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Abstract Book



INVITED SPEAKERS

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CHANGING EFFORTS DEDICATED TO THE KNOWLEDGE OF THE WORLD MESOSTIGMATID FAUNA, WITH EMPHASIS ON THE PHYTOSEIIDS

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Mites of the order Mesostigmata are mostly edaphic, but also common on plants and associated with other animals. The objective of this presentation is to highlight the milestones leading to the present stage of the knowledge about them, discussing future scientific endeavours. Early efforts to classify these mites were spent mostly by European researchers, tied to the development of the microscope. Of the 31 species listed by Linnaeus in the 10th edition of his *SYSTEMA NATURAE*, only three belonged to this order. Dugès seems to have been the first to refer to the group, naming it Gamasei; the term Mesostigmata was first used by Canestrini. It is presently composed of nearly 12,000 species of 110 families. About half of the families were described in 1859–1950; the remaining, after 1950. The most numerous

families are Phytoseiidae, accounting for almost a quarter of all species, followed by Laelapidae, with about 12%. Phytoseiidae is also the most extensively studied family, for the potential of comprising members as biological control agents; almost 20 phytoseiid species have been used worldwide to control agricultural pests. *AMBLYSEIUS* and *TYPHLODROMUS* are the largest genera, together comprising about a third of all phytoseiid species. Initial interest in the laelapids relates strongly to the parasitic habits of part of the species. Continued field surveys followed by biological evaluations and syntheses of information, made available as catalogues and databases, seem crucial to facilitate mitigation of undesirable effects of parasitic mesostigmatids and to develop prospective biological control agents.



Peter Schausberger

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PARENTAL AND EARLY-LIFE EXPERIENCES DRIVE PREDATORY MITE PERSONALITIES

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Animals are said to have personality if they exhibit behaviors that are consistent within individuals and consistently variable among individuals over time and across contexts. Canonical behavioral categories that are typically used to characterize animal personalities are activity, exploration, boldness (risk-taking behavior), aggressiveness (against conspecifics), and sociability. Here, we document that key environmental factors such as food, predation risk and social circumstances, experienced in the parental generation and/or in early life, critically influence behavioral repeatability and personality trajectories in plant-inhabiting predatory mites. In the omnivore *Amblyseius swirskii*, the diet options experienced early in life mediate adult personality expression in activity, aggressiveness and exploration; personality expression covaries with the individual foraging niches in thrips-experienced predators; the parental diet influences the activity

personalities of offspring. In the spider mite specialists *Phytoseiulus persimilis* and *P. macropilis*, the prey life stage experienced by parents leads to covariation of prey stage preference and personality expression in activity and exploration. In *P. persimilis*, intraguild predation risk experienced early in life shifts the personalities towards bolder and more aggressive types; early social isolation disrupts adult female personality expression in group-living and sociability; intriguingly, also the early social conditions experienced by the mates of the females influences the females' personalities. In *P. macropilis*, the parental social conditions determine offspring personality in sociability, activity and oviposition. By affecting personality occurrence and expression, parental and transient personal experiences early in life are critical determinants of fine-scale phenotypic structure and diversification within local groups and populations of predatory mites.



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ORAL PRESENTATIONS

BIOGEOGRAPHY & BIODIVERSITY

OP-01

A RED LIST FOR MITES AND TICKS

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Habitat destruction, invasive species, overexploitation, illegal wildlife trade, pollution and climate change put the survival of species at risk and result in an overall decline in biodiversity. The extinction risk assessments focus mainly on vertebrates and large invertebrate species (mollusks, crustaceans, spiders, insects etc.), while small arthropods such as Acari are usually excluded from the Red Lists of endangered species. A total of 296 species of Acari (25 endemic and 271 non-endemic) have been assessed for the National Red list of Greece. Species assessed include representatives from different groups i.e. soil mites, plant-inhabiting mites, water mites, agricultural pests, predatory mites, and animal

parasites. The evaluation of the conservation status of the analyzed species was compiled based on criteria proposed by the International Union for Conservation of Nature (IUCN). The 25 endemic species have been assessed as follows: 8 Near Threatened (NT), 7 Least Concern (LC) and 10 Data Deficient (DD). The 271 non-endemic species have been assessed as follows: 29 Near Threatened (NT), 221 Least Concern (LC) and 21 Data Deficient (DD). Although, the number of species assessed is small, corresponding to almost one fifth of species reported from Greece, such research may encourage other researchers and experts to include mites and ticks in similar lists.



OP-02

MITES ASSOCIATED TO AMBROSIA BEETLES OF THE GENUS *XYLEBORUS* (CURCULIONIDAE: SCOLYTINAE) ON AVOCADO (*PERSEA AMERICANA*) IN MEXICO.

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Insect-mite associations has been studied in different natural ecosystems and in avocado orchards. Recently this group of insects has become relevant mainly due to a couple of species of quarantine importance; *Xyleborus glabratus* and *Euwallacea kuroshio* (already present in Mexico; Ensenada, Baja California). We are currently developing a project, "Mites associated with bark and ambrosial beetles in avocado in Mexico". 18 species of the genus *Xyleborus* are present in the country, our interest is to study the phoretic mites associated to them, particularly those present in avocado. The insects were collected mainly from infested avocado logs that were placed into emergency chambers. Orchards have been visited in the main avocado producing areas in the country.

The states of Colima, Mexico, Puebla, Michoacán, Veracruz, and Jalisco were visited. We have recorded phoretic mites in four species of *Xyleborus* (*X. torquatus* in Colima; *X. affinis* and *X. volvulus* in Jalisco; *X. affinis* and *X. bispinatus* in Veracruz; *X. affinis* and *X. volvulus* in the state of Mexico). Species of four families (Ascidae, Tarsonemidae, Pigmephoridae, Melicharidae) until now were recorded. Our explorations on other regions of avocado producing areas continue to extend our knowledge on this associations in México. No predation by the mites on the immature of these insects has been documented yet, but cases on bark beetles are well documented. Up to now *Xyleborus affinis* is the species in which more phoretic mites have been found.



OP-03

GLOBAL STUDIES OF THE HOST-PARASITE RELATIONSHIPS BETWEEN ECTOPARASITIC MITES OF THE SUBFAMILY PICOBIINAE AND THE STARLING BIRDS

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Quill mites belonging to the subfamily Picobiinae (Prostigmata: Syringophilidae) are obligate ectoparasites of birds. They inhabit quills of the contour feathers, where they spend their whole life cycle. During our studies, we conducted global research on picobiine mites associated with starling birds.

Mite material was collected from dry bird skins housed at the Natural History Museums in Germany, Kenya, and Belgium. In our studies we analysed a total of 414 individuals of starlings belonging to the 44 species from all zoogeographical regions of starlings occurrence. The Picobiinae–Sturnidae network was composed of seven mite species parasitising 24 host species. The prevalence of host infestation by syringophilid mites varied from 5.9% to 100% (95% confidence interval (CI Sterne method) = 0.3–100). To describe patterns within the studied host-parasite ecological two-way web, the bipartite network was characterized by a

high network level specialization $H2'=1$ (for null model = 0.036; $t = -6626.61$, $P < 0.0001$); nestedness $N=34.15$, connectance $C=1$. Normalized specialization level d' in all cases was 1.

In our analyses, only one picobine species was monoxenous, whereas six were oligoxenous parasites. Network analyses indicate that each of these parasite species has unique ways of interacting with the host in the network (d'). High nestedness (N) indicates the moderate internal organization of the network, and connectance (C) indicates that picobiine mites parasitising this group of birds have fully non-co-occurring tendencies.

The research was carried out with the financial support of ID-UB AMU - Excellence Initiative-Research University, grant no. 118/34/UAM/0056.



OP-04

MITES IN GREATER SPOTTED EAGLE NESTS: A COMPARISON AFTER 30 YEARS

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The Greater Spotted Eagle (*Clanga clanga*) is the rarest bird of prey in the world's northern hemisphere. Its nesting in European Union only in Poland and also through Belarus, Ukraine and Russia to the pacific coast and the entire global population is currently estimated at less than 3000 pairs.

In 1994 and 1995 two samples of lining from the two different nests were collected. In the material collected 1267 mites from the order Mesostigmata and 646 from the subclass Actinotrichida were found. Mites from the order Mesostigmata were determined to the species and genus level and the mites were represented by 21 species from the 12 families. *Macrocheles ancyλεύs*, *Nenteria floralis* and *Parasitus consanguineus* were species new to Polish fauna. Very specific for eagle nests *Nenteria*

pandioni, previously found in the nests of Ospreys (*Pandion haliaetus*) and White-tailed Sea Eagles (*Haliaeetus albicilla*), also was found. In 2023, the project 101113849 - LIFE22-NAT-PL-GSELIFEAboveBorders (Above Borders: conservation of Greater Spotted Eagles in breeding and wintering areas and along the flyway) was launched, coordinated by Poznan University of Life Sciences, and our team obtained permission to collect material in this summer from 5 Greater Spotted Eagle nests in the same conservation area in Biebrza National Park (Poland) as 30 years ago.

This presentation will be a comparison of obtained results from this unique microhabitats now and 30 years ago.



OP-05

ZOOGEOGRAPHY AND CATALOGUE OF FAMILY ZERCONIDAE (MESOSTIGMATA)

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Zerconidae is considered to be holarctic family of mites. They are best known from Europe, as there were many authors researching this group. Nonetheless, there is also decent amount of knowledge of this group from North America and Asia. Based on gathered literature, we created catalogue of family Zerconidae, which

contains 486 species in 46 genera. We also summarized zoogeography of zerconids. Creating catalogue of family Zerconidae is the first step in developing determination key of this family, which will help to resolve many problems inside the family. Key of all species is needed, as to prevent misidentifications of species.



OP-06

BIODIVERSITY AND BIOGEOGRAPHY OF THE OPIILIOACARIDAE FAMILY IN MEXICO

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The Opilioacaridae family was described by With (1902) from north Africa, with 2 new species under the genus *Opilioacarus* With 1902. *O. segmentatus* With, 1902 and *O. italicus*, With 1904. In 1905 was described the first species from the neotropical region, *O. platensis* (Silvestri 1905), from Uruguay and Argentina.

In 1986 beginning a series of studies in order to know the species richness of the Opilioacaridae family and its description in several ecosystems from Mexico such as: Pine-oak forest, tropical forest and coastal dunes. In all sites, collects were taken out handle searching under, trunks, stones, moss, and litter processed by Berlese funnels.

Mexico has 10 spp in only one genus: *Neocarus*. The gennus *Caribeacarus*, have 2 spp in the

Caribbean region and probably this genus is also present in Cozumel and Puerto Morelos, Quintana Roo, Mexico.

On the Neotropical region are 26 spp, described, being this region the best studied and with the highest biodiversity of the Opilioacaridae family. The species described occupied a very wide range of microhabitats in dunes (Mexico) at the sea level, in mangrove litter, pine-oak forest, tropical forest and even in hot springs (Nicaragua), as well in rainfalls (Argentina and Brazil).

The Neotropical region have the higher biodiversity and a very interesting biogeography.



AGRICULTURAL & FORESTRY ACAROLOGY

OP-07

PREVALENCE, SPATIO-TEMPORAL DISTRIBUTION, VECTORIAL POTENTIAL AND RISK FACTORS FOR THE *DERMANYSSUS GALLINAE* MITE IN LAYING HENS IN GREECE

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Dermanyssus gallinae, the poultry red mite (PRM), is the most prevalent and harmful ectoparasite of laying hens globally. PRM is a vector of various microorganisms, with some being important for production losses and public health. Prevalence and risk factor studies can help veterinarians make decisions regarding farm treatments.

The present study aimed to investigate: 1) the prevalence and infestation severity of PRM in poultry farms across Greece and examine potential risk factors, 2) the presence of specific pathogens, including *Staphylococcus* spp., *Escherichia coli*, *Salmonella* spp., and *Listeria* spp., carried by PRM.

AviVet traps were used to sample 84 farms (51 backyard, 33 industrial) from 2021-2023 across Greece. Mites were identified as *D. gallinae* using morphological keys and COI DNA barcoding. Farm altitude, temperature, humidity, production systems and other relevant data were recorded for each farm and

assessed as potential risk factors. Unwashed PRM were homogenized and used for microbiological cultures, carried out on general and selective substrates to detect the above-mentioned bacteria.

Overall PRM prevalence was 75.0% and was higher in backyard (80.4%) than industrial farms (66.7%), varying regionally from 66.7-90.9%. Different risk factors significantly increased infestation risk. Microbiological cultures and PCR assays were positive for *Staphylococcus aureus*, *E. coli* and *Listeria monocytogenes*.

In the future, global warming, reduced acaricide options, and a ban on cage systems all threaten a wider spatio-temporal distribution of the PRM. Effective monitoring and control methods are required to minimize any possible contamination risk of poultry products, protect hen production and welfare and workers' health.



OP-08

COVER CROPS IN VITICULTURE: EXPLORING RELATIONSHIP BETWEEN HOST PLANTS AND PHYTOSEIIDAE COMMUNITIES USING TAXONOMIC AND FUNCTIONAL APPROACHES

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The use of pesticides in viticulture can affect natural enemies and thus the success of conservation biological control. Increasing plant diversity in agroecosystems could provide refuges and food resources for natural enemies. Although this hypothesis has been confirmed in several meta-analyses, less information exists on the effect of cover crops on Phytoseiidae mites – known to be efficient predators in vineyards. Most Phytoseiidae are generalist predators, feeding on prey or pollen, and strongly influenced by plant leaf characteristics. Some studies highlighted the positive impact of cover crops in vineyards on Phytoseiidae communities, but information on the effect of traits of these non-crop plants on Phytoseiidae communities is lacking. This study aims to characterize beneficial weeds for predatory mites in a Mediterranean vineyard using both a

taxonomic and functional approach through the measurement of six functional traits related to habitat quality, food quantity and quality, for the nine most abundant plant species in cover crops. In 2023, four plants harbored a high abundance and diversity of Phytoseiidae mites. Sixteen Phytoseiidae species were retrieved, the most abundant being *Typhlodromus recki* and *Phytoseius finitimus*. Phytoseiidae density were (i) positively correlated to the mean pollen grain number produced by the plant and (ii) negatively correlated to trichomes density of the leaf veins. The next step is to investigate whether improving Phytoseiidae communities on cover crops has a direct positive effect on Phytoseiidae on vine and the associated natural regulation. Results of this study are assumed to provide advice to growers when establishing cover crops.



OP-09

THE AGROECOLOGICAL TRANSITION IN FRENCH MEDITERRANEAN VINEYARDS: HOW ARE SOIL PREDATORY MITE COMMUNITIES AFFECTED IN DIFFERENT AGRICULTURAL SYSTEMS?

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Soil mites play pivotal roles in agro-systems, providing ecosystem services. Many species can prey on invertebrates, contributing for their regulation. However, agricultural intensification threatens soil biodiversity and associated services. This study aims to characterize the abundance of soil predatory mites (Mesostigmata and Prostigmata) in Mediterranean vineyards (Hérault) under different management practices, vegetation covers, with different levels of soil aggregate stability (based on mean-weight diameter). Soil samples were taken in autumn 2023 from 30 plots (0-5 cm soil layer) across different agroecological systems (conventional vs organic, vegetation cover vs bare soil) and from garrigue vegetation. Arthropods were extracted using a modified Berlese-Tullgren funnel, and the mites were counted and identified. In total, 1,592 Mesostigmata and 723 Prostigmata were collected. The abundance of predators was analysed by fitting Generalized Linear Mixed

Models (GLMM) with Negative Binomial distribution. Mesostigmata abundances did not differ significantly across all studied systems. This could contribute to the maintenance of regulation services regardless of the agriculture practices. Differently, the abundance of Prostigmata was higher in garrigue (mean of 7.03) compared to vineyards (organic: 1.70, conventional: 1.42). While organic vs. conventional management did not differ significantly, permanent cover crops yielded abundances that did not differ from the garrigue, while bare soil had the lowest. Additionally, higher soil stability was positively correlated with Prostigmata abundances. Agroecological practices favoring natural vegetation might benefit predatory Prostigmata communities, potentially enhancing vineyard regulation services. The completion of the analysis at a lower-level taxonomic identification will allow for a better comprehension of these communities.



OP-10

WHAT IS GOING ON UNDER THE CHARMING FRENCH MEDITERRANEAN VINEYARDS? ASSESSING THE EFFECT OF AGRICULTURAL PRACTICES ON ORIBATIDA MITE COMMUNITIES

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Oribatid mites play a major role in soil functioning, facilitating decomposition and nutrient cycling. This study aims to assess the effect of agricultural practices on oribatid mite communities in mediterranean vineyards (Hérault) in the context of the agroecological transition. In autumn 2023, soil samples were collected from 30 plots across various production systems (conventional and organic, different vegetation cover management practices, varying levels of soil aggregate stability, and other agricultural practices), as well as in garrigue vegetation. A total of 9 soil samples were collected per plot within the 0-5 cm soil layer using a 9 cm diameter cylinder. Arthropods were extracted using a modified Berlese-Tullgren funnel and counted. A total of 7,562 oribatids was collected. The abundance was analysed by fitting a Generalized Linear Mixed Model (GLMM) with a Negative Binomial

distribution for each explanatory variable. The highest oribatid abundance was found in the soils of garrigue vegetation (mean of 59.83), significantly differing from the vineyards (mean of 23.44 and 12.23 for organic and conventional, respectively). Despite no significant difference being found between oribatid abundance in soils under conventional and organic systems, differences between the vegetation cover management were observed. Higher abundances were found in soils with permanent cover crops than in bare soils. The Oribatid numbers was also the highest in soils with the highest stability levels. These results highlight the impact of agricultural practices on oribatid communities, emphasizing the need for further studies on species richness and population dynamics to better understand the effect on functional diversity.



OP-11

SOIL MITES (ORIDATIDA, MESOSTIGMATA) REACTION TO FOREST FIRE DYNAMICS

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Forest fires are an important and growing threat to temperate forests. Knowledge about soil mites' reaction to different types of fires can help with planning regeneration processes. Our goal is to test the hypothesis that soil mites survival is related to the energy flux delivered to the ground and soil by wildfires. Study plot is located in close proximity to the Miasteczko Śląskie Zinc plant, in this very polluted area. In May 2022 a big (40 hectares) forest fire occurred in Scots pine stand. Soon after this event we collected charred fragments from burned ground and measured the reflectance properties of the representative sample of charcoal. Based on that we determined the relative differences in energy fluxes (and to some extent max fire temperature) in different

locations of the burned area. Mites (Oribatida and Mesostigmata) population (number and species present) was investigated twice: in the fall of 2022 i spring of 2023 along the same three 80 m long transects (40 meters in the forest and 40 meters in the burned area). In order to obtain reasonable population statistics, a set of four soil samples was collected every 10 meters. Our results show that: 1) the correlation between energy flux proxies by the charcoal reflectance and mites population requires more analysis, 2) the number of soil mites was higher shortly after the fire and decreased over time in the burned area. This study emphasizes the importance of better understanding the long-term response of temperate forest ecosystems to wildfires.



OP-12

ROLE OF SOIL MITES' COMMUNITY TO ASSESS THE STANDARDS OF GOOD AGRICULTURAL AND ENVIRONMENTAL CONDITIONS (GAEC)

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Sustainable land use requires the protection of soil biodiversity for its importance in the delivery of ecosystem services. Soil mite communities are efficient bioindicators of soil functionality. In this study, it was evaluated the effect of different soil management for Good Agricultural and Environmental Conditions (GAECs) on mites' functional biodiversity. Two areas, with two applications of standard and one control for each GAEC, were selected. In Spring and Autumn (2009-2011), five soil samples/plots/area were collected. Mesofauna was extracted using Berlese-Tullgren funnels: arthropod abundance was calculated; soil mites were identified at different taxonomical and trophic level.

Set-aside areas had higher arthropod abundance and biodiversity than conventional durum wheat fields: notwithstanding GAEC, monosuccesional fields led to low arthropod biodiversity. The oribatid community was represented by 46 species. In tilled soil,

Tectocephaeus and *Punctoribates* were dominant species and the community was quite simplified. The Astigmata were registered only by hypopus form. Considering Mesostigmata, 15 families were detected, with *Hypoaspis aculeifer* and *Rhodacarellus silesiacus* as more abundant species. Endeostigmata and Prostigmata comprised 17 families, with 10 predator families; the most abundant was Nanorchestidae followed by Eupodidae, Pygmephoridae and Scutacaridae.

As the abundance fluctuations of soil mites respond to climate and habitat conditions, biodiversity indices may be good indicators of long-term practices. However, the edaphic mite community structure, based on their trophic niche, closely reflects the resource availability in soil and exhibits a rapid response to management practices with implications for soil ecosystem functioning.



OP-13

HOST PLANTS AND PEST STATUS OF THE INVASIVE LEWIS SPIDER MITE, *EOTETRANYCHUS LEWISI* (MCGREGOR, 1943) (ACARI; TETRANYCHIDAE), IN MAINLAND PORTUGAL AND MADEIRA ISLAND.

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Introduction. The Lewis spider mite, *Eotetranychus lewisi*, is native to central America and despite being mainly associated with poinsettia (*Euphorbia pulcherrima*) plants, it can attack and cause damages to several crops. In the European Union it's a quarantine-regulated pest, being present in Madeira Island and mainland Portugal.

Methods and Results. We conducted field samplings to identify plant hosts in Madeira and mainland Portugal (Algarve and Lisboa Districts), surveying different local crops and non-cultivated plants, with leaves collected from plants near or in direct contact with mite-infested poinsettias. Our results confirm the association of *E. lewisi* with *E. pulcherrima* and *Ricinus communis*. No damages were observed on agricultural crops.

In addition to sampling, the risk of crop infestation and sustaining *E. lewisi* populations

was studied with an outdoor experiment where potted “trap-plants” (strawberry, grape vine and poinsettia) were placed in direct contact with mite-infested poinsettias (“donor” plants). Two months after the start of the experiment, the mite was detected on the three recipient plant species, with low infestation rates in the two crops and without causing damages.

Conclusions. *Eotetranychus lewisi* is mainly associated with poinsettia and *R. communis*. The Lewis mite is absent or rarely found (and in low numbers) on agricultural plants, and currently is not causing damages to crops. This is an important information for Portugal and also the rest of Europe considering the EU-regulated status of this exotic mite.

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OP-14

CHOICE TESTS TO DETERMINE THE PREFERENCE BEHAVIOR OF THE PHYTOSEIIDAE SPECIES *TYPHLODROMUS (ANTHOSEIUS) RECKI* (WAINSTEIN) AMONG A COMBINATION OF PLANTS AND FOOD

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Recent studies have shown *Typhlodromus (Anthoseius) recki*'s ability to feed on pest mites on tomatoes and its potential introduction into crops via two banker plants (*Mentha suaveolens* and *Phlomis fruticosa*). The aim of this project was to assess predator dispersal from banker to tomato plants. Choice experiments were carried out in the lab, exposing predatory females to *Typha angustifolia* pollen vs *Aculops lycopersici* or *Tetranychus urticae*, using leaf disks of *M. suaveolens*, *P. fruticosa* and *Solanum nigrum*. After 5 days, predator position, number of eggs laid and the number of *T. urticae* eggs consumed were assessed. When comparing predator feeding preferences between pollen and *A. lycopersici* or *T. urticae*, a higher abundance of predators and their eggs were observed on disks with prey. However, this was not the case with

P. fruticosa, where higher predator densities were reported on leaf disks with pollen. In the choice tests, predators consumed a higher percentage of *T. urticae* eggs when offered *A. lycopersici* than when offered pollen. Regarding banker plant preference, predators seem to prefer *M. suaveolens* over *P. fruticosa*. Predator dispersal seems to be positively influenced by the offered prey; however, dispersal from *P. fruticosa* to *S. nigrum* seems less effective, as predators preferred pollen and stayed on this plant rather than moving to the infested *S. nigrum*. Thus, *Mentha suaveolens* would be a better bank plant, but further experiments are needed to characterize the predator's development on this latter plant in greenhouse conditions.



OP-15

GENETIC VARIABILITY AMONG POPULATIONS OF *AMBLYSEIUS SWIRSKII* ATHIAS-HENRIOT (ACARI: PHYTOSEIIDAE) FROM TURKEY

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Amblyseius swirskii is one of the most important Phytoseiidae mites commercialized worldwide for the control of mites and small insect pests. The study aims to (i) investigate genetic variation among seven populations collected from different locations and crops (cotton, orange) in Turkey and (ii) compare them with commercial populations, based on 12S rRNA and Cytb mitochondrial DNA sequences. The mean genetic distances among the Turkish populations were very low (0.7% for 12S rRNA and 0.9% for Cytb mtDNA), ranging from 0 to 2.8% and 0 to 1.5%, respectively. The two phylogenetic trees show two distinct groups containing the same samples for the two fragments. These clades are separated by a genetic distance of 0.9% and 1.3% for the 12S rRNA and the Cytb mtDNA fragments,

respectively. The genetic differences were not explained by location or host plant. However, samples from some populations were exclusively or predominantly included in one of the two clades. When compared with DNA sequences of *A. swirskii* from commercialized populations, the latter were included in only one clade, as were all samples collected in orange orchards. In cotton fields, as well as on *Solanum nigrum*, samples from both clades coexist, but in different proportions. These results show a globally low genetic diversity within *A. swirskii* for the two DNA fragments. The two clades question the existence of a clade derived from commercial releases. However, this result may be related to other factors and additional morphological phenotyping are planned in future studies.



OP-16

PREVALENCE OF *TETRANYCHUS URTICAE* KOCH AND *T. TURKESTANI* (UGAROV & NIKOLSKII) (ACARI: TETRANYCHIDAE) AND THEIR ENDOSYMBIOTIC BACTERIA IN COTTON FIELDS OF AYDIN, TÜRKİYE

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Spider mites are important pests of cotton, a vital fiber crop cultivated in sun-drenched regions. This study investigated the prevalence and distribution of spider mite species infesting cotton fields in Aydin province, Türkiye. Spider mites were found in a significant portion (89%) of the surveyed fields. The two most abundant mite species were the red form (RF) of *Tetranychus urticae* (57.1%) and *T. turkestanii* (39.3%). A minor presence of *T. urticae* green form (GF) (3.6%) was observed. *Tetranychus urticae* RF was more prevalent in coastal areas, while *T. turkestanii* was more common inland. Field surveys demonstrated that areas with higher *T. urticae* RF prevalence exhibited more frequent spraying, potentially due to this species' greater capacity to develop resistance

compared to *T. turkestanii*. This study also investigated the prevalence of *Wolbachia*, *Rickettsia*, *Cardinium* and *Spiroplasma* endosymbionts, which are linked with pesticide resistance due to their ability to degrade pesticides, in these mite populations. The study confirmed the presence of *Wolbachia* and *Rickettsia* endosymbionts in spider mite populations in Türkiye. However, no *Cardinium* or *Spiroplasma* were detected in any of the populations. Infection rates of the detected endosymbionts differed between *T. urticae* and *T. turkestanii*. Future studies should investigate the resistance levels of these tetranychid mite species as well as the role of their endosymbiotic bacteria in resistance in cotton-growing areas.



FORENSIC ACAROLOGY

OP-17

FORENSIC ACAROLOGY IN SLOVAKIA: THE BEGINNING OF THE RESEARCH

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In Slovakia, there are known multiple species of mesostigmatic mites associated with the variability of decaying substrates also found in carcasses, but there was no study concentrated on the range of mite species associated with the different stages of decomposition. The intensive forensic research in this area started in 2021. That year we started a pilot study on decaying rats. Each of five rats were collected in different stages of decomposition, rats and rat-soil samples separately to detect possible differences. Then we continued with three pig carcasses, two in spring and summer 2022 and one in winter 2023. Samples were taken in various intervals. Alongside the pigs, we had installed traps with bait of pork meat for catching the insect and phoretically active mites.

The traps were collected every week for two months and the bait was changed with a fresh one. From pilot study we collected 2617 individuals, 191 found on rats and 2060 found in the rat-soil samples. We confirmed forensically important species in both types of samples in different numbers. The research with pig carcasses ended in november 2023, altogether 356 samples were collected. The processing of the material is in progress. From 234 trap samples we collected 2705 individuals with 414 phoresis interactions. The present species from pigs and traps will be compared. The aim of our research was to detect mesostigmatic mites associated with different stages of decomposition in our area and to use this knowledge in the continuing research.



OP-18

BIODIVERSITY OF MITES ASSOCIATED WITH THE CADAVERIC DECOMPOSITION OF PIGS (*Sus scrofa domestica*) IN TEXCOCO, MEXICO

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Forensic Acarology is a new area under development in Latin America and in Mexico only a few studies have been developed (Blé, 20218; Bonilla-Hernández et al., 2020; Estrada-Venegas et al., 2022). Mites are present in different habitats, they are associated to the process of decomposition of plants and animals. Through the diversity along the process, they can provide relevant information to forensic investigations, such as post-mortem time, causes of death or temporal and geographical conditions when the body was found. Despite this importance, studies on the diversity of the group associated with decomposing bodies are considerably scarce. A study on cadaveric decomposition of pig heads was established in San Nicolás Huexotla, Texcoco, Mexico. The decomposition was evaluated along the process, in three

treatments: exposed, buried, and exposed for a week and later buried (semi-exposed). Three soil samples per treatment plus a control, were collected and processed in Berlese and Tullgren funnels. The collected organisms in alcohol were reviewed, quantified, and a representative portion of the mites was mounted in permanent preparations. Mites were identified using different keys and original descriptions. A total of 37 families and 48 genera and 53 species were found, belonging to: Mesostigmata (11 families and 14 genera), Prostigmata (15 families and 21 genera) and Oribatida (11 families and 15 genera). This work is part of a Project on Forensic Acarology in Mexico, in order to establish information of mites involved in the cadaveric decomposition under different conditions in the country.



OP-19

THE INCREASING UTILITY OF MITES IN FORENSIC INVESTIGATIONS

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Whenever and wherever insects are rare, compromised or absent, mites might hold valuable forensic information no other source can provide. For a long time solely depending on casework, upstarting research in forensic acarology is poised to increase the utility and value of mites in forensic investigations.

Since 1878, mites have provided time of death estimations of human corpses. Mites can do much more than that. They can provide information on pre-mortem conditions, abandonment, torture, unsanitary conditions. They might indicate the place of death, any relocation, the extend and nature of concealment like how a corpse was wrapped or packaged. Information of when a corpse has been burned might be retrieved from mites. Mites are important when bodies have been completely destroyed as with woodchippers.

When a corpse is relocated, it takes with it the mites from that environment, but it also leaves mites behind. While maggots from hanged bodies fall underdeveloped, mites concentrate on the ground below.

Aside from corpses, when money had temporarily been hidden by burying it in the ground, mites might indicate the environment in which it has been buried, as well the continent and area.

Research in forensic acarology is investigating the complex histories of mass graves and mite fragments in the air. The increasing use of mites in forensic investigation is an international phenomenon. This calls for the urgent training of acarologists in forensic acarology, especially for different regions of the world. A huge diversity of mites demands local expertise explaining local crime scenes.



OP-65

FORENSIC ACAROLOGY AS A TOOL IN CASES OF CONCEALMENT FOLLOWING INFANTICIDE

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Infanticide refers to the act of killing a child under the age of one year, and most commonly occurs in the first 24 hours of life. Children in this age bracket are more than twice as likely than any other age group to be a victim of homicide, and infanticide is considered to be one of the least preventable crimes. The prevalence of this crime is difficult to predict, as the body is often intentionally concealed, preventing discovery. Births are rarely reported in these cases, meaning even if the body is discovered, it cannot be corroborated with a missing persons report, complicating identification, and event reconstruction.

To solve these uniquely challenging and distressing cases, forensic evidence becomes important. Post-mortem interval (PMI) estimations, facilitated by insect evidence, are

instrumental in event reconstruction, ultimately assisting in solving the crime. However, the concealment methods implemented in these cases, often restrict insect access. Mites, owing to their minute size and abundance, have been reported in multiple cases of concealment following infanticide, and have been successfully used to not only predict PMI, but also provide information such as location provenance due to the habitat specificity of mites. However, there is a lack of research exploring how mite colonies develop in these cases. To address this, an experiment is being conducted using neonate porcine carcasses as a proxy for infant human remains, concealed using methods observed in infanticide casework. This presentation will discuss the preliminary findings of this study, and the implications for forensic acarology.



BEHAVIOUR, ECOLOGY AND LIFE HISTORY STRATEGIES

OP-20

MATERNAL DIET MEDIATES OFFSPRING PERSONALITY IN THE PREDATORY MITE *AMBLYSEIUS SWIRSKII*

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Animal personality is defined by consistent behavior within individuals and consistently variable behavior among individuals in a population across time and/or contexts. Genetic determination, transgenerational effects, and personal experience are three major pathways that may shape animal personalities. Among these pathways, little attention has been paid to environmental factors in the parental generation affecting offspring personality. We tested the effects of the maternal diet on offspring personality in the plant-inhabiting predatory mite *Amblyseius swirskii*. Mated females and males, whose mothers were fed during egg production on either cattail pollen, two-spotted spider mites, or thrips, were subjected to a battery of three to five tests each for activity, exploration, and boldness. Movement activity was assessed in the mites' familiar environment. Exploration was quantified by the latency to emerge from a

shelter in open-field tests and to leave the release site in closed acrylic cages. Boldness was evaluated by residence in risky versus benign sites. Mean behaviors were analyzed by generalized linear models (GLMs); repeatability was assessed by intraclass correlation coefficients (ICCs). On average, offspring from spider mite-fed mothers were the most active, and those from pollen-fed mothers were the shyest. Offspring from thrips-fed mothers were more repeatable in activity than offspring from pollen- and spider mite-fed mothers. Only offspring from pollen-fed mothers were repeatable in boldness. Offspring from spider mite- but not pollen- and thrips-fed mothers showed personality in exploration. Taken together, our research suggests that the maternal diet critically influences both the average behavior and the personality expressed by offspring.



OP-21

HOW DO INTERACTIONS BETWEEN INDIVIDUALS OF THE PHYTOSEIIDAE SPECIES *TYPHLODROMUS (ANTHOSEIUS) RECKI* (WAINSTEIN) AND *PHYTOSEIULUS PERSIMILIS* AFFECT THEIR EFFECTIVENESS AS PREDATORS?

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Recent studies have shown *Typhlodromus (Anthoseius) recki*'s ability to feed on pest mites on tomato plants. However, the effects of coexistence with other predatory mite species, such as *Phytoseiulus persimilis*, was never assessed. This study aimed to determine the influence of *P. persimilis* on the population development and predation efficiency of *T. (A.) recki* on Solanaceae plants. Laboratory experiments were conducted, using leaf disks from *Solanum nigrum*, where a total of 8 treatments (combinations of *T. urticae* eggs with or without pollen, and different ratios of predatory mites from both species) were tested. Daily observations recorded the consumption of *T. urticae* eggs and the number of eggs laid by each predator species under the different treatment conditions. Results indicated that

treatments with multiple mite individuals on a leaf exhibited higher rates of *T. urticae* egg consumption compared to single-individual treatments. Additionally, temporal consumption dynamics varied across treatments. However, *T. (A.) recki* consumption was always lower in presence of pollen. Interestingly, food type rather than interspecies interactions primarily influenced egg-laying behavior. It thus seems that in the presence of pollen, competitive interactions between the predator species diminished, facilitating coexistence. These findings suggest that under conditions where alternative food sources are available, both predator species can coexist, offering promising implications for biological pest control strategies.



OP-22

THE FIRST RECORD OF THE EFFECT OF TEMPERATURE AND HUMIDITY ON THE FUNCTIONAL RESPONSE OF A PREDATORY SOIL MITE

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a. Introduction

The fluctuations of temperature and humidity can significantly influence physiology and behaviour of arthropods including their functional responses to prey. The current research aimed to investigate the functional response of the predatory soil mite *Blattisocius mali* foraging on its common prey, the mold mite *Tyrophagus putrescentiae* at different temperatures between 10° C and 35° C, and at different humidity levels between 32% and 92%.

b. Methods and Results

The predatory female was exposed to varying densities of prey eggs or prey males across different temperatures at 85% relative humidity, or to varying densities of prey eggs at different relative humidity levels and the temperature of 25°C. At varying humidities, the predators displayed Type III functional response towards prey eggs except the lowest humidity of 32%, at

which they changed their response to Type II. By contrast, across all tested temperatures the predators performed Type III towards prey eggs and Type II when preying on prey males. The handling time was longer at lower temperatures when *B. mali* preyed on either eggs or males. In contrast, the potential for prey mortality and the attack rate were higher at higher temperatures. The potential for prey mortality was higher and the handling time was shorter at higher humidity levels compared to lower humidity levels.

c. Conclusions

Functional response type did not change with warmer temperatures but varied with both changing humidity levels and prey types. *Blattisocius mali* was more efficient in reducing prey densities at higher temperatures and higher humidity levels.



OP-23

DIVING IN THE BIOLOGY AND ECOLOGY OF THE LYCHEE ERINOSE MITE (*ACERIA LITCHII* KEIFER; ACARI: ERIOPHYIDAE)

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The lychee erinose mite (LEM), *Aceria litchii* (Keifer), is an economically important pest of lychee plants (*Litchi chinensis*) that induces the formation of open galls, also known as erineae. The erineae change color over time and four distinct stages can be observed: hyaline, white, amber and dark brown. Little is known regarding the role of erineae in this mite-plant interaction and several aspects of its biology and ecology remain to be elucidated. Herein, we evaluated how temperature (15, 25, and 35 °C) can influence LEM populations and erineae development by measuring mite population size and developmental time of the four erineum stages. The mite population was lower at 35 °C than at 15 and 25 °C. Subsequently, we investigated changes in the volatile profile of

lychee plants infested by LEM and their role on mite behavior. The volatile profile of uninfested and infested plant tissue was characterized, and 58 volatiles were identified. Using dual-choice bioassays, we investigated the preference of LEM for the six most abundant plant volatiles identified. We observed that LEM attraction or repellence to volatiles was mostly influenced by compound concentration. Lastly, we investigated the spatiotemporal infestation patterns of the LEM in a lychee orchard with 190 trees. While LEM required 78.6 days to infest 10% of the trees, it was able to infest 90% of the plants within just 100 additional days. The relevance of these findings for integrated pest management will be discussed.



OP-24

ACALITUS SIMPLEX (ERIOPHYIDAE) ON *RUELLIA SIMPLEX* (ACANTHACEAE): A CLOSER LOOK TO THE TAXONOMY AND MITE-HOST INTERACTIONS

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Acalitus simplex, an oligophagous pest of the genus *Ruellia*, causes the development of open galls (erinea), on the plant tissue. The erinea progress through four distinct stages: hyaline, white, purple, and silver, although the purple may be absent under certain environmental conditions. Little is known about the taxonomical status of *A. simplex* and no data are available about its interactions with *Ruellia* species. The study aims to: i) clarify the uncertain taxonomy ii) investigate population density inside each erineum stage and iii) assess the erinea development time. Specimens of *A. simplex* from Brazil, Florida, and Hawaii were compared by sequencing the CO1 gene and using different microscope techniques. Population density in each erineum stage was investigated by placing individual leaf discs on a

plastic tile and recording the emergence of *A. simplex* every 24 hours. Erinea developmental time was assessed after infesting *R. simplex* with 30 adult *A. simplex* females. The progression of the erinea was recorded every 72 hours until all reached the silver stage. All *A. simplex* specimens showed close morphological and molecular similarity, sharing the same epigynium reticulation and 95% sequence similarity. The population density varied across the erineum stages, with white and purple containing the highest number *A. simplex* while the hyaline and silver had the lowest. The white stage persists longer on the plant than the hyaline and silver. The research outcomes will enhance understanding of *A. simplex* taxonomy and the role of erinea, aiding the development of mitigation strategies against this pest.



OP-25

EXTENDING LIFESPAN: EXAMPLES FROM MITES AS EXPERIMENTAL ANIMALS

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Life-extending interventions have been studied in many model animal species, but surprisingly, mites are rarely present in this large body of literature. Many hypotheses on aging and lifespan have been proposed and tested, and several measures of interventions to extend lifespan are well studied in animal models. For example, diet restriction or intermittent fasting has been shown in a large number of animal taxa to increase lifespan.

In this study, we used a number of mite species to test effects of several factors on lifespan: diet restriction, moderate fasting, reduced frequency of mating and mild stress. These species belong to a wide range of taxonomic groups with different feeding habits and biology:

phytophagous mites such as the twospotted spider mite *Tetranychus urticae* (Trombidiformes: Tetranychidae), predatory mites such as *Phytoseiulus persimilis* and *Neoseiulus cucumeris* (Mesostigmata: Phytoseiidae), and fungivores such as *Tyrophagus putrescentiae* (Sarcoptiformes: Acaridae).

We demonstrated that mites are excellent model systems for experimental studies on lifespan and highlighted sex-specific effects (Li & Zhang 2019) and transgenerational effects ((Li & Zhang 2020; Lee et al. 2020) on lifespan in mites. The importance of early-life experience on lifespan was confirmed in multiple mite species (Wei et al. 2022).



OP-26

THE BIOLOGY OF AUGUSTSONELLA (PARASITENGONA: ERYTHRAEIDAE)

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Introduction

Augustsonella tuberculatus (Augustson 1940) was described from specimens collected on coastal sand dunes in Southern California (USA). This mite is unique in the Erythraeidae in having tuberculate setae on the distodorsal palpgenu and dorsal palptibia (Fig. 1). In 1973 Hoffmann & Menendez described *A. southcotti* from Morelos, Mexico suggesting *Augustsonella* was a wide-ranging genus.

Methods and Results

Field collections revealed additional species from various habitats ranging from sea level to over 3300 m and the inland deserts of southwestern USA. Live specimens from coastal sand dunes and desert areas were obtained using dry pitfall traps. Some specimens were prepared for morphological study using the LTSEM and others were kept alive for observation. Field collections and laboratory

rearing confirmed the absence of an active larval instar as eggs developed directly into deutonymphs. At least one species was observed feeding on a dead insect. In the laboratory these mites were only active under bright light and in the field, they were never active at night. One desert species was observed running on the soil surface that registered a temperature of 61.7°C. When not active *Augustsonella* spp. bury themselves in the substrate by digging with their palps and pushing themselves into the substrate with legs II-IV. Leg I is not used in digging.

Conclusions

Augustsonella is unique among the Erythraeidae in their palpal morphology and the absence of an active larval instar. They have adapted to a variety of habits from the cool moist seashore to high mountains and hot deserts.



OP-27

TRADE-OFF BETWEEN HOST SPECIALISATION AND THERMAL NICHE BREADTH IN A GLOBAL MITE PEST OF CEREALS

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Introduction: Unraveling the mechanisms underlying the evolution of ecological niche is fundamental to understanding the ability of species to adapt to environmental change and to explain patterns of their diversification and distribution. Organisms are constantly exposed to environmental variability, which imposes adaptive pressure. Usually, constant environments favor specialization, whereas fluctuating environments select for generalists. In this study we aim to understand how divergent environments (constant vs. fluctuating) shape biotic (host range) and abiotic (thermal range) niche dimensions.

Methods and results: We used the plant-feeding mite *Aceria tosichella*, the significant cereal pest, as a study system. Specifically, we used replicated mite populations that were experimentally evolved over 150 generations under constant (single host plant) or fluctuating

(alternation of two plant species) conditions. We then assessed the fitness of these experimentally evolved lineages (i) on different host plant species, and (ii) over a range of temperatures from 12°C to 36°C. Our results show that the niche breadth of *A. tosichella* underwent evolutionary changes in response to environmental variability. Host specialization led to a broadening of thermal tolerance, whereas host generalization led to a narrowing of thermal tolerance. This suggests trade-offs between biotic and abiotic niche dimensions.

Conclusion: Our study contributes to understanding mechanisms underlying adaptation in response to environmental heterogeneity as well as niche and range expansions and contraction. The study was supported by the National Science Centre, Poland (grant no. 2021/41/B/NZ8/01703).



FIELD ECOLOGY & MORPHOLOGY

OP-28

THE IMPACT OF TILLAGE, INSECTICIDES AND HERBICIDES ON ORIBATID MITE (ACARI: ORIBATIDA) COMMUNITIES EXPERIMENT IN NATURAL FIELDS LEADS TO THE SURPRISING FINDINGS

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a. Introduction. The agricultural practices affect non target soil fauna either by altering soil physical structure, or by application of chemicals. The effects of tillage, insecticide and herbicide applications on oribatid mites was studied over three years (2020, 2021, 2022).

b. Methods and results. The experiment was carried out at two natural fields. Three types of treatment (tillage, insecticides, herbicides) and their combinations were applied. A natural meadow without any treatment was used as control. Each treatment was repeated for three times at each site resulting in 48 plots overall (Figure 1). Oribatid diversity and density steadily declined from 2020 to 2022 due to increased average annual temperature and decreased precipitation. Herbicide and insecticide application had significant negative effect on the species number and abundance, while

combination of tillage with herbicide and insecticide had mitigating effect as tillage increases the rate of pesticide degradation and reduces by that direct exposure to soil fauna. Herbicides had significant positive effect on parthenogenetic species by immediate increase of resources (dead plant matter) while tillage lead to resource depletion and thus, to the higher proportion of sexual species. Annual decline of the oribatid diversity was expressed by loss of oribatids with thin cuticle and those, who are sensitive towards disturbance.

c. Conclusions. The study indicates on the change of local ecosystem from meadow to dry steppe enhanced by intensive agricultural interference. In a long term perspective, this will affect ecological services performed by these animals and change decomposition rates and nutrient turnover in soil systems



OP-29

ACAROFAUNA ON PRUNUS LAUROCERASUS: FROM TREE TO POTENTIAL BIOCONTROL PRODUCT

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a. Introduction: Cherry laurel, *Prunus laurocerasus* L., is an evergreen shrub native to Eastern Europe and is a popular ornamental in temperate regions. Here, we followed the acarofauna on a cherry laurel tree from an urban garden in Belgium on a monthly basis over a 3 year period. For two species of mites, we explored the potential to be used in biocontrol.

b. Material and methods: The first species, *Czenspinskia transversostriata* (Oudemans) (Acari: Winterschmidtidae), was tested as a feed mite for *Amblyseius swirskii* in the laboratory and in a greenhouse trial on cucumber. Based on previous reports on its fungivorous feeding behavior, we assessed its potential to feed, reproduce and control

powdery mildew on cucumber plants. The second species, *Amblyseius herbicolus* (Chant) (Acari: Phytoseiidae) was tested as a potential biocontrol agent against a range of pest at different climate conditions.

c. Conclusion: When served as a feed mite, *C. transversostriata* proved to be an excellent food source for *A. swirskii*, both in the laboratory experiment and in the greenhouse trial. Furthermore, *C. transversostriata* was able to feed, reproduce and limit the spread of powdery mildew on cucumber plants. *Amblyseius herbicolus* showed potential to be used for controlling thrips and whitefly, particularly at lower temperature conditions.



OP-30

FURTHER MECHANISTIC INSIGHTS INTO THE TROPHIC DESIGN OF FREE LIVING MITES

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Recent advances in the ecomorphological understanding of how gnathosomal features work as food processing tools relevant for astigmatan mites of economic importance and their mesostigmatid predators are described.

Engineering analysis is used. New unpublished acarine morphological results are included. Underbite and overbite in cheliceral chelae are exemplified and their function debated.

Features for acarologists to search for in fluid handling are highlighted. The Rollplatte is re evaluated. Designs for browsing, grazing and liquid feeding are critically discussed in detail. Other topics covered include mites in cadavers and sword like designs.

A variety of tool types remain to be found in acarines.



OP-31

GRIP, HOOK, PULL, SCRATCH – CLAWS OF ORIBATID MITES AND THEIR CORRELATION WITH ECOLOGY AND FUNCTION

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Claws are biological tools which can be found across the animal kingdom. These biological appendages serve a multitude of functions, including digging, climbing, and capturing prey. Mites also possess hooked claws and they are generally used for attachment, which is why not much attention has been paid to these morphological structures. However, studies on claws of other organisms have shown that claws may contain information about ecology and biology. Mites mostly dwell in microhabitats which are difficult to observe and therefore studying their claws may provide important insights into their cryptic lifestyles. We used geometric morphometrics to document and compare the shapes of over 50 species from various environments. We found a significant correlation between claw morphology and environment. Littoral mites exhibit notably larger claws compared to their terrestrial

counterparts, with aquatic species presenting intermediate traits. In littoral oribatids, substrate properties of the microhabitat have a strong influence on claw characteristics, whereas in terrestrial mites other factors apparently also contribute to claw shape. We also discovered that claw shapes remain constant during development when juveniles and adults share the same environment and ecology, but in case of ecological shifts between immature and adult stages, claw shapes also show significant differences. Although claws of mites are used only for attachment, considerable variation can be found in their characteristics. Different microhabitats and different lifestyles cause specific differences in claw shapes. These differences may allow us to learn more about the biology of these tiny creatures, which usually remains hidden from our eyes.



OP-32

INTRASPECIFIC VARIATIONS IN ROSETTE PATTERNS OF FEMALE FAVOGNATHUS AMYGDALUS (TROMBIDIFORMES: CRYPTOGNATHIDAE)

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Introduction

Favognathus amygdalus (Cryptognathidae) has been known from Iran and Turkey (Beron, 2020). It can be recognized by evenly distributed pores on the dorsum, partly reticulate patterns formed by polygonal dimples or cells, cluster of cells associated with setae c1 and d1, central area of dorsum none reticulate venter with lateral reticulation, prosternal apron with fourteen dimples; femur II with three setae, and dissimilar addorsal setae tc on tarsus II (Doğan and Ayyıldız, 2004). In this study, intraspecific variations in rosette patterns of female *Favognathus amygdalus* were investigated.

Methods and Results

In total, 45 female specimens of *F. amygdalus* were examined. The specimens were extracted by using Berlese Tullgren during a study on the raphignathoid mites in the Karasu Valley (Türkiye), cleared in 60% lactic acid and mounted in Hoyer's medium on microscopic slides. The variations were photographed with the aid an Olympus BX63 differential interference contrast (DIC) microscope.

Figures 1–2. Variations in rosette shaped patterns on dorsum of *Favognathus amygdalus* (female). 1. The rosette lacks a central cell, 2. The second rosette on the right side consists of only one cell.

Conclusion

Some species of *Favognathus* bear one or two pairs of dorsal rosette shaped patterns in a cellular structure, and these patterns have taxonomic significance. There are typically two pairs of rosettes on the dorsal surface of *F. amygdalus*. They consist of 7 or 8 cells and have a central cell according to Doğan and Ayyıldız (2004). Intraspecific variations were detected in these patterns of some specimens examined. The cells range in number from 1 to 10 in the specimens. The rosettes of some specimens lack a central cell (Fig. 1), and the second rosette on the right side of one specimen consists of only one cell (Fig. 2).

The rosettes consist of 3 to 5 cells in *F. rosulatus* (Doğan and Doğan, 2020a), 4 in *F. insularis* (Paktinat Saeij et al., 2020), 2 to 6 in *F. bafranus* (Doğan and Doğan, 2020b), 3 to 7 in *F. manisaensis* (Akyol and Koç, 2017), 3 to 8 in *F. esfahaniensis* (Khanjani et al., 2014), 6 to 8 in *F. hyrcanensis* (Mohajer et al., 2014), 7 or 8 in *F. turcicus* (Koç and Ayyıldız, 1999), and 7 to 9 in *F. distinctus* (Swift, 1996). In conclusion, as the number of cells in the rosettes in the genus *Favognathus* can vary, caution is required when identifying or describing new species based on a few specimens, particularly when their distinctive characters are related the rosette patterns.

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TAXONOMY, SYSTEMATIC & PHYLOGENY

OP-33

WHERE ARE WE NOW? ABOUT MICROTROMBIDIIDAE (TROMBIDIFORMES: PARASITENGONA) SYSTEMATICS AND RELATIONSHIPS FROM A MORPHOLOGICAL AND MOLECULAR POINT OF VIEW

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With about 500 species assigned to more than 120 genera the Microtrombidiidae constitute the most speciose family next to Trombiculidae within terrestrial parasitengone mites. However, numbers bear huge uncertainties because of poor evidence on species boundaries and the fact that about 90% of the species are only known for a postlarval instar [Figure 1] or the heteromorphic larva.

Concerning the more recently published hypotheses on relationships at inter- and intrafamily level ([2], [3]) our knowledge remains rather incomplete due to the limited data, which include mostly ectomorphological characters of which only a few seem useful. In the last decades, the progress in phylogenetic analyses using molecular data led to new insights into evolutionary relationships and processes; however, their application in Microtrombidiidae and Parasitengona, in general, is still limited and often burdened with contradictory results.

We will evaluate published phylogenetic hypotheses related to Microtrombidiidae with regard to the suitability of included characters and applied methods. Moreover, we will review possibilities to use molecular data for better detection of species and for phylogenetic analyses and will discuss the problems related to an integrative approach, combining molecular techniques with traditionally used morphological data.

In morphological analyses the standard microscopic techniques are applied; the protocol for molecular analyses, employing markers suitable for various taxonomic levels, follows [1], [4], with modifications.

New findings, juxtaposed with the hitherto views on the relationships within Microtrombidiidae, confirm the monophyly of all subfamilies hitherto distinguished. Our studies constitute the step forward to a deeper insight into microtrombiid systematics.



OP-34

MORPHOLOGICAL AND MOLECULAR VARIATIONS OF SPECIMENS IDENTIFIED AS *Protogamasellopsis zaheri* (Rhodacaridae: Mesostigmata) FROM DIFFERENT BRAZILIAN BIOMA

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Protogamasellopsis zaheri (Rhodacaridae) is one of the mesostigmatid species most frequently and abundantly found throughout Brazil. The objective of this work was to study the morphological and molecular characteristics of specimens from four Brazilian bioma (Caatinga, Cerrado, Atlantic Forest and Pantanal). Specimens from rearing colonies were mounted on slides for measurements of selected structures using a graduated eyepiece. No major morphological differences were observed, suggesting that all the mites belong to the same species. In regards to the molecular analyses, total genomic DNA was extracted using a QIAGEN DNeasy kit. Five DNA fragments were amplified (the mitochondrial fragments mtDNA Cytb, 12S rRNA and COI, and the nuclear fragments 28S, ITSS) and sequenced. Genetic distances were calculated applying the Kimura-two-parameter (K2P) and phylogenetic trees

were constructed (Maximum Likelihood). The specimens collected in the Caatinga, Atlantic Forest and Pantanal were very similar, genetic distance being close to 0% for all the DNA markers used. The specimens collected in Cerrado were however very different from specimens from the other locations. The mean genetic distance between Cerrado specimens and the others were very high for all primers (mean genetic distance were between of 0.150 for the marker 28S and of 0.269 for the marker Cytb). Such genetic distances correspond to interspecific distances, suggesting that the specimens from Cerrado are actually another species. New morphological observations confirmed this conclusion and this new cryptic species is morphologically distinguishable mainly by the greater length of the setae on podonotal and opistonotal shields, especially of the "S".



OP-36

MITOGENOMIC EVIDENCE FOR THE MONOPHYLY OF THE SUBFAMILY CECIDOPHYINAE (ERIOPHYOIDEA, ERIOPHYIDAE)

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Introduction

Eriophyoidea (four-legged or gall mites) is a large superfamily (about 5000 species) of highly host-specific phytoparasitic acariform mites. Some species of gall mites are economically important pests. Phylogeny of Eriophyoidea is poorly resolved. Subfamily Cecidophyinae is one of the few morphologically distinct and putatively monophyletic suprageneric taxa of Eriophyoidea. Cecidophyines have uniquely modified female spermathecal apparatus and external genitalia appressed to coxae II. Remarkably, a recent comprehensive mitogenomic study focused on resolving basal divergence of Eriophyoidea, rejected the monophyly of Cecidophyinae. Our research is aimed at retesting the hypothesis of monophyly of Cecidophyinae based on new mitogenomic dataset.

Methods and results

Mitogenomes of five Cecidophyinae species from three genera (*Cecidophyes*, *Cecidophyopsis* and *Coptophylla*) were obtained and annotated. The mitogenomes have the same gene order, except translocations of tRNA Cys gene and control region in *Coptophylla*. We compared the new mitogenomes with those from previous research, performed molecular phylogenetic analyses of the sequences of 12 protein-coding and 2 rRNA genes and obtained a ML tree showing high support for the clade comprising all mitogenomes of cecidophyines.

Conclusions

Our analyses confirm the monophyly of subfamily Cecidophyinae. We showed the consistency of the morphology based diagnosis of this taxon and the unique structure of cecidophyine mitogenomes. Overall, our study shows that comparative mitogenomics is a promising tool for investigating the phylogeny of Eriophyoidea.



OP-37

ESCAPE FROM A VICIOUS CIRCLE - ABOUT TROMBICULIDAE (TROMBIDIFORMES: PARASITENGONA) IN A SLIGHTLY DIFFERENT WAY

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The Trombiculidae with ca. 3300 nominal species, constitute the most speciose family of terrestrial Parasitengona. The actual number of species may significantly depart from published data, because of basing the descriptions almost exclusively on morphological characters of larvae.

The Palearctic *Hirsutiella* comprises 11 nominal species. Despite numerous records on *Hirsutiella* spp., available in taxonomic and faunistic works, the status of several species requires verification. At poorly marked species boundaries and the confirmed phenomenon of phenotypic plasticity, the correct identification is challenging for researchers and votes for referring to additional diagnostic criteria.

Hirsutiella zachvatkini, considered the only representative of the genus in Poland, has been known for the widest distribution range, covering most of Europe and Asia. Larvae of *H.*

zachvatkini parasitize a wide variety of hosts, including rodents and insectivores. A wide host spectrum, and the observed scope of intraspecific variation constitute the background for hypothesis on the presence of *H. zachvatkini* species complex.

We aimed to verify the actual representation of *Hirsutiella* in Poland. Larvae collected from different host species were preliminarily assigned to *H. zachvatkini* based on morphology. Three different methods of delimitation employing the COI sequences pointed to the presence of three potential species. The latter was contradicted by analyses based on the p28S marker which did not confirm the presence of distinct species. The results vote for considering *H. zachvatkini* the only representative of the genus in Poland and, at the same time, support the integrative approach in the verification of the species status in Trombiculidae.



BIOLOGICAL CONTROL & INTEGRATED PEST MANAGEMENT

OP-38

REASSIGNMENT OF *EPITRIMERUS VIOLARIUS* LIRO, 1941 (ACARIFORMES: ERIOPHYOIDEA) TO THE GENUS *LEIPOTHRIX*

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Epitrimerus violarius Liro, 1941 is a free-living eriophyoid mite inhabiting plants from the genus *Viola*. This species was reported for the first time in Poland and collected from *Viola uliginosa* Besser's leaves in Cracow. Examination of the collected specimens and analysis of the original description revealed incorrect placement of this species within the genus *Epitrimerus*. These findings aimed to provide a comprehensive description of this species, including morphological and genetic analysis and illustrations of all developmental instars. Mite colony was carried out directly on plants and in Munger cages and kept in a microclimate chamber Panasonic MLR-352PE under controlled conditions at $25 \pm 1^\circ\text{C}$, humidity of $60 \pm 10\%$ and 16-hour photoperiod. Specimens from the colony were mounted in Berlese

medium and morphological traits of 13 females, 5 males, 5 nymphs and 4 larvae were measured. Single specimens were also used for nucleic acid extraction and the D1D2 region of the 28S rDNA was sequenced.

Morphological traits of studied specimens, especially the absence of the femoral seta (bv) on both pairs of legs, and the presence of bifurcate gnathosomal seta, clearly indicate the necessity of reassignment of the species from the genus *Epitrimerus* to *Leipothrix*. These findings were also supported by molecular analysis, which showed 94.97% affinity of the D1D2 region to the sequence of *Leipothrix* sp. deposited in GenBank. As a consequence of this study, the valid name of the species is currently *Leipothrix violarius* (Liro, 1941).



OP-39

INNOVATIVE TOOLS TO COMBAT KEY TOMATO PESTS

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Tomato is a crop of high economic importance; however, it is damaged by several herbivorous arthropods, while alternatives to chemical control are often rare or not effective enough. In this study, we assessed the effects of novel pest control tools on tomato key pests such as the two-spotted spider mite *Tetranychus urticae* and the tomato russet mite *Aculops lycopersici*. Specifically, we treated plants with peptides, a metabolites and beneficial soil fungal strains, and recorded the number of mite individuals, as well as spider mite eggs on plants of the different treatments. We found a lower number

of mites of both species as well as number of spider mite eggs on treated plants as compared to control (untreated) plants. As a next step, we will study the molecular and chemical mechanisms underlying the most promising tools. Our results highlight the role of peptides, metabolites and beneficial soil microbes in suppressing mite populations. Furthermore, our study aims to identify specific molecular and chemical components of tomato direct and indirect defense that are differentially affected by treating tomato plants with the different pest control tools.

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OP-40

THE BLACK NIGHTSHADE (*SOLANUM NIGRUM*) AS GREEN BRIDGE OF TOMATO RUSSET MITE (*ACULOPS LYCOPERSICI*)

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The tomato russet mite (TRM), *Aculops lycopersici* (Tryon) (Acariformes: Eriophyoidea), is widely acknowledged as a significant pest afflicting tomato (*Solanum lycopersicum*) crops. Nevertheless, its presence has been often documented on various weed species within the Solanaceae and Convolvulaceae families. Our observations reveal a notable affinity of TRM towards black solanaceous (*Solanum nigrum*), a frequently encountered weed alongside tomato cultivations in Italy: this suggests its potential role as a green bridge facilitating TRM persistence in the absence of tomato as primary host. Hence, this investigation aimed to compare the developmental parameters of TRM populations on tomato and on black nightshade while also exploring TRM adaptability to colonise alternative hosts.

Life tables were calculated based on age-specific survival rates and specific fecundity rates for TRM developed on tomatoes and black

nightshade. Concurrently, the capacity for TRM to exploit alternative hosts was gauged by determining population growth rates. Our findings revealed that black nightshade was a slightly worse host plant for TRM mites than tomato: the intrinsic rate of population increase was 0.24 and 0.25, with population doubling times of 2.92 and 2.75, for black nightshade and tomato, respectively. Furthermore, the population growth rate of the tomato-adopted population developed on black nightshade was not significantly different than that on tomato. Additionally, our investigations showed that the size of this population still increased on pepper (*Capsicum annuum* 'Clavesol'), convolvulus (*Convolvulus arvensis*), tobacco (*Nicotiana tabacum* 'Xanti'), and petunia (*Petunia × hybrida* 'Starlet F2') while on white goosefoot (*Chenopodium album*) it survived just for two weeks.



OP-41

FUNCTIONAL RESPONSE OF A TOMATO-SELECTED POPULATION OF THE PREDATORY MITE *AMBLYSEIUS ANDERSONI* (ACARI: PHYTOSEIIDAE)

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Tomato is a hostile crop plant for phytoseiid predators mainly because of its chemical and morphological defenses. On the other hand, tomato is damaged by a series of arthropod pests, among which the two-spotted spider mite *Tetranychus urticae*. *Amblyseius andersoni* is an important biological control agent of spider mites. With the aim to establish a lab rearing of a field-collected population of the mite, an extended survey was conducted in tomato fields throughout continental Greece. This population was further selected for increased survival on commercial tomato lines and a small-scale mass rearing was established on plastic arenas. *Typha angustifolia* pollen supplemented with juveniles and eggs of the spider mite or the alternative prey *Carphoglypus lactis* were used as food

source for the predator. In this study, we assessed the effects of each diet on the performance of the mite specifically, its predation efficiency. Functional response experiments were conducted using predators reared on the two diets for more than 5 generations, at several spider mite egg densities on tomato leaflets, and prey consumption was recorded daily. Data analysis revealed a type II functional response curve, and the random predator equation was used to estimate searching efficiency and the handling time indices. Overall, we show that no significant diet effects on the predation efficiency and functional response of the predator under lab conditions. Field trials are required to confirm these results under realistic conditions.

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OP-42

HYPERPREDATION OF *APHIDOLETES APHIDIMYZA* EGGS BY GENERALIST PHYTOSEIID MITES; A THREAT TO APHID BIOCONTROL IN SWEET PEPPER?

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Biocontrol in sweet pepper relies on a range of biocontrol agents for a variety of pests. Aphids are a major issue in greenhouse cropping systems. Generalist predatory mites, *Amblydromalus limonicus*, *Amblyseius swirskii* and *Transeius montdorensis* are used to control thrips and whiteflies and the gall midge *Aphidoletes aphidimyza* is an important component of aphid control. Biological control of aphids has become even more important since the emergence of a flonicamid-resistant strain of *Myzus persicae* in European greenhouses. It is known that generalist predatory mites predate on *A. aphidimyza* and that this can potentially disrupt aphid predation. We investigated the predation capacity and oviposition of *A. limonicus*, *A. swirskii* and *T. montdorensis* on *A. aphidimyza* eggs in

laboratory experiments and interactions of *A. aphidimyza* with the different phytoseiid mites and the effect on *M. persicae* control on sweet pepper plants in a greenhouse cage trial.

We found significantly higher predation rates on *A. aphidimyza* eggs of *A. limonicus* and *T. montdorensis* of 15.8 eggs per day compared to *A. swirskii* with 12.6 eggs per day. However, the oviposition rate did not differ between the three phytoseiid species. Furthermore, *A. aphidimyza* population development was significantly inhibited by all phytoseiid mite species on sweet pepper plants in the cage experiment. We conclude that hyperpredation by phytoseiid mites may negatively affect aphid control. Further research is necessary to understand this interaction and its effect on aphid biocontrol in commercial greenhouses.



OP-43

PLANT-MEDIATED EFFECTS OF SOIL MICROBES TO ENHANCE PEPPER PERISTANCE

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Unable to run away from their enemies, plants have evolved a series of sophisticated mechanisms to defend themselves against herbivory. Besides herbivorous arthropods, plants also interact with beneficial organisms such as soil microbes which are known to improve plant growth, antagonize pathogens and prime plants against future attackers via plant defense elicitation. In this study, we assessed the plant-mediated effects of beneficial fungal strains against a key pest of pepper, namely the two spotted spider mite *Tetranychus urticae*. For this, we inoculated (or not) plants with the microbes, infested them (or not) with mite individuals, and recorded the

number of live adults and eggs laid on plants of the different treatments. To assess the effects of the most promising fungal strain on indirect defenses of pepper, plants were prepared as above and then we recorded the behavior of natural enemies towards plants of the different treatments with olfactometer experiments. Results show that inoculating plants with different fungal strains differentially affect spider mites via the plant, as well as the behavior of their natural enemies, highlighting the role of soil microbes in suppressing herbivore populations, possibly via the induction of plant defenses.

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OP-44

BEYOND DISCOVERY: FINDINGS FROM 15 YEARS OF SURVEYS REVEAL NEW PHYTOSEIID MITES (ACARI: MESOSTIGMATA), AND THEIR PROMISING POTENTIAL IN BIOLOGICAL PEST CONTROL

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The demand for sustainable pest control methods is steadily increasing due to growing environmental concerns related to usage of chemical pesticides. The predatory mites in the family Phytoseiidae (Acari: Mesostigmata), on the other hand, play a crucial role in the management of phytophagous mites and some other pests such as thrips and whiteflies. Studying, discovering, and accurately identifying, the biodiversity and functions of these natural predators are in line with broader environmental objectives, such as the European Green Deal's ambition for a "climate-neutral bloc" by 2050. Over 15 years, our extensive surveys have resulted in the identification of approximately 40 new species and over 100 new records within the predatory mite family Phytoseiidae in several countries, especially in

Turkey and Russia. These findings significantly contribute to our understanding of the biodiversity and ecological dynamics of this important group of natural enemies in a variety of ecosystems including agricultural, arid, forest, terrestrial, urban, and wetland. Through meticulous fieldwork and taxonomic analyses, we have identified previously unknown or poorly known species and expanded the known distribution ranges of numerous phytoseiid mites. Some of the new species and records we have discovered may share similarities with well-known phytoseiids that are available in the international market, particularly in terms of their lifestyle, ecology, and food habits. Therefore, conducting research on these species to assess their potential as local biological control agents is crucial.



OP-45

POTENTIAL OF COMMERCIALY AVAILABLE AND NATURALLY OCCURRING PREDATORY MITES AGAINST *THRIPS PARVISPINUS* KARNY (THYSANOPTERA: THIRIPIDAE)

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Thrips parvispinus has emerged as a major agricultural pest and it is regulated in Florida. It exhibits characteristics of high invasiveness with a worldwide distribution and a broad host range. In Florida, it was first reported in ornamental plants in 2020. The damage caused by *T. parvispinus* is by feeding on young leaves, buds, and flowers causing dark spots, reddish-brown discoloration, and curling of leaves. Phytoseiid and laelapid mites play a significant role in pest management with demonstrated efficacy against numerous thrips species, as well as other significant pests. Commercially available phytoseiid and laelapid mites and those naturally occurring in the environment are good candidates for thrips control. Little is known regarding the potential of predatory mites as biological control agents of *T. parvispinus*. The aim of this study is to determine which

predators are most likely to be effective in controlling this pest. Under contained conditions, eight commercially available predatory mites: *Neoseiulus californicus*, *N. longispinosus*, *N. cucumeris*, *Amblyseius swirskii*, *A. andersoni*, *Amblydromalus limonicus*, *Iphiseius degenerans*, and *Stratiolaelaps scimitus*, and two naturally occurring: *Proprioseiopsis ovatus* and *Amblyseius largoensis* were offered first (L1) and second (L2) instar larvae of *T. parvispinus* (two-choice experiments). The predator choice was scored every five minutes for the first half hour and every hour after that for a total period of six hours. Preliminary findings indicate that *A. swirskii*, *A. andersoni*, and *P. ovatus* prefer to feed on L1. The predators *N. californicus* and *N. longispinosus* did not feed on *T. parvispinus* larvae during the experiment.



OP-46

FITNESS COMPARISON IN *AMBLYSEIUS SWIRSKII* POPULATIONS RESISTANT AND SUSCEPTIBLE TO AN ABAMECTIN AND BIFENAZATE MIXTURE FORMULATION

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The predacious mite *Amblyseius swirskii* Athias-Henriot (Acari: Phytoseiidae) is an effective biocontrol agent of whiteflies, thrips and spider mites. A native Turkish population of the predator were artificially selected by an acaricide formulation that is a mixture of bifenazate and abamectin. Compared with its native population, selections in the laboratory for 6 consecutive generations resulted in 25 folds bifenazate and abamectin resistance. To examine the relative fitness of the abamectin and bifenazate-resistant population of *A. swirskii*, the life table parameters of resistant and susceptible populations of *A. swirskii* feed on eggs of *Tetranychus urticae* (Koch) (Acari: Tetranychidae) were observed under controlled conditions (27±1°C, 80±5% RH, L:D, 16:8). The analyses showed that the developmental duration, longevity and prey consumption of the

resistant population did not seem altered with developing acaricide resistance. The mean fecundity and oviposition duration of the resistant population were significantly higher than that of the susceptible population. The resistant population had significantly higher the intrinsic rate of increase ($r_m=0.154 \text{ d}^{-1}$) and the finite rate of increase ($\lambda=1.166 \text{ d}^{-1}$) than the sensitive population ($r_m=0.147 \text{ d}^{-1}$; $\lambda=1.159 \text{ d}^{-1}$). The net reproductive rate ($R_0=10.00$ offspring) and the mean generation time ($T=15.65 \text{ d}$) of the susceptible population were only slightly higher than those of the resistant population ($R_0=9.75$ offspring, $T=14.81 \text{ d}$). The study showed that acaricide resistance of *A. swirskii* can be increased artificially without adversely affecting their main fitness components. This study was funded by TUBITAK with the grant number of 122R115.



OP-47

PHYTOSEIID MITES ASSOCIATED WITH OAK, POPLAR AND WALNUT TREES IN TURKIYE*

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The leaf surfaces of wild and cultivated plants worldwide provide billions of square meters of potential habitat and microhabitat for mites, but variations in their abiotic and biotic environments can pose extreme challenges. The phytoseiid mites (Acari: Phytoseiidae), an extremely species-rich group of mostly generalist predators, provide vital ecosystem services worth hundreds of millions of dollars yearly by suppressing phytophagous mites and insects in native and planted forests, field crops, green-houses and home gardens. In this study, the phytoseiid mites on the leaves and shoots of four species of common tree species - oak (*Quercus cerris*), poplar (*Populus deltoides*, *P. nigra*) and walnut (*Juglans regia*), were

compared. The three data sets used were from three seasonal studies in Samsun Province, Turkiye, between 2018 and 2023. In total, 19 phytoseiid species in 13 genera were collected. Only *Eusieus amissibilis* was collected from all three tree genera. Reasons for the distinct differences in the phytoseiid complexes on the oak, two poplars and walnut, including leaf morphology, lifestyle, feeding behaviour and abiotic factors, are discussed. Global biodiversity, likely including many undescribed phytoseiid species, is being lost to habitat destruction and climate change, especially in the tropics. Urgent, integrated actions from the local scale to global initiatives are required in response.



OP-48

MITIGATION STRATEGIES FOR ACARINE PESTS OF HEMP (*CANNABIS SATIVA*)

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Industrial hemp (*Cannabis sativa*) is cultivated in Florida for fiber, seeds, resin, and medicinal compounds. Distinguishing it from Marijuana is its low delta-9 tetrahydrocannabinol (THC) concentration, mandated to be under 0.3%. Hemp is attractive to acarine pests, including spider mites (*Tetranychus urticae*, *Tetranychus gloveri*), broad mites (*Polyphagotarsonemus latus*), and russet mites (*Aculops cannabicola*). Chemical control is limited and regulated by the Florida Department of Agriculture and Consumer Services – Division of Plant Industry (FDACS-DPI). Our study assessed approved biorational pesticides against common acarine pests, and predatory mites for managing the regulated pest *A. cannabicola*. Single active ingredient products: citric acid, rosemary, thyme, sesame, and garlic oil (table 1.) were applied at the maximum label rate. Mites placed on leaf discs were sprayed with each treatment,

and mortality was recorded after 4, 24, 48, 72, and 96 hours. Citric acid, garlic, and thyme oil were most efficacious against the evaluated species. Subsequent greenhouse trials confirmed the efficacy of garlic oil against *T. urticae*, and these oils demonstrated potential for producing mite-free cuttings for propagation. Predatory mites were evaluated against *A. cannabicola*. Thirty *A. cannabicola* mites were placed on leaf discs and offered to one female in a hermetic arena. *Amblyseius swirskii* showed the highest predation rate and managed to lay eggs. The effect of biorational pesticides on *A. swirskii* showed no significant differences between thyme and garlic compared to the water control over the experimental time. Our findings provide practical solutions for the hemp industry, assisting growers in managing acarine pests.



OP-49

BIOLOGICAL CONTROL OF INVASIVE THRIPS WITH PREDATORY MITES IN ORNAMENTAL CROPS: SUCCESSES AND CHALLENGES

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Predatory mites of the family Phytoseiidae are among the most commonly used predators for biological thrips control. In recent years, several invasive thrips species have established in ornamental crops in Dutch greenhouses, causing a lot of damage. The goal of our study was to explore the potential of phytoseiid mites as predators of 3 invasive thrips species (*Thrips parvispinus*, *Thrips setosus*, *Dichromothrips corbetti*) in 3 ornamental crops: anthurium, lily and orchids. We carried out greenhouse experiments with different predatory mite species (*Amblyseius swirskii*, *Transeius montdorensis*, *Neoseiulus cucumeris*), supplementary food treatments (Artemia cysts, pollen, prey mites) and climatic conditions. In parallel, we performed laboratory experiments to study the predation capacity of invasive thrips on predatory mite eggs. Our results show that

phytoseiid mites can be used as effective biological control agents of *T. parvispinus*, *T. setosus* and *D. corbetti*. However, the establishment of phytoseiid mite populations in crops such as anthurium, lily and orchid remains difficult and many repeated mite introductions are necessary to ensure thrips control. Anthurium, lily and orchid plants have glabrous leaves (without trichomes or domatia), which might partly explain why predatory mites struggle to establish in these crops. We also showed that some thrips species are able to predate on predatory mite eggs, depending on the host plant. Our study highlights the need to develop artificial microhabitats mimicking trichomes and domatia for predatory mites in ornamental crops. These microhabitats would act as shelters, protecting them against unfavourable climatic conditions and predators.



OP-50

ACARICIDES RESIDUE IN MILK IN THE CHEMICAL AND BIOLOGICAL CONTROL OF THE TICK *RHIPICEPHALUS (BOOPHILUS) MICROPLUS* (ACARI: IXODIDAE)

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Brazil ranks as the third largest milk producer globally. The Instituto Biológico has been actively investigating the management of *Rhipicephalus (Boophilus) microplus* ticks by employing fungi in pasture environments. This study aimed to assess milk samples from cows (BT) treated with acaricides containing chlorpyrifos, cypermethrin, and piperonyl butoxide, and compare them with milk from cows (BF) grazing in pastures treated with *Metarhizium anisopliae* fungus (IBCB 425), which was applied using a drone. The experiment took place in Pindamonhangaba, São Paulo, Brazil. In both BT and BF groups, comprising 7 animals each, three treatments were administered at 21-day intervals. Six samples were collected from each animal (0, 1, 2, 3, 4, and 7 days after treatment), totaling 252

samples. Tick counts were conducted throughout the experiment to evaluate infestation levels. The analysis of acaricide residues in milk samples employed the QuEChERS and LC-MS/MS method. While milk samples from group BT displayed residues of all three active ingredients across the three treatments, they remained compliant with regulations and fell below Maximum Residue Limits. Conversely, samples from group BF exhibited no detectable residues. In terms of tick counts, both groups experienced a reduction in infestation without significant difference between them ($p=0.870$). The application of the *M. anisopliae* fungus for tick control substantially mitigates the risk of residues in milk and offers an effective, environmentally safe alternative for tick management.



CHEMICAL CONTROL, RESISTANCE & TOXICOLOGY

OP-66

MOLECULAR MECHANISMS OF GENE EXPRESSION VARIATION ASSOCIATED WITH RESISTANCE IN TETRANYCHUS URTICAE

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Spider mites are important crop pests that can mount a strong transcriptional response when challenged with a novel host, or after adaptation to acaricides. Resistance is therefore a worldwide serious problem. However, gene regulatory mechanisms underlying this plasticity and adaptation potential are not well studied. We have started to unravel the global architecture of gene expression variation in these generalist herbivores. An eQTL analysis revealed that a single trans eQTL hotspot

controlled large differences in the expression of a subset of genes in different detoxification gene families. Additional genetic approaches identified a duplicated HR96-related gene as causal for the expression differences between strains. The presence of a large family of HR96-related genes in *T. urticae* may enable modular control of detoxification and facilitating this species' known and rapid evolution to diverse pesticides and host plants.



OP-51

RESISTANCE TO COMPLEX II INHIBITORS IN *TETRANYCHUS URTICAE*

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Acaricides inhibiting the mitochondrial electron transport system at complex II (METI-II), commonly known as succinate dehydrogenase inhibitors (SDHI), constitute a recently developed class of acaricides. This class includes cyflumetofen, cyenopyrafen, pyflubumide, and cyetpyrafen. Despite their efficacy, resistance to complex II has been observed in European *Tetranychus urticae* populations, even in the absence of prior exposure. A long-term monitoring of cyflumetofen resistance in Turkish populations of *T. urticae* showed the development of high levels of resistance only three years after the registration of cyflumetofen. Subsequent investigations revealed the involvement of target-site mutations as a primary mechanism of resistance to SDHI. Intriguingly, these mutations often confer resistance selectively, with some variants

displaying even a negative cross-resistance pattern among complex II inhibitors. More recently, we uncovered a novel mutation located outside the ubiquinone binding site of succinate dehydrogenase. Functional validation via marker-assisted backcrossing and biochemical assays confirmed its role in resistance to cyflumetofen and pyflubumide. Furthermore, CRISPR-Cas9 gene editing were used to reveal the role of several complex II mutations. All these findings underscore the complex interplay between target-site mutations and SDHI resistance. Future studies on SDHI resistance and resistance mechanisms in field populations are imperative for a comprehensive understanding and the development of robust resistance management strategies.



OP-52

TWO SPOTTED SPIDER MITE SUBJECTED TO SUBLETHAL ABAMECTIN TREATMENTS: EVALUATION OF TRANSGENERATIONAL PHENOTYPIC PLASTICITY

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Transgenerational phenotypic plasticity is the phenomenon by which an organism can show phenotypic difference in response to environmental stimuli experienced by previous generations.

Tetranychus urticae Koch, the two-spotted spider mite (TSSM), is a polyphagous agricultural pest known to rapidly develop resistance to acaricides. The aim of the present research was to evaluate if and how transgenerational phenotypic plasticity affects the response of TSSM to repeated sublethal acaricide treatments.

A homozygous *T. urticae* line was developed by repeatedly crossing full siblings. Thereafter, the homozygous mites were subdivided in eight independent lines. Half lines were successively treated for seven consecutive generations with water (control lines) and half with sublethal concentrations of abamectin (abamectin lines),

respectively. Then, a Common Garden Experiment (CGE) was performed by treating both groups either with abamectin or with water (factorial design 2 x 2). CGE was repeated for two consecutive generations after the end of abamectin or control treatments.

The evidence acquired leads to conclude that transgenerational phenotypic plasticity is involved in *T. urticae* response to the acaricide treatment. During CGEs, mites previously treated with abamectin showed a maladaptive response, depositing, if further treated, fewer eggs than mites never treated with abamectin ($p < 0.05$). This phenotype, observed for two following generations, suggests the involvement of epigenetic based information in the observed transgenerational phenotype. The adaptive and evolutionary implication of these observations need to be further deepened in the framework of *T. urticae* response to acaricides.



OP-53

USEFULNESS OF DEET (N,N-DIETHYL-META-TOLUAMIDE) IN THE DIRECTED EXPULSION OF DIFFERENT GROUPS OF MITES AND INVERTEBRATES IN BERLESE-TULLGREN FUNNELS

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Collecting mite samples using methods known today is effective, but lacks the ability to target specific groups of organisms we might be interested in. Previous studies conducted on DEET as a repellent factor showed promising results in terms of repelling efficiency compared to using a light bulb in these extractors. In order to obtain more reliable measurements, new research was conducted, focused on measuring effectiveness of different concentrations of DEET for different invertebrates.

The methods used in this study involved taking soil samples once a month for six months on a specific day from a 2 m diameter area - always at three locations and four samples at each location. One sample was spudded conventionally using a light bulb (control

sample) and the others were spudded at different concentrations of DEET- sequentially: 2.5ml, 3.5ml and 5ml DEET. A total of 72 samples (12x6) were collected. All samples were then dissected, the animals counted and sorted according to taxonomic groups. For mites, individuals from the orders Astigmata, Oribatida and Mesostigmata were counted separately.

The results indicate that the efficacy of DEET as a repellent is higher than the use of a light bulb and that different concentrations of DEET have different efficacy on different groups of mites. Thus, DEET may be a selective agent for repelling specific groups of animals. Further research could surely delve into optimizing DEET concentrations for different groups of soil organisms.

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OP-54

MOLECULAR CHARACTERIZATION OF ACARICIDE RESISTANCE MECHANISMS IN THE MAJOR BEE PARASITE *VARROA DESTRUCTOR*

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Varroa destructor is the primary pest of the European honeybee (*Apis mellifera* L). Several synthetic acaricides have been used for its control in Europe, such as the organophosphate coumaphos, the pyrethroid tau-fluvalinate and the formamidine amitraz. However, their intensive use has selected for acaricide resistance in several occasions. By using bioassays, as well as molecular approaches, we monitor the presence and frequency of insecticide resistance phenotypes and alleles in a number of parasitic mite populations. High levels of coumaphos, tau-fluvalinate and amitraz resistance has been identified in some regions, often associated with

the history of spraying application. The presence of pyrethroid resistance mutations in the voltage-gated sodium channel of pyrethroid-resistant *Varroa destructor* has been recorded, at various frequencies in several populations from Europe. Acaricide resistance mechanisms have been characterized at the molecular and functional level, with emphasis on cytochrome P450s. The results will help beekeepers with their decision making as to when to include or exclude certain acaricide control products and thereby facilitate the application of effective and sustainable management programs.



OP-55

MONITORING OF ACARICIDE RESISTANCE ON *DERMANYSSUS GALLINAE* IN TURKEY

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Turkey ranks among the top ten countries worldwide in egg production. Despite various factors affecting poultry yield, *Dermanyssus gallinae* (commonly known as Poultry Red Mite, PRM) stands out as a significant ectoparasite, imposing substantial economic losses. The control of PRM infestations in poultry houses often relies on chemical acaricides, both during egg production and in empty facilities. However, Turkish *D. gallinae* populations exhibit considerable levels of resistance to pyrethroid and organophosphate acaricides associated with the widespread occurrence of target-site mutations. In this study, we assessed the efficacy of next-generation neurotoxic

pesticides, such as fluralaner and isocycloseram, alongside traditional options like pyridaben and fipronil, against Turkish PRM populations. Our findings revealed varying degrees of efficacy among these acaricides, with some demonstrating promising results across all tested populations. Nevertheless, decreased susceptibility was observed in certain instances such as pyridaben and fipronil. Furthermore, synergism assays showed the involvement of P450 monooxygenases in fluralaner toxicity. Regular monitoring of acaricide toxicity in PRM populations should be continued in future studies.



OP-56

MOLECULAR SCREENING AND GENETIC MECHANISMS OF PESTICIDE RESISTANCE IN FIELD-EVOLVED PREDATORY MITE *AMBLYSEIUS ANDERSONI* (ACARI: PHYTOSEIIDAE)

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Many arthropod pest species develop pesticide resistance, causing the inefficiency of pest control measures and dramatic losses in cropping systems. Pesticide resistance is the key factor causing secondary pest outbreaks. *Amblyseius andersoni* (Chant) is a generalist predatory mite that naturally occurs in orchards and vineyards. It is considered a key natural enemy of spider mites and other arthropod pests. Its conservation is thus fundamental for successful pest management strategies. In European orchards and vineyards, synthetic insecticides are particularly important in the management of quarantine and invasive pests (i.e., against *Halyomorpha halys* (Stål) and *Scaphoideus titanus* Ball). Synthetic pesticides can be detrimental to beneficial mites, increasing the risk of spider mite outbreaks. Understanding whether predatory mites

develop pesticide resistance can be important for their conservation and implementation of IPM strategies. In this study, we screened for target-site resistance mutations in four field-collected and two commercial *A. andersoni* strains. We assessed the incidence of mutations in VGSC, CHS-1, SdhB/C, ATP synthase, CytB, ACCase and PSST. Results showed that the well-known super-kdr mutation (M918L) was present in pyrethroid resistant strains of the predatory mite, while absent in a commercial susceptible strain. We also detected the mutation L925V, which seems to be associated with resistance against pyrethroids, as it was not detected in the susceptible strain. In addition, we looked at linking resistant/susceptible phenotype to genotype by crossing experiments. Our results are discussed in the context of integrated pest management programs.



MITE VECTORS IN AGRICULTURE

OP-57

MITE BE MORE INTERESTING THAN YOU THINK: EXPLORING MITE-DRIVEN VIRUS TRANSMISSION

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Phytophagous mites are known to transmit several plant viruses, but the mechanisms are largely unknown. Eriophyoid mites (Acari: Eriophyoidea) and flat mites (Acari: Tenuipalpidae) are the primary vectors, with sporadic reports suggesting that spider mites (Acari: Tetranychidae) could also vector some viruses. The challenges in working with mites, particularly in rearing and setting up transmission experiments, combined with their minute size, have hindered broader research efforts. Even with advancements in molecular identification methods like DNA barcoding, the study of mite vectors is lagging behind their insect counterparts.

Approximately sixty plant viruses have been associated with mites; however, two-thirds lack

verified vectors, indicating the rudimentary state of our understanding of the virus-mite interactome.

This lecture will discuss the current state of knowledge on mite-driven virus transmission, emphasizing the need to understand the molecular and ecological dynamics involved. Recent research shows that viruses like the rose rosette emaravirus (RRV, family Fimoviridae) or wheat streak mosaic virus (WSMV, family Potyviridae) actively replicate within certain mite vectors, influencing the spread and severity of diseases. By exploring these intricate interactions, we aim to pave the way for new research directions and address knowledge gaps essential for developing innovative and sustainable control measures.



OP-58

INSIGHTS INTO EMARAVIRUS VIRAL DYNAMICS AND ERIOPHYOID MITES VECTOR COMPETENCY USING THE ROSE ROSETTE EMARAVIRUS (RRV)/*PHYLLOCOPTES FRUCTIPHILUS* PATHOSYSTEM PARADIGM

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Introduction: Understanding the interaction between rose rosette emaravirus (RRV) and its vectors is pivotal in addressing the epidemic outbreak of rose rosette disease in the United States. This study aimed to assess RRV replication in *Phyllocoptes fructiphilus* and *P. adalius* (Acariformes: Eriophyoidea), providing insights into viral dynamics and vector competency.

Methods and Results: Quantitative real-time RT-PCR was employed to measure RRV genome copy numbers in the two mite species. Our findings suggest active virus replication within *P. fructiphilus*, a confirmed vector species, unlike *P. adalius*, highlighting its non-vector status. Furthermore, the study revealed variability in

virus concentration in mites over time, underlining possible developmental stage-specific responses and the influence of mite lifestyle on RRV retention and replication.

Conclusions: This research is the first step in understanding the virus-mite interactome, which is essential for developing effective management strategies against rose rosette and potentially other emaravirus-caused diseases. Our work significantly enhances the understanding of the dynamics between RRV and its eriophyoid mite vectors, paving the way for the creation of targeted management approaches to mitigate the impact of rose rosette and other emaravirus-caused diseases.



OP-59

PHYLLOCOPTES PARVIFLORI IS A DISTINCT SPECIES AND THE VECTOR OF A WIDESPREAD BLACKBERRY VIRUS THAT CAN SOLELY CAUSE BLACKBERRY YELLOW VEIN DISEASE

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Blackberry leaf mottle-associated emaravirus (BLMaV, *Emaravirus rubi*, family Fimoviridae), transmitted by an unidentified species of eriophyoid mite (Acariformes: Eriophyoidea), is implicated in the emergence of blackberry yellow vein disease (BYVD), a highly destructive malady prevalent in the southeastern United States. This study evaluates the potential of an eriophyoid mite *Phyllocoptes parviflori*, as a vector of BLMaV while verifying its taxonomic validity, previously synonymized with *P. gracilis*. Our findings demonstrate that *P. parviflori* effectively transmits BLMaV, inducing characteristic yellow vein disease symptoms on

'Ouachita' blackberry without the presence of other viruses. This discovery challenges existing paradigms, as disease symptoms have conventionally been attributed to multiple virus infections. Consequently, we propose renaming the virus to blackberry leaf mottle virus (BLMV). Our research, backed by molecular analyses, refutes the previous synonymization of *P. parviflori* with *P. gracilis*, establishing them as distinct species. The widespread presence of *P. parviflori* on both wild and cultivated blackberries and its ability to infest other *Rubus* species underscores its significance as a primary agent in disseminating BYVD.



OP-60

THE TWO-SPOTTED SPIDER MITE AS A VECTOR OF ZUCCHINI YELLOW MOSAIC VIRUS (ZYMV)

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Zucchini Yellow Mosaic Virus (ZYMV), *Potyvirus cucurbitaflaviteselati*, a member of the Potyviridae family, was first identified in zucchini squash plants in northern Italy. Typical symptoms of ZYMV infection include yellow mosaic patterns, severe malformations, and blisters. ZYMV is an aphid-borne virus and is considered a major pathogen of cucurbits in many regions worldwide. Previous laboratory experiments have shown that cucumber plants infected with ZYMV are preferred by the spider mite *Tetranychus urticae*, which benefits from the infection by living longer and laying significantly more eggs on infected plants. Our study aimed to determine whether *T. urticae* can act as a vector for ZYMV. We conducted greenhouse transmission trials using potted cucumber plants that were mechanically

inoculated with ZYMV. The symptomatic plants were subsequently infested with spider mites and placed next to healthy plants on a table or in a simple wind tunnel to encourage the aerial dispersal of mites from infected to healthy plants. The presence of ZYMV in both donor and recipient plants was evaluated based on symptom expression and DAS-ELISA. Additionally, the presence of the virus in mites after feeding on infected plants was assessed using RT-PCR and transmission electron microscopy. The obtained results confirmed that *T. urticae* can acquire ZYMV and transmit it to healthy cucumber plants. This finding suggests that spider mites should also be considered in ZYMV management, in addition to aphid vectors.



OP-61

UNRAVELING THE ROLE OF ERIOPHYOID MITES IN THE SPREAD OF RASPBERRY LEAF BLOTCH EMARAVIRUS (RLBV)

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Raspberry leaf blotch emaravirus (RLBV, *Emaravirus idaeobati*, family Fimoviridae) affects raspberry plants across Europe. It negatively affects plant growth and fruit quality, reducing raspberry yields [1]. Poland is one of the largest berry producers in the world; therefore, a better understanding of RLBV and improved virus eradication efforts are crucial for domestic berry growers. It has been long suspected that the raspberry leaf and bud mite (*Phyllocoptes gracilis*) is involved in the natural spread of RLBV; however, transmission tests conducted for this species were inconclusive [2]. This study aimed to (A) identify the fauna of eriophyoid mites present in raspberries and blackberries in Poland, (B) conduct RLBV transmission tests with mite species or genotypes predominant on infected plants, (C) examine the possibility of RLBV replication within the body of a vectoring mite.

For this purpose, we have collected 200 samples in Poland, both from cultivated and naturally growing raspberry and blackberry plants. Samples were tested for RLBV using RT-PCR, with 26 raspberries and one blackberry being infected. Barcoding of mites and phylogenetic analysis revealed two species of eriophyoids being associated with raspberry, whereas only one species was present on blackberry plants. RLBV transmission tests unequivocally confirmed vector-competence of *P. gracilis*, and virus quantification assay within individual mites provided a new perspective on RLBV accumulation and retention. Identification of RLBV vector and improved understanding of transmission mechanisms are crucial for developing effective control strategies that could be used in the field.



OP-62

GENETIC DIVERSITY OF *COLOMERUS VITIS* (ERIOPHYIDAE) IN FRANCE AND ITS RELATION WITH THE GRAPEVINE PINOT GRIS VIRUS INCIDENCE

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The eriophyid mite *Colomerus vitis* is the vector of the Grapevine Pinot Gris virus (GPGV), a phytovirus emergent in France and in Europe associated with Grapevine Leaf Mottling and Deformation disease. Previous studies considering populations from South Africa, Iran, Egypt, Israel, Spain and USA showed that this mite constitutes a complex of cryptic species, including five genetic lineages. French populations have not been characterized to date. In France, the status of GPGV is contrasting among regions, possibly due to differences in virus transmission efficiency among eriophyid mite genetic lineages. The aims of this study were to i) characterize the genetic diversity of *Col. vitis* from France; and ii) check for a relation between the genetic pool of *Col. vitis* and the incidence of GPGV. For this, populations from 44

vineyards on 17 departments were sampled. For each plot, around 10 specimens from 5 vines were isolated for DNA extraction and COI sequencing. GPGV rt-PCR tests were conducted to detect the virus in sampled vines. A total of 574 sequences were obtained. Phylogenetic analysis, which datasets included all public sequences available in GenBank and previously obtained by the team, revealed the co-occurrence of the five divergent COI genetic lineages in France, with two dominant lineages - G1 and G5. Statistical analysis suggests a significant association between the presence of GPGV and group G1 within a vine ($p=0.02$), indicating that G1 is most strongly associated with virus transmission. Further studies should investigate the efficiency of virus transmission by the two dominant lineages.



OP-63

COMPARISON OF WHEAT STREAK MOSAIC VIRUS INFECTION LEVELS IN WHEAT AFTER NATURAL AND ARTIFICIAL INOCULATION IN DIFFERENT GROWTH STAGES – THE ROLE OF WHEAT CURL MITE IN EFFECTIVE VIRUS TRANSMISSION

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Wheat streak mosaic virus (WSMV), transmitted by the wheat curl mite (WCM) *Aceria tosichella* Keifer (Fig. 1), frequently causes loss in winter wheat. Previous field studies which compared the relationship between the timing of infection of winter wheat with WSMV and the method of inoculation, natural (vector) or artificial (manual inoculation), showed significant differences in the extent of losses. However, there is little data that defines which stages of wheat development are the most susceptible for different infection scenarios. Therefore, the aim of the study was to examine the effect of WSMV inoculation method and timing on the condition of wheat and assessment of the WCM population development. Experimental assays were performed in the greenhouse conditions, with wheat *Triticum aestivum* L., WCM lineage MT-1 and the WSMV-Sze isolate. To assess the degree

of plant infection, ELISA tests were performed and chlorophyll content and oxidative stress were measured. The results showed that the WSMV infection had a positive effect on mite population density, especially in plants infested at earlier stage (avg. 0.11 mites/mm² on WSMV-positive plants vs avg. 0.04 on non-infected plants) and chlorophyll levels were lowest in plants that were infected by vectors. Moreover, superoxide anion levels were also higher in plants inoculated with WSMV by vectors regardless of the growth phase. The study indicates that the impact of WSMV vector transmission by mites and mite presence itself on plant condition decreases as the plant age at the infestation and inoculation timing increases. Furthermore, the combined mite and virus effects on plant exceed mechanical inoculation effects.



OP-64

UNVEILING THE ENIGMATIC MITE VECTOR OF BLUEBERRY NECROTIC RING BLOTCH VIRUS

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Global blueberry (*Vaccinium sp.*) cultivation has grown exponentially in the past decade. Several viruses are known to infect blueberries, most of which occur in the United States, the world's largest producer and the country of origin of the crop. *Blunervirus vaccinii* (family Kitaviridae), causing Blueberry necrotic ring blotch virus, was detected in Florida in 2006, but until recently, its vector was unknown. The first report of *B. vaccinii* also mentioned its association with an undescribed eriophyoid mite. However, Kitaviruses are usually linked to mites in the genus *Brevipalpus* (Family Tenuipalpidae).

Brevipalpus yothersi is considered a pest of blueberries and is common in areas where *B. vaccinii* has been reported. We evaluated the vector competency of *B. yothersi* and the undescribed eriophyoid mite. Controlled transmission studies revealed that the eriophyoid mite and not *B. yothersi* is the vector of *B. vaccinii*. The mite, belonging to the genus *Calacarus*, is being described. This is the first determination of a Blunervirus vector, and the first Kitavirus known to be vector by mites outside of the *Brevipalpus* genus. Other peculiarities of this pathosystem are discussed.



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AGRICULTURAL & FORESTRY ACAROLOGY

PP-01

ECOLOGICAL RESPONSE OF SOIL MITE COMMUNITIES STRUCTURE (ACARI, MESOSTIGMATA) IN THE ENVIRONMENT SHAPED BY THE SEA BUCKTHORN SHRUBS (*HIPPOPHAË RHAMNOIDES* L.) GROWING ON RECLAIMED POST-MINING LAND

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Fruit shrubs play an extremely important role as biocenotic admixtures, for example as a source of food for many organisms, including soil fauna. Their impact and importance have been studied many times in relation to vertebrate animals, although the impact on soil fauna communities, including mites, are relatively poorly understood, especially in disturbed ecological systems, such as post-mining areas. Therefore, the aim of our study was to examine the mite communities structure (Acari, Mesostigmata) at different distance from forest trees and fruit shrubs, as well as from the biogroups center formed by them, growing on reclaimed post-mining land.

The work scope included the mesostigmatid mite communities structure analysis, inhabiting the top soil layer in Scots pine (*Pinus sylvestris* L.) and silver birch (*Betula pendula* Roth) stands,

and buckthorn shrubs (*Hippophaë rhamnoides* L.), growing on the external spoil heap created as a result of brown coal opencast mining. The study was conducted on the "Bełchatów" lignite mine external spoil heap (Central Poland). A total of 128 soil samples were collected for further analysis. Soil fauna, including mesostigmatid mites, inhabiting the samples was isolated using the Berlese-Tullgren apparatus. Developmental stage and taxonomic unit of individuals have been classified.

In total, 252 individuals were described as 26 taxa (21 species, four genera and one suborder). The results revealed that the sea buckthorn presence in pine and birch stands growing on post-mining area had a positive effect on the abundance and species richness of mesostigmatid mites.



PP-02

FLOTAC APPARATUS APPLICATION FOR DETECTION BY FLOTATION METHODS OF MITES (ACARI: ERIOPHYOIDEA, PHYTOSEIIDAE) ASSOCIATED WITH HAZELNUT

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Typically, eriophyoid detection is operator-dependent and is done by a manual separation and counting of mites from symptomatic and non-symptomatic plant materials directly under a dissecting microscope or after an extraction procedure. Collection/observation is often time-consuming and requires training to observe and handle small specimens under a dissecting microscope. Several alternative methods have been developed and some are applied (Monfreda et al. 2009).

FLOTAC is a recent technique developed to separate and count fecal parasites like protists and helminths (Cringoli et al., 2010). It involves a special apparatus to separate and view specimens at composite microscope in one step after a simple procedure.

To detect mites, the FLOTAC procedure has been modified in part and it has been validated for accuracy (i.e. number of individuals detected out of a known number of stages added to the plant samples) and sensitivity (the smallest value of individuals measurable with the instrument). Eriophyoid and Phytoseiid mites were quantified from *Phytoptus avellanae* infested plant material processed by the mite extraction washing protocol previously applied by Monfreda et al. (2007).

This flotation procedure shows to be promising for a faster quantification and a more practical detection than the other techniques currently applied.

The research leading to these results has received funding from the project “Innovative Management Strategies of Eriophyoid mites affecting hazel-NUT (MASTER-NUT)” CUP H53D23007270001 funded by the Italian PRIN-PNRR 2022 – DD 1409/2023.



PP-03

SOIL MITE ASSEMBLAGES (ACARI, MESOSTIGMATA) IN DIFFERENT TYPES OF COPPER SMELTER POLLUTED HABITATS

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The areas adjacent to the copper smelter are subject to contamination by elements such as sulphur, arsenic, cadmium and lead. Contamination of the soil may disrupt the functioning of soil trophic network. The aim of our study was to compare Mesostigmata mite communities inhabiting three different habitats under the equal influence of copper smelter pollution. The study included [1] a 51-yo pine stand (*Pinus sylvestris* L.), [2] a 66-yo black locust stand (*Robinia pseudoacacia* L.) and [3] an area of spontaneous succession, overgrown with shrub forms: blackthorn (*Prunus spinosa* L.), common hawthorn (*Crataegus monogyna* Jacq.), black locust, birch (*Betula pendula* Roth.) and white willow (*Salix alba* L.) among others. 72 soil samples were eventually collected – 24

samples from each habitat (3 plots × 8 samples). Soil fauna was extracted using Berlese-Tullgren apparatus. In total, 370 individuals were described as 33 taxa (29 species, four genera). The highest mite abundance was found in the area under spontaneous succession, while the highest number of species was described in the black locust stand. The lowest abundance and species richness were described in the pine stand. The mite communities structure was similar in the black locust stand and on area with spontaneous succession. In the pine stand, ecological features of mite communities were much lower. The results of the study indicate a positive effect of deciduous species, compared to coniferous, on soil biodiversity in heavily transformed and industrially polluted areas.



PP-04

SOIL MITES (ORIBATIDA, MESOSTIGMATA) AND NEMATODES (NEMATODA) IN EUROPEAN SCOTS PINE (*PINUS SYLVESTRIS* L.) FORESTS

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Climate changes influence the location, composition, structure and function of forests in many parts of the world, including the high-latitude forests dominated by boreal species with Scots pine (*Pinus sylvestris* L.) forests. The literature on belowground soil mites (decomposers and predators), and nematodes in such forests is scarce. We focused on Scots pine forests based on soil fauna sampling along a 2000 km latitudinal transect as this tree is one of the most widespread conifer species on Earth and also on various soil fauna groups as they greatly increase the global turnover of dead organic matter and provide key ecosystem processes such as the decomposition of organic matter and the recycling of nutrients.

We aimed to characterise the mite and nematode communities from soils of mature

Scots pine forests based on samples collected during summer field campaign in 2013. Soil samples come from 22 location between west Poland and northern Finland. Mites were processed in „portable extractor”, whereas nematodes using the centrifugal method. After extraction soil fauna was preserved in liquid solution and finally mounted on slides and identified. We analysed relationships between soil fauna characteristics and environmental factors such as longitude and meteorological data.

We recorded that soil fauna density in Scots pine forests depended on latitude, annual temperature, precipitation but the responses are differentiated within analysed soil fauna groups.

This research was supported by the National Science Center, Poland (2011/02/A/NZ9/00108)



PP-05

THE EFFICACY OF THE TANSY-BASED TREATMENT IN DECREASING THE DEVELOPMENTAL POTENTIAL OF THE TWO-SPOTTED SPIDER MITE

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The tansy (*Tanacetum vulgare* L.) is a herb whose volatiles can repel or be toxic to pest-arthropods. The study aimed to verify if tansy essential oil water-based solutions and hydrolate reduced the development the two-spotted spider mite (*Tetranychus urticae* Koch, Tetranychidae).

The essential oil and hydrolate were isolated from fresh herb using two-column distillation apparatus Innotec Tetekov TWE 250–2000 VA. The solutions (0.25; 0.5; 0.75; 1% in 0.05% Tween) and hydrolate were applied either directly on females or indirectly by transferring females on previously sprayed bean (*Phaseolus vulgaris* L.) leaf discs. Mite fecundity and survival were assessed every day, for 7 days under controlled conditions.

Direct bioassay showed that neither concentrations of oil solutions lower than 0.75%, nor hydrolate affected mite fecundity

and survival, while 0.75% and 1% solutions decreased fecundity by 50%-60% and survival by 40-52%, respectively after 6-7 days. Residual bioassay showed that feeding on bean leaves previously treated with 0.75 and 1% solutions resulted in 3-fold and 6-fold decrease in fecundity after 4 and 6 days, respectively. Probit Analysis Method showed that after 4 and 6 days of direct treatment, the LC50 equalled 2581µl/100ml and 1507µl/100ml, respectively, and that those values were higher by 26% and 81% in comparison to the LC50 values determined in residual bioassays.

The efficacy of tansy oil could be increased by using greater concentrations. Furthermore, indirect effects of tansy oil on mite reproduction should not be neglected due to a likely repellent/deterrent effect of bean leaves previously treated with tansy oil.



MEDICAL & VETERINARY ACAROLOGY

PP-06

COMPARATIVE STUDY OF CONVENTIONAL VS. INNOVATIVE METHODS FOR CONTROLLING *VARROA DESTRUCTOR* (ANDERSON AND TRUEMAN) (MESOSTIGMATA: VARROIDAE)

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Introduction

The Varroa mite poses one of the greatest threats to beekeeping worldwide. This issue is due to the ectoparasitic mite *Varroa destructor*, which targets both brood and adult bees. It was first observed in 1904 in Southeast Asia parasitizing the Indian honey bee *Apis cerana*, and after 1960, its transfer to the honey bee *Apis mellifera* resulted in its global spread. The mite reproduces within brood cells, making treatment difficult. This is why beekeepers prefer to manage the infestation when there is little or no brood. Historically, synthetic chemical pesticides (acaricides) were used to combat the mite. However, due to a shift in consumer preference towards organic products, oxalic acid has become one of the most widely used treatments worldwide.

Methods and Results

This study employs a comparison control group design with two groups of bee colonies: one treated conventionally and the other using an innovative method. In the latter, the queen bee is confined in a cage, and when the colony is broodless, oxalic acid treatment is administered. The experiment involves 20 beehives (two groups of 10), equal in population, with sister queens and similar *V. destructor* infestation levels. Measurements include colony size (brood, population, and weight) and honey production.

Conclusion

The anticipated results are promising, suggesting that healthy and productive colonies can be maintained without the use of chemical pesticides.



PP-07

FEASIBILITY ASSESSMENT OF AUTOMATED DETECTION OF *RIPHICEPHALUS (BOOPHILUS) MICROPLUS* TICK LARVAE IN INFESTED PASTURES

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The *Rhipicephalus (Boophilus) microplus* tick is a significant parasite in cattle farming, with about 95% found in pastures at various stages like larvae, engorged females, and eggs. This study assesses the potential of using Unmanned Aerial Vehicles (UAVs) for automated detection of *R. microplus* larvae in infested pastures. A 2m by 4m area of pasture was marked and divided into eight equal squares and two cameras were installed for observation. To emulate a typical low-flying UAV application in a controlled environment, two commercial lightweight, visible-light spectrum cameras (“C1”, “C2”) were used for time-lapse imaging: C1 was placed at 2.25m high, with a full overhead view, while C2

was placed at 1.10m, focusing on the two areas of the highest concentration of larvae. The experiment was designed with two control squares without larvae and six squares containing larvae in varying amounts: 150, 250, and 400. Observations from 6 a.m. to 6 p.m. revealed that, against prevailing beliefs, tick larvae were present on foliage throughout the day, especially in areas not directly exposed to sunlight. In this specific configuration, this experiment showed that automated detection using various machine learning methods was much worse than human identification, therefore a similar UAV application is not commercially viable.



PP-08

MICROBIAL AGENTS IN ARGASID TICK *ORNITHODOROS FONSECAI* WITH NOTES ABOUT ITS KARIOTYPE

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Ornithodoros fonsecai is an argasid tick described from larvae collected parasitizing bats and from adults found free-living in caves inhabited by these hosts, in the Central-West and Northeast regions of Brazil. This study aimed to characterize the bacteriome of this species, with the help of Next Generation Sequencing, and present the karyotype of this tick. The specimens used in this study come from São Miguel Cave, Bonito, state of Mato Grosso do Sul, Brazil. Two males were dissected to karyotype study, and 2 males and 2 females were submitted to microbiome analyses. Specimens were individualized and cleaned (1% sodium hypochlorite, 70% ethanol, followed by rinsing with sterilized distilled water three times, 2 min each), and then were subjected to DNA extraction, using the QIAGEN® - DNeasy Blood & Tissue kit, following the manufacturer's

protocol. PCR was performed and the V3-V4 region of 16S rRNA gene was used to detect prokaryotes. Sequences analyses were conducted with DADA2 pipeline, and taxonomic assignments were performed using Silva database. It was possible to obtain many different bacteria from the samples, with emphasis on *Coxiella* genus. Further investigations will be carried out to try to characterize this *Coxiella* sequence. Submitting more samples for microbiome analysis will certainly expand our knowledge about this bacterial diversity in these ticks. Meiotic cells from *O. fonsecai* were obtained and stained with DAPI, demonstrating diakinesis and metaphase I initial. The diploid number for this species was $2n=20$, with the occurrence of 2 sex chromosomes.



PP-09

MICROBIAL AGENTS IN BAT-ASSOCIATED MACRONYSSID MITES (ACARI: MESOSTIGMATA) FROM BRAZIL

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Twenty-six species of macronyssid mites have been reported to Brazil, from which 15 were collected from bats. Although *Bartonella* spp., *Anaplasma* spp., and *Ehrlichia* spp. were molecularly detected in bat-associated macronyssid mites in the state of Mato Grosso do Sul, central-western Brazil, the true role of these mite species on the epidemiology of pathogens is still unknown. This study aimed to characterize the bacteriome of Macronyssidae with the help of Next Generation Sequencing. The mite specimens used in the present study were stored and deposited in the Acari Collection of the Instituto Butantan and they were identified according to the most recent review carried out for the family. After cleaned with 1% sodium hypochlorite, 70% ethanol, and rinsing with sterilized distilled water three

times, mites were subjected to DNA extraction, using the QIAGEN® - DNeasy Blood & Tissue kit, following the manufacturer's protocol. Each mite DNA sample was subjected to a conventional endogenous control PCR (18S rRNA gene) and the 16S rRNA gene (region V3-V4) was also used to detect prokaryotes. Finally, the Next Generation Sequence was carried out to perform the bacterial microbiome of the samples. It was possible to obtain an average of 200 different bacteria belonging to 45 families from the samples sequenced, with emphasis on the genus *Wolbachia*. Further investigations will be carried out to try to characterize these *Wolbachia* sequences. Submitting more samples for microbiome analysis will certainly expand our knowledge, which is still so incipient, about this bacterial diversity in these ticks.



PP-10

PROTEOMIC INVESTIGATION OF EMBRYONIC TICK CELL LINE DERIVED FROM *AMBLIOMMA SCULPTUM* BERLESE INFECTED WITH *ANAPLASMA MARGINALE*

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Tick cell lines, exemplified by the ASE-14 line derived from *Amblyomma sculptum* Berlese, play a crucial role in manipulating pathogens genetically and studying protein expression. This investigation aimed to delve into the proteomic profile of ASE-14 cells during *Anaplasma marginale* infection, unraveling differentially expressed proteins and their involvement in host-pathogen dynamics. Infected cells at 5, 7, and 10 days, and uninfected controls, were analyzed using Giemsa-stained slides to trace infection progression. Protein extraction was followed by LC-MS/MS analysis. The eggNOG platform facilitated functional annotation of proteins showing differential abundance. Findings revealed that the top ten up-regulated proteins in infected cells were associated with translation, ribosomal structure, biogenesis,

post-translational modification, protein turnover, chaperone, and cytoskeletal functions. Conversely, down-regulated proteins were linked to energy production, conversion, post-translational modification, protein renewal, and chaperone functions. Proteomic analysis unveiled dynamic shifts in protein expression over time post-infection, with functional annotation highlighting cellular defense mechanisms against bacterial invasion. Additionally, *A. marginale* proteins involved in pathogen invasion and evasion of immune responses were identified. This comprehensive understanding of host-pathogen interactions provides valuable insights for vaccine development, with this study marking the initial exploration of the protein profile of ASE-14 cells infected with *A. marginale*.



PP-11

MOLECULAR DETECTION OF *BARTONELLA SPP.* IN CHIGGER MITES (ACARI: TROMBICULIDAE) ASSOCIATED WITH RODENT FROM SOUTHERN BRAZIL

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Chiggers (Trombiculidae) are well-adapted parasites, mainly vertebrates, and can play a role as potential vectors for pathogens. In Brazil, 74 species of chiggers have been cataloged, most of them parasites of rodents, and some of them associated with some Bacteria. The DNA of '*Candidatus Rickettsia colombianensi*'-like was detected in the species *Herpetacarus hertigi* (Brennan), *Quadrasetta trapezoides* (Brennan and Jones), and *Trombewingia bakeri* (Fonseca). However, chigger mites associated with rodents have never been detected with Bartonella in the national territory. The mite specimens used in the present study were stored and deposited in the Acari Collection of the Instituto Butantan (IBSP), São Paulo. For DNA extraction, the 'DNeasy Blood & Tissue' kit was used, following the manufacturer's instructions. Each mite DNA sample was subjected to a conventional

endogenous control PCR (18S rRNA gene). For Bartonella, the positive samples were subjected to a real-time quantitative PCR for Bartonella spp. based on the nuoG gene followed by additional molecular characterization using conventional PCR – cPCR. In total, out of 33 chigger mite samples submitted to the molecular analysis, 20 (60.60%) showed a positive result for the endogenous control. Of all these, three chigger mites identified as a new species of Parasecia were positive in the qPCR and cPCR for Bartonella spp. based on the nuoG gene. Unfortunately, the lack of amplification in PCR assays targeting other molecular markers might have been due to the low bacteremia in the samples. In the future, new attempts should be performed aiming to obtain other Bartonella genes



PP-12

USE OF MALDI-TOF/MS IN THE IDENTIFICATION OF EMERGING PATHOGENIC MICROORGANISMS IN *AMBLIOMMA SCULPTUM* (ACARI: IXODIDAE)

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Ticks are ectoparasites of the Ixodida order, vectors of various microorganisms, making them relevant to public health and the global economy not only due to the number of species acting as transmitters, but also because of the wide variety of microorganisms they can transmit or carry. Microorganism exchange between hosts and ticks occurs during the hematophagous phase. This study aims to characterize emerging pathogens present in the salivary glands and ovaries of *Amblyomma sculptum* ticks collected from the field (group 1) and maintained in the laboratory for one year (group 2), both collected from the Tietê Ecological Park, São Paulo (SP), Brazil (23° 29' 46" S 46° 31' 10" W). Salivary gland and ovary extracts were obtained from 20 unfed females

under laminar flow using a stereomicroscope (Leica-EZ4). Colonies were isolated using the Petri dish exhaustion technique containing soybean tryptone agar and incubated in a BOD incubator (25°C). Ribosomal protein extraction from isolates and their identification using mass spectrometry (MALDI-TOF/MS) - (Bruker-Daltonics) were performed. Nine microorganisms were isolated, including *Candida haemulonii*, a pathogenic yeast resistant to antifungals, *Microbacterium paraxydans*, and *Gordonia terrae*, bacteria associated with long-term infections and nosocomial infections, respectively. These findings highlight the potential of ticks such as *A. sculptum* to host pathogenic microorganisms, posing a risk to public health.

Keywords: emerging pathogenic, *Amblyomma sculptum*, mass spectrometry



PP-13

COMPARISON BETWEEN ARTIFICIAL AND NATURAL FEEDING PROTOCOLS IN *ORNITHODOROS BRