were smaller in the colonies with permanently inserted pollen trap than in the control group. With the temporarily inserted pollen trap, the harvest was very efficient with an average of 694g +/- 299g in 16 days compared to the permanently inserted pollen trap with 803g +/- 408g in 24 days. The selected pollen trap with a hole size of 4.55 mm allows a sufficient pollen supply to the bee colonies. Regular interruptions of pollen collection reduce the pollen harvest only slightly.

Keywords: pollen nutrition, colony development, chronic bee paralysis virus

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P 22 Brood activity in winter accelerates ageing and shortens the lifespan of winter bees and increases infestation with Varroa destructor, which can be prevented by caging the queen (N)

Brutaktivität im Winter beschleunigt die Alterung und verkürzt die Lebensspanne von Winterbienen und erhöht den Befall mit Varroa destructor und kann durch Käfigen der Königin verhindert werden

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Keywords: winter bees; fat body, immunity, climate change, aging

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P 23 Development of a climate-friendly and economically resilient beekeeping practice (N)

Entwicklung einer klimaschonenden und ökonomisch resilienten imkerlichen Betriebsweise

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Keywords: extensive resilient beekeeping, honey bee vitality, climate change, *Varroa destructor*, honey yield

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Genetik & Zucht

P 24 What makes the difference? Molecular insights into early diploid drone larvae of the western honey bee *Apis mellifera* (N)

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The molecular basis of sex determination is well understood in the western honey bee *Apis mellifera* in which the *complementary sex determiner (csd)* gene acts as the primary signal of sex determination. The following downstream gene regulatory cascade is based on the allelic endowment. Heterozygosity at *csd* initiates female development (2nF), while hemi- (1nM) and homozygosity (2nM) leads to male development. *Csd* homozygous individuals develop into diploid drones and have zero fitness. They are recognized and removed by worker bees shortly after hatching. The signal which triggers this behavior 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 the changed expression of the phenotype.

We used different early larval stages from an inbred cross reared *in-vitro* for transcriptome sequencing to investigate gene expression differences between the different genotypes. 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 supports the hypothesis that the detection might be linked to differences in the CHC profiles. Consequently, additional biochemical and functional analyses will pave the way for a comprehensive picture of the underlying genetic network that leads to the discrimination of diploid drone larvae in *Apis mellifera*.

Keywords: Apis mellifera, diploide drones, gene expression, transcriptome sequencing

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Bienenschutz & Pflanzenschutz

P 25 **Analyse von Einflüssen des Klimawandels auf die Imkerei und Entwicklung von Handlungsoptionen für die Imkerschaft**

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

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In this project we analyse the influence of aridity and high temperatures caused by the climate change on *Apis mellifera* at a hive and individual level. At the same time, we are investigating possible solutions for practical beekeeping to counteract potential negative effects.

One approach is to reduce the heat, that is transferred into the hive – to make it easier for *Apis mellifera* to maintain the climate in the hive despite hot periods. Different sheet metal roofs as well as variable hive-colours or isolations are tested. First results indicate that painting the metal roof with white colour can clearly reduce temperature in and on top of the beehives during hot periods. Another way to support *Apis mellifera* is by providing a watering place. To increase the attractiveness of the watering places different substances will be tested. To investigate the impact of the currently observed heat and drought conditions on the development of *Apis mellifera*, these conditions are simulated in laboratory experiments. Subsequently, various parameters such as size weight or learning ability will be measured. For drones, the focus is on the reproductive ability, the sperm number, and sperm vitality. The effects of drought and heat on colonies will be investigated by measuring lifetime, population development and pathogen load. In field experiments, we test the use of thermal sheaths in the brood nest for its effect on brood development and population strength.

Keywords: climate change, Apis mellifera

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P 26 The German Bee Monitoring Project: Analysis of pesticide residues in stored pollen

Das Deutsche Bienen Monitoring Projekt: Ergebnisse der Pflanzenschutzmittel Rückstände im Pollen

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The German Bee Monitoring has been in existence for 20 years to better understand drivers of colony losses, especially during winter. We have been collecting health measures, such as *Varroa destructor* infestation, pathogen presence, viral infections, and overwintering success since 2004. Over 120 beekeepers are currently involved nationwide with more than 1,200 colonies monitored annually. The overwintering dynamics of these colonies are monitored. Bee, honey and pollen samples for disease and residue analyses are taken up to three times per year in spring, summer and fall. Although pesticide residue analysis was first added in 2006, it has regularly been part of the annual analysis since 2009. Here we report the preliminary pesticide residue results for N = 2,211 apiary samples. In the last few years, our multi-residue analysis has been able to look for residues in stored pollen of 475 different pesticides and their metabolites. Honey bees function like environmental monitors, foraging in a wide radius from their point-source colony. The residues detected thus essentially reflect current agricultural practices within a 2-6 km radius of the apiary, the typical foraging distance of honey bees.
A total of 75 of the 475 active substances and metabolites were detected in the bee bread samples from 2022, 12 fewer than in 2021. The residues were mostly in the trace range, though 61 active substances were detected at least once above the limit of quantification. All together 90.7% of the samples contained at least one pesticide residue, though only in 67.4% of the samples was at least one active substance above the limit of quantification, 9.3 percentage points less than in the previous year (76.7%). We will also report on the overall trends of pesticide residues from 2009-2023, where insecticide residues are decreasing over time, while fungicide residues are increasing, a trend that matches current agricultural plant protection policies.

Keywords: honey bee health, pesticides, pollen, German bee monitoring

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P 27 Do certain insecticide tank mixtures used in organic apple orchards pose a risk to honey bees (*Apis mellifera*)?

Stellen bestimmte insektizide Tankmischungen aus dem ökologischen Apfelanbau ein Risiko für Honigbienen (*Apis mellifera*) dar?

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P 28 Test design for a long-term exposure of large earth bumblebees (*Bombus terrestris*) to microbial pesticides in semi-field effect studies

Testdesign für eine Langzeit-Exposition von dunklen Erdhummeln (*Bombus terrestris*) gegenüber Pflanzenschutzmitteln aus Mikroorganismen in Halbfreilandstudien

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Biological plant protection products (biocontrol agents) play an increasingly important role for sustainable crop production following the farm-to-fork strategy set in 2020 in the EU. Microbial pesticides for example consist of bacteria, fungi or viruses and have to fulfil the approval criteria laid down in (EC) 1107/2009 like all other active substances used in synthetic chemical plant protection products (PPP). However, due to their different modes of action, test designs have to be adapted.

One essential adaptation in study designs is the duration of the exposure period. In pollinator semi-field effect studies (e.g. OECD75 / EPPO170 for honey bees or ICPPR ring-tested study designs for mason bees and bumblebees) the exposure period is normally set to 7-10 days, assuming that the highest exposure is given directly after application of the PPP. For testing microbials this would not be sufficient in most cases as viruses, bacteria or fungi are continuously multiplying after application and thus exposure increases accordingly over time.

For an exposure study with the large earth bumblebee (*Bombus terrestris*) to an insectivorous entomopathogenic fungus we developed a semi-field test design with a long-term exposure period of up to 30 days. It requires permanent flowering of crops inside the tunnels to prevent starvation of the bumblebees and additionally modified research and development hives (R&D hives) to ensure a maximum synchronized development of bumblebee colonies with minimum disturbance during assessments.

Keywords: bumblebee, semi-field, microbial pesticides, long-term exposure

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P 29 **Digital assessment of solitary bees in semi-field trials, *Osmia* spp.**

Digitale Auswertung von Solitärbienen in Semi-Feld Studien, *Osmia* spp.

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Solitary bee semi-field studies have been successfully conducted in the past. The assessments of flight activity and nesting behavior of solitary cavity-nesting bees in semi-field trials is time consuming and depends e.g. on weather conditions. First attempts for a digital assessment have been conducted using 3D-printed bee counters. These counters were originally designed to measure honey bee activity at the hive entrance, but with a slight adaptation our aim was to evaluate their potential use in semi-field trials with solitary bees (*Osmia spp*). With these counters the flight activity of solitary bees can be assessed without the need of manual observation. The counters results were validated by manually counting bees entering the nesting cavities through the counters by comparing it to the "count-in" value of the counter. Although the "count-in" value was slightly higher than the "count-out" value, it was possible to show a good correlation between the manual assessment and the results of the counter. In addition, we used Dimethoate as a positive control in 4 tunnels (Dimethoate EC 400, 145g/ha) and compared nesting success, flight activity and reproduction of the bees to 4 untreated tunnels. In a period of 14 days following the application the number of female solitary bees actively using the nesting blocks was slightly lower in the dimethoate treated tunnels (mean: 16 bees) compared to the control (mean: 19 bees), but the flight activity was significantly higher (mean: 15 bees/15min), compared to the control (mean: 12 bees/15min). The number of cocoons collected was significantly lower in the Dimethoate treated tunnels (mean: 67 cocoons) compared to the control (mean: 116 cocoons). Digital counters proved to be an efficient tool in semi-field trials with solitary bees although further validation and improvement is necessary.

Keywords: risk assessment, electronic bee counter, semi-field, solitary bees, non-Apis bees

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P 30 Does pollen availability and fungicide exposure during the larval stages influence the life span of adult honey bees? (N)

Beeinflusst die Pollenverfügbarkeit und eine Fungizidexposition während der Larvalstadien die Lebenserwartung von adulten Honigbienen?

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Honey bee health is influenced by multiple factors, such as a limited pollen supply, caused by breaks in floral resources, and the use of plant protection products. Using a full factorial experimental design, we investigated whether these two stressors, pollen shortage and fungicide exposure during larval development, influence the life span of adult honey bees. In spring we collected newly emerged bees from large and small colonies that had previously been placed next to rapeseed fields, which were subject to a fungicide treatment during bloom in comparison to control fields without treatment. Half of the colonies were equipped with pollen traps to create a pollen dearth. For every single group we investigated four to six cages with 25 newly emerged bees each (n bees = 2,000). The cages were placed in an incubator for 28 days and the daily mortality was recorded. We also conducted field studies, in which we added 25 young marked bees per group into five small colonies in Miniplus hives (n bees = 920). The number of marked bees still alive was recorded every second day over a period of four weeks. The experiments were carried out simultaneously at three different locations: Hohenheim, Veitshöchheim, and Braunschweig. The results of the cage experiments show that young bees from the smaller experimental colonies live slightly longer than the bees from the commercial colonies. In the field trials, there were no significant differences in the recovery rate of bees in observation colonies. Hence, the fungicide treatment and the pollen trap had no effect on mortality or recovery rates, although there were differences between locations. The results show that bee colonies can compensate temporary pollen limitation during brood rearing.

Keywords: pollen limitation, stress, hive size, cage assay, survival

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P 31 Species-specific sensitivity of different bee species after a field-realistic application of an insecticide

Artspezifische Sensitivitätsunterschiede verschiedener Bienenarten nach feldrealistischer Anwendung eines Insektizids

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In the registration process of pesticides in the EU, mainly honey bees are used to assess the ecotoxicological effects of pesticides on bees. Data on wild bees are often lacking. Therefore, it remains unclear whether the honey bee can adequately serve as surrogate for wild bee species.

In a series of laboratory trials, we tested the effects of a pyrethroid insecticide, containing lambda-cyhalothrin, on various bee species with different life history characteristics (*Apis mellifera*, *Andrena vaga*, *Bombus terrestris*, *Colletes cunicularius*, *Megachile rotundata*, *Osmia bicornis*, *Osmia cornuta*).

Our results on mortality and sublethal effects showed significant species-specific responses. The survival probability of bumble bees and mason bees was least affected, whereas leaf-cutting bees were affected the most. The honey bee showed medium sensitivity compared to the other bee species.

The majority of sublethal effects, i.e. behavioral abnormalities, was observed within the first hours after application. In some of the solitary species, for example mason bees, such effects were evident over a longer time until the end of the observation period.

While individual weight of the bee species explained some of the observed mortality patterns, differences were likely depended on other ecological, phylogenetic or toxicogenomic parameters as well.

Our results support the suitability of the honey bee as surrogate for some bee species, especially when using safety factors. However, a larger set of bee species is required in order to cover species that are more sensitive. In addition, the inclusion of sublethal effects in sensitivity estimations provides a more comprehensive approach to risk assessment.

Keywords: honey bee, wild bees, risk assessment, plant protection products, insecticide

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P 32 Oilseed rape cropping systems with companion plants for insect pest control and insecticide reduction (oilseed rape OP) (N)

Rapsanbausysteme mit Begleitpflanzen zur Schadinsektenabwehr und Insektizid-Reduktion (Raps-OP)

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Insect pests have a major impact on oilseed rape cultivation. Increasing resistance and the limited choice of insecticides are exacerbating the problem. At the same time, pollinator species are disappearing, especially in poorly structured agricultural landscapes. An innovative solution would be to grow plants that are more attractive to oilseed rape pests than the oilseed rape itself, so-called trap plants ("sacrificial plants") as "diversionary feeding" in mixtures or alongside the oilseed rape. These can either be tolerated or specifically controlled ("attract and kill"). At the same time, these plants, such as turnip rape, early oilseed rape varieties, pith stem cabbage, etc., extend the flowering horizon, which, together with a significant reduction in insecticides, should have a positive effect on pollinators and antagonists of oilseed rape pests.

In order to qualitatively and quantitatively investigate the measures described with regard to their attractiveness for pollinating insects, the respective trial plots and the insect flight are filmed once a week during the individual flowering phases with a camera and evaluated.

After the first year of the trial, it became apparent, especially later in the flowering period, that the variants with the early oilseed rape variety, marrowstem kale and turnip rape were visited 1.5 - 7 times more frequently by wild pollinators than the main crop, oilseed rape. Honey bees also particularly preferred turnip rape and pithy stem cabbage (1.5 and 2.8 times more frequently than the main crop).

No correlation between the flowering intensity of the experimental plots and the frequency of insect visits can currently be deduced from the results to date. A possible cause could be the distribution effect with regard to insect visits with increasing flowering intensity or nectar supply playing a greater role. It is also conceivable that the nectar supply of the respective companion plants varies greatly.

Keywords: Biodiversität, Pflanzenschutz, Bestäuberschutz, Kamerabeobachtung

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P 33 Der Einfluss von Pflanzenschutzmittel-Mischungen auf die Flugaktivität von Honigbienen (N)

The effect of plant protection product mixtures on the flight activity of honey bees

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There has been a significant decline in pollinating insects in recent decades. In addition to factors such as changes in land use, climate change and various diseases, the use of plant protection products (PPPs) is regarded as a major factor in this decline. The effects of PPP mixtures, in particular, are difficult to predict. However, mixtures occur naturally in the field, and this is why bees are exposed to multiple PPPs at the same time. The consumption of mixtures can lead to unexpected harmful effects. In this study, the flight activity of honey bees was investigated after chronic treatment with two PPP mixtures. RFID technology was used, in which individual bees can be precisely identified by a chip and their flight activity can be accurately recorded by scanners at the hive entrance. While the mixture of neonicotinoid (Mospilan®, active ingredient (a.i.) acetamiprid) and non-SBI (sterol biosynthesis inhibiting) fungicide (Cantus® Gold, a.i. boscalid and dimoxystrobin) had no negative effects on bees, the mixture of neonicotinoid (Mospilan®, a.i. acetamiprid) and SBI fungicide (Difcor®, a.i. difenoconazole) had a negative effect on the number of foraging trips. Bees that consumed the mixture performed significantly fewer foraging trips (GLMM, $p < 0.05$). Such an effect could be due to the interaction of the SBI fungicide with the detoxification mechanism which leads to an inhibition of crucial detoxification enzymes. The study shows that more detailed investigations into the effect of PPP mixtures are needed in order to be able to make a suitable risk assessment.

Keywords: insecticide, fungicide, plant protection product mixtures, flight activity, RFID

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Bienenpathologie

P 34 Characterization of microbial collagenase (ColA) secreted from *Paenibacillus larvae* (N)

Charakterisierung der von *Paenibacillus larvae* sezernierten, mikrobiellen Kollagenase (ColA)

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One of the most devastating bee diseases responsible for significant colony losses is American Foulbrood, caused by the gram-positive, spore-forming bacterium *Paenibacillus larvae*, which only affects the larval stages of honeybees. The two epidemiologically relevant genotypes, *P. larvae* ERIC I and ERIC II, differ in their virulence as they differ in the suite of virulence factors used during pathogenesis. For the development of effective treatment methods, it is important to understand the molecular mechanisms of pathogenesis and to identify crucial bacterial virulence factors. Secreted proteases have long been assumed to play a role as virulence factors in the infection by *P. larvae*, but none has been identified so far. We here present our results on putative protease virulence factors obtained by analysing the protease profiles of culture supernatants of *P. larvae* ERIC I and ERIC II cultures. Using degradation assays and zymograms, we identified a protease exhibiting gelatinolytic activity in the supernatants. *In silico* analyses identified it as microbial collagenase (*Pl*ColA), and a member of the M9 metalloprotease family. Differences in zymogram banding patterns suggested that *Pl*ColA differs between *P. larvae* ERIC I and ERIC II which was confirmed by *in silico* structural analysis. In both genotypes, all required domains for collagenolytic activity were encoded, but the proteins deduced from the genomic data differed in size. To substantiate that the identified gene encodes *Pl*ColA and that this protease is responsible for the observed gelatinolytic activity, gene activation mutants for *Pl*ColA were constructed and tested in different functional assays. In the upcoming season, we will use the *Pl*ColA-deficient *P. larvae* mutants to verify the role of *Pl*ColA as virulence factors for both genotypes.

Keywords: *Paenibacillus larvae*, American Foulbrood, Virulence factors, Proteolytic enzymes

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P 35 Multiple locus VNTR analysis - a good option for epidemiological studies of *Paenibacillus larvae*

Multiple Locus VNTR Analyse - eine gute Option für epidemiologische Untersuchungen von *Paenibacillus larvae*

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Various genotyping methods exist for the pathogen that causes American Foulbrood, the Gram-positive bacterium *Paenibacillus larvae*. The first protocol developed for *P. larvae* genotyping was repetitive element PCR (repPCR) performed with Enterobacterial Repetitive Intergenic Consensus (ERIC) primers, which led to the identification of several ERIC-genotypes. Among those, *P. larvae* ERIC I and II are the only ones found in diseased colonies since more than 50 years. *P. larvae* ERIC III-V are hypervirulent and represented by only a few strains isolated from honey. The next genotyping method developed for *P. larvae* was Multi Locus Sequence Typing (MLST). The established MLST scheme, which is based on the analysis of seven housekeeping genes, identified 48 *P. larvae* MLST types which grouped according to the ERIC classification thus confirming and extending it. However, we felt that MLST was not able to sufficiently reflect the genetic variance of *P. larvae* ERIC II. In order to achieve a better resolution of the genetic variability of the *P. larvae*, we established and optimized multiple locus VNTR analysis (MLVA) for this species. MLVA is a PCR-based method that analyzes the number of tandem repeats (VNTR, variable number of tandem repeats) in different regions of the genome. During the adaptation and optimization of the MLVA, we selected 11 sequence regions that reproducibly yielded different VNTR patterns enabling the fine-typing of *P. larvae*. By analyzing more than 1,000 *P. larvae* strains with this optimized method, we identified more than 300 MLVA types. Hence, the resolution power of this method comes close to whole genome sequencing but is much cheaper and faster. The classification into the ERIC genotypes remained unchanged but it became clear that the two practically relevant genotypes, ERIC I and II, exhibit similar genetic variability, which could not previously be demonstrated by MLST analyses.

Keywords: *P. larvae*, molecular typing, MLVA

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P 36 Antimicrobial peptides as part of the immune response in honey bee larvae (N)

Antimikrobielle Peptide als Teil der Immunantwort in Honigbienenlarven

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Antimicrobial peptides (AMPs) are a class of small peptides that play an important role in the innate immune system of invertebrates. They have a broad spectrum of inhibitory effects against bacteria (Gram+ and Gram-), fungi, parasites, and viruses. The innate immune response of invertebrates include the local and the systemic immune response. For both, the detection of pathogens triggers the corresponding immune signalling pathways and subsequently the secretion of AMPs. The signalling cascades are mostly studied in Drosophila. However, it is known from the honey bee that not only are all the necessary components of the signalling pathways present in the genome, but also that various AMPs serve the local and systemic defence against invading pathogens.

Paenibacillus larvae, the causative agent of American Foulbrood, is one of the most relevant pathogens of honey bees. Infection with *P. larvae* leads to a massive proliferation of vegetative bacteria in the midgut, which is likely to trigger a local immune response. A very high accumulation of pathogens in the intestinal lumen can also trigger a systemic immune response. And indeed, previous studies have shown that AMPs are differentially upregulated during *P. larvae* infection in larvae. However, since *P. larvae* is a very successful pathogen and obligate killer, we hypothesized that it should rather not be affected by the secreted AMPs. To test this hypothesis, we analysed the susceptibility of *P. larvae* ERIC I and II against four larval AMPs: defensin1, abaecin, apidaecin, and hymenoptaecin. We performed different inhibition assays and tested the AMPs individually and at different concentrations as well as in combination. Our results show that *P. larvae* is resistant to all four AMPs and combinations thereof, which explains the extraordinary success of *P. larvae* as larval pathogen.

Keywords: antimicrobial peptide, Inhibition assay, *Paenibacillus larvae*

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P 37 Evolution of virulence in *Paenibacillus larvae*, a honey bee pathogenic bacterium (N)

Evolution der Virulenz von *Paenibacillus larvae*, einem für Honigbienen pathogenen Bakterium

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Paenibacillus larvae is a Gram-positive, spore-forming bacterium and the causative agent of the notifiable epizootic American Foulbrood (AFB). There is no niche or known host for *P. larvae* other than honey bee larvae, indicating that this pathogen is a highly specialized obligate pathogen. These characteristics promote genome reduction and can result in genetic minimalism through major loss of genes. The infection cycle shows that *P. larvae* is also adapted to the eusocial behavior of honey bees, as the spread of spores is linked to the hygiene behavior of the bees. An infection starts when first instar larvae ingest food contaminated with *P. larvae* spores, which then germinate in the midgut. Massive proliferation is eventually followed by an infiltration of the hemocoel, causing the death of the infected larva. *P. larvae* decomposes the larval cadaver to a ropy mass, which dries into the so-called foulbrood scale containing millions of newly generated spores. These spores are the source of intra- and intercolonial horizontal transmission.

To understand the evolutionary processes between the host and the pathogen, we established an *in vivo* assay in order to serially passage *P. larvae* through honey bee larvae, mimicking the natural infection cycle in a colony. Our experimental design eliminates cultivation of *P. larvae* in the laboratory and, instead allows *P. larvae* to decompose the larval cadaver to a ropy mass that dries into the foulbrood scale. Spores are isolated from these scales, counted and used for the next round of infection. Using statistical analyses we assessed whether the survival rate systematically changed during the evolution experiment. The initial results of the survival analysis show a decreasing relative mortality risk over the experimental evolutionary period. Interestingly, we also found that sporulation did not occur in all larvae that died from *P. larvae*.

Keywords: *Paenibacillus larvae*, *in vivo* assay, serial passages

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P 38 Secondary metabolites produced by *Paenibacillus larvae* as potential virulence factors in American Foulbrood (N)

Die Sekundärmetabolite von *Paenibacillus larvae* als potenzielle Virulenzfaktoren der Amerikanischen Faulbrut

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The Gram-positive and spore-forming bacterium *Paenibacillus larvae* (*P. larvae*) is pathogenic only to honey bee larvae and causes the epizootic American Foulbrood (AFB). Using repPCR performed with enterobacterial repetitive intergenic consensus (ERIC) primers, several ERIC genotypes can be defined which also differ phenotypically, most importantly in virulence. Two *P. larvae* ERIC genotypes, ERIC I and II, are of epidemiological relevance and have therefore been analyzed in detail over the last two decades. *P. larvae* ERIC I and ERIC II both follow different pathogenesis strategies due to their different genomic and metabolomic setup resulting in the described differences in virulence. Several virulence factors have been described and functionally analyzed for *P. larvae* (e.g. chitin-degrading enzyme, AB toxins, S-layer protein), but little information is available on the role of *P. larvae* secondary metabolites in AFB pathogenesis. In general, secondary metabolites have been already shown as potential virulence factors (e.g. in regulation). A few of them are peptides synthesized ribosomally and post-translationally modified (RiPPs) or produced by multimodular enzymes called non-ribosomal peptide synthetases (NRPS). Genome mining of *P. larvae* ERIC II has revealed six potential RiPP-like and five potential NRPS-derived compounds. To date, four NRPS-derived compounds could be isolated and characterized for *P. larvae* ERIC II (including their potential functions): sevadicin (antibacterial), bacillibactin (siderophore), paenilamicin (antibacterial), paenilarvin (antifungal). The fifth NRPS-derived compound has been unveiled as a volatile compound. However, the RiPPs produced by *P. larvae* ERIC II remain elusive. The search for the link between secondary metabolites and AFB pathogenesis plays a pivotal role to understand the host-pathogen relationship, which in turn is a prerequisite for finding efficient treatment strategies against AFB.

Keywords: *Paenibacillus larvae*, AFB, virulence, secondary metabolites, peptides

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P 39 Sevadicin and Paenilamicin, key factors for the successful infection cycle of *Paenibacillus larvae*? (N)

Sevadicin und Paenilamicin: Schlüsselfaktoren für den erfolgreichen Infektionszyklus von *Paenibacillus larvae*?

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Keywords: *Paenibacillus larvae,* fluorescence *in situ*-hybridization, honey bee larvae, microbiota

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P 40 Establishment of an exposure bioassay for experimental infection of honey bee larvae with SBV (N)

Entwicklung eines Expositionsbioassays für die experimentelle Infektion von Honigbienenlarven mit SBV

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Keywords: Virus, pathogen, protein expression, immunofluorescence

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P 41 Analysis of the genetic diversity of *Nosema apis* based on Short Tandem Repeats (STR)

Analyse der genetischen Vielfalt von *Nosema apis* mit Hilfe von Short Tandem Repeats (STR)

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Nosema apis and *Nosema ceranae* are microsporidian parasites of the Western honey bee (*Apis mellifera*), which infect the epithelial cells of the midgut of adult bees. While *N. apis* is known as a pathogen specific for *A. mellifera* since more than 100 years, *N. ceranae* was originally described as a pathogen of the Eastern honey bee *A. cerana*, but obviously switched host several decades ago and by now is even more prevalent than *N. apis* in many *A. mellifera* populations. Results on the differences in virulence between *N. ceranae* and *N. apis* are contradictory as are reports on the replacement of *N. apis* through *N. ceranae* in *A. mellifera* populations. One possible explanation for these contradictory results is the described sensitivity of *N. ceranae* spores to cold, which could have a climate-dependent effect on the spread and virulence of *N. ceranae*. It was also suggested, that assertiveness and virulence differ between different populations of *N. apis* and *N. ceranae*, which would indicate a population genetic effect in the two species. Several studies attempted to characterize *Nosema* spp. on a population genetics level in order to investigate the genetic differentiation between phenotypically different or geographically distant *N. ceranae*- or *N. apis*-populations. While the results for *N. ceranae* are contradictory, there is evidence for genetic variance between *N. apis*-isolates from geographically distinct *A. mellifera* samples. This prompted us to develop a short tandem repeat (STR) -based analysis adapted to the characterization of the genetic diversity of *N. apis*. We tested 60 pairs of primers flanking putative STR-regions of the *N. apis* genome and after evaluation and optimization, five pairs of primers were identified which were suitable to identify genetic variants. We present here our data from the STR-based analysis of the *N. apis* population circulating in the *A. mellifera* population in northeastern Germany.

Keywords: *Nosema apis*, short tandem repeats, genetic diversity

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P 42 Development of a tool for the study of genetic diversity of *N. ceranae* populations, based on micro and minisatelite markers (N)

Entwicklung eines Instruments zur Untersuchung der genetischen Vielfalt von *N. ceranae*-Populationen auf der Grundlage von STRs

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Nosema ceranae is an obligate intracellular microsporidian parasite of honeybees. In Germany, this invasive species showed an increasing beehive prevalence over the last 20 years, essentially replacing its congener *N. apis*. This population growth has led to increased scientific interest in further studies on the genetic nature of *N. ceranae* populations and their potential association with beehive health. Since typically millions of *Nosema* spores are processed per sample, only co-dominant typing methods, such as those based on short tandem repeats (STRs), are suitable to capture the true species diversity. Using the available *N. ceranae* genome sequence, we designed a total of 112 primer pairs against flanking sequences of micro- and minisatellite regions. Primer pairs showing potential cross-amplification as determined by BLASTn were discarded and remaining 89 sets of primers flanking *N. ceranae* STRs were further analysed. PCR amplicons using these primers were first subjected to high-concentration agarose gel electrophoresis to check for reliable amplification, and then analyzed by capillary electrophoresis to detect length polymorphism. The following selection criteria were used to identify the most informative STRs markers: (i) presence of multiple amplicons for a given STR per sample, (ii) consistency between triplicate runs for each STR marker and sample, and (iii) observation of length polymorphism of the same STR marker between samples. This resulted in a final set of 6 STR markers (out of 112). Selected candidates were further optimized for annealing temperature and sensitivity. The application of these STR markers to typify genomic DNA extracted from *N. ceranae* positive bees from different regions of Germany is in progress. Preliminary results suggest the presence of genetic clusters when analysing samples of different geographic origin. The development of this tool will facilitate future epidemiologic studies of bee nosemosis.

Keywords: *Nosema ceranae*, SRT, genetic diversity

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P 43 **Development of a DWV-specific immunohistochemistry protocol to analyze tissue and cell tropism of DWV (N)**

Entwicklung einer DWV-spezifischen Immunhistochemie zur Analyse des Gewebe- und Zelltropismus von DWV

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Infections with deformed wing virus (DWV) are one of the major threats to honey bees, as clinically relevant DWV-infections in conjunction with *Varroa destructor* infestation correlate significantly with honey bee colony losses. Overt DWV infections depend on the transmission of the virus to bee pupae by *V. destructor* and are characterized by pupal death or adult bees emerging with deformed wings and a shortened abdomen. To better understand the pathogenesis of DWV infections, we aimed at identifying tissues and cells which can be infected by DWV und permit replication of the virus. We previously established fluorescence *in situ* hybridization (FISH) analysis for the detection of infected cells and here aimed at developing a DWV-specific immunohistochemistry protocol. Immunohistochemistry is an antibody-based method that allows to visualize proteins in tissues while preserving its microstructure. Firstly, we recombinantly expressed and purified the capsid protein recDWV-VP2 for the commercial (ASKA Biotech) production of monoclonal antibodies. One of the antibodies obtained showed high specificity for the recDWV-VP2 antigen in dot blots and Western blots and was able to distinguish between bees that had tested DWV- positive and DWV- negative in RT-PCR assays. We next tested this antibody in immunohistochemistry using sections of brain, thorax and intestine of crippled (DWV-positive in PCR) and healthy (symptomless and DWV-negative in PCR) bees. DWV was detected in the epithelial cells of the intestine and in the cells of various regions of the brain of crippled bees. In thorax sections, signals were detected only in the connective tissue surrounding the muscle cells, the perimysium and endomysium, but not inside the muscle cells. These results confirm and extend previous findings on midgut- and neurotropism of DWV by showing clear cell tropism: DWV can infect epithelial and neuronal cells, but not muscle cells.

Keywords: Virus, pathogen, protein expression, immunofluorescence

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P 44 American Foulbrood monitoring in Berlin: results of molecular epidemiological analyses

AFB-Monitoring in Berlin: Ergebnisse zur molekularen Epidemiologie

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American Foulbrood is a disease of honey bee larvae that occurs worldwide and is caused by the Gram-positive bacterium *Paenibacillus larvae*. Five genotypes of *P. larvae* have been described, which differ from each other not only at the genomic level, but also in their phenotype. The differences include the metabolism, morphology and above all the virulence of the bacteria. The spores of *P. larvae* can be detected in various materials, of which brood comb honey in particular is used for the early diagnosis of American foulbrood.

In the course of an AFB-monitoring program, which has been carried out continuously at the Institute for Bee Research Hohen Neuendorf for more than 20 years, around 1,000 brood comb honey samples were examined for *P. larvae* each year. For species determination, we used classical microbiological cultivation techniques in combination with species-specific PCR protocols. For a more detailed epidemiology, we not only determined the ERIC-genotype by rep-PCR and the sequence type (ST) by multi-locus sequence typing (MLST), but also used the recently established and optimized MLVA (multi locus variable number of tandem repeats) analysis. Using the example of our AFB-monitoring in Berlin, we will demonstrate the power of these methods for the molecular epidemiology of *P. larvae*. Samples from the years 2002-2023 were analyzed and the MLVA types of the isolated *P. larvae* strains were determined. The location data of the analyzed samples allowed a geographical evaluation of the epidemiological situation of *P. larvae* in all 12 districts of Berlin over 20 years.

Keywords: American Foulbrood, epidemiology, MLVA

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P 45 20 Jahre – Monitoring der Amerikanischen Faulbrut in Niedersachsen

20 years - Monitoring of American foulbrood in Lower Saxony

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American foulbrood (AFB) of honey bees caused by the spore-forming bacterium *Paenibacillus larvae* is a notifiable epizootic disease in most countries. The control of American foulbrood in Lower Saxony is based on three pillars: 1. early diagnosis by the detection of spores in honey samples gained from brood combs (AFB-monitoring), 2. the beekeeping advisory service of the LAVES and 3. the sanitation of bee colonies instead of killing them. The early diagnosis of AFB spores in honey samples allows the detection of the pathogen shortly after infection and before a visible outbreak of the disease in infested colonies.

In 2004, a state-funded AFB-monitoring project was started in Lower Saxony. On a voluntary basis, the district beekeepers' associations take samples from around 10% of their beekeepers (one apiary per beekeeper) annually. Examination costs are funded by the Federal Ministry of Agriculture. In principle, the apiaries should be permanent. One apiary represents one measuring point. These points should be evenly distributed over the area and should change from year to year. Samples should be taken after the summer harvest and before the feeding period.

In the time before this monitoring-project (1999 – 2003), the foulbrood pathogen was detected in 25% of all honey samples analyzed. Since the beginning of the monitoring project, a noticeable downward trend in positive samples has been observed. The data also agree with the numerous other samples that were routinely examined at the institute. Only in the case of samples that originate from AFB-restricted zones sent by veterinary service higher proportions of positive samples were found.

In the AFB monitoring project, a regular and systematic examination of suspicion-free areas is achieved. Examination of honey samples is an excellent tool for the early diagnosis of AFB. However, the pathogen cannot be eliminated. There are still individual outbreaks of the disease, which are usually limited to a few bee colonies.

Keywords: American foulbrood, brood comb honey samples, Lower Saxony, monitoring, *Paenibacillus larvae*

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P 46 Schadschwellenorientierte Varroabekämpfung: Ein Citizen Science Projekt zur Erforschung und Evaluierung eines neuen Ansatzes in der Imkerei (N)

Damage threshold oriented varroa control: A citizen science project to research and evaluate a new approach in beekeeping.

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Die Varroamilbe (*Varroa destructor*) stellt eine erhebliche Bedrohung für die Honigbiene dar. Angesichts der immer wieder auftretenden hohen Überwinterungsverluste von Bienenvölkern ist eine Überprüfung der etablierten Varroabekämpfungsstrategien dringend erforderlich. In enger Zusammenarbeit mit Imkern aus Berlin und Brandenburg führen wir ein Citizen Science Projekt durch, um die Wirksamkeit eines neuen Ansatzes zur schadschwellenorientierten Varroabekämpfung zu untersuchen und zu validieren. Unter wissenschaftlicher Leitung der Freien Universität Berlin erfolgt eine kontinuierliche Erfassung des Varroabefalls und relevanter Parameter. Die Varroabekämpfung erfolgt ausschließlich auf Basis der individuellen Varroabelastung. Mit diesem innovativen Ansatz soll nicht nur die Überlebensrate der Bienenvölker verbessert werden. Die erfassten Daten sollen auch das Verständnis der Populationsdynamik der Varroamilbe erweitern. Die gewonnenen Erkenntnisse werden helfen, die imkerliche Praxis weiterzuentwickeln und langfristig gesunde und stabile Bienenvölker zu fördern.

Keywords: Varroabekämpfung, Citizen Science, Schadschwelle, schadschwellenorientiert

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P 47 **Liquid and solid matrix formic acid treatment comparison against Varroa mites in honey bee colonies**

Im Vergleich: Flüssige und feste Matrix-Ameisensäurebehandlung gegen Varroamilben in Bienenvölkern

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Beekeepers use organic acids to control the invasive parasitic mite *Varroa destructor* (Varroa mite) in honey bee colonies (*Apis mellifera*), as an alternative to synthetic acaricides, to which Varroa mites can develop resistance. Here, we tested the efficacy of two formic acid treatments for Varroa mite control: a solid matrix product (Formic Pro; $n = 10$ colonies) and a liquid product (Formivar 60; $n = 10$ colonies), relative to control colonies that were not treated with formic acid ($n = 10$). Both formic acid treatments killed >95% of the mites, however, the use of formic acid also resulted in 1.6 times more brood loss and 30% queen loss, relative to control colonies. Although the solid application was perceived as being more practical to use for treating against Varroa mites, both the solid and liquid application methods were equally effective and had similar negative side effects on honey bee colonies.

Keywords: Formic Acid, Varroa, Mite treatment, Efficacy, Honey bee

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P 48 Winter treatment of Varroa with oxalic acid: trickling once or twice vs. vaporizing once or twice

Varroa-Winterbehandlung mit Oxalsäure: ein- oder zweimal Beträufeln gegenüber ein- oder zweimal Verdampfen

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In many regions in Europe, beekeeping advisors recommend a treatment against *Varroa* in winter. Oxalic acid is preferentially used, as it has a high efficacy against *Varroa* mites in brood-free colonies. When colonies are highly infested with *Varroa* mites, a second treatment might be desired for increased efficacy. According to label instructions, trickling oxalic acid should be done only once. Even a single trickling treatment may harm honey bees. In 2023, vaporizing oxalic acid became a legal treatment in Germany. According to the medication's instructions, colonies may be treated twice if needed.

We evaluated the efficacy and the side effects of treating honey bee colonies in winter with oxalic acid using either single or double trickling or vaporizing treatments.

Across two apiaries, we compared five experimental groups: 1x trickling, 2x trickling, 1x vaporizing, 2x vaporizing, untreated control. At each apiary, we used 5 colonies per group (i.e. 10 colonies in total per group), for a total of 50 colonies. After the treatment, the efficacy was determined using a control treatment (Apivar). We estimated colony size before treatment (Liebefeld method) and will estimate colony size again at the beginning of spring (overwintering quotient), to determine if there are negative impacts of multiple treatments on colony development. We also counted dead bees in front of the colonies as proxy for side effects. The treatment efficacy and honey bee tolerance of single and double winter treatments with oxalic acid will be discussed.

Keywords: Honey bee; Varroa; organic acid; vaporization; veterinary drug

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P 49 Reliable detection of Tropilaelaps with the soapy water method is possible, but not with honey douple sieves!

Eine sichere Feststellung von Tropilaelaps-Milben mit der Auswaschmethode ist möglich, jedoch nicht mit dem Honig-Doppelsieb!

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Tropilaelaps mites are parasites of eastern honey bees. However, it has made the transition to the western honey bee and there are indications that it is already outside Asia. Introducing this mite to other regions can lead to a threat to bee colonies there. Therefore, a suitable detection technique is required, even before *Tropilaelaps* reach Europe. To be prepared, we tested the washing method with two sieves, known for measuring the infestation rate of adult honey bees with *Varroa* mites, which is also recommended for the detection of *Tropilaelaps* mites. However, we did not find any *Tropilaelaps* mites in the bee samples, to which we actively added dead *Tropilaelaps* and *Varroa* mites. It is known that the sieve must have a mesh size of less than 0.5mm. Most commercially available honey double sieves, which are often used for measuring the infestation rate with Varroa mites, show mesh sizes of 0.5mm upwards (specifications: 0.5 to 0.7mm). Therefore, honey double sieves cannot be used to detect *Tropilaelaps*, because the adult females are only 0.5mm in width. Sieve towers, used in geology, have defined and standardized mesh sizes. Finally, we used a sieve tower consisting of three sieves (bees: 2.0mm; *Varroa:* 0.5mm and *Tropilaelaps:* 0.25mm). In our experiment, we prepared mite-free bee samples. These samples were artificially mixed with dead *Varroa* and *Tropilaelaps* mites. In 27 runs we found 168 of 175 added *Tropilaelaps* mites in the 0.25mm sieve (recovery rate: 96.00%). Of 242 added *Varroa* mites, 238 were recovered in the 0.5mm sieve (recovery rate: 98.35%). For reliable identification of *Tropilaelaps* mites in the 0.25mm-sieve, we also recommend a good lighting and the use of a 10x magnifying glass.

Keywords: Tropilaelaps Mite; Soapy water method, washing method; Varroa destructor

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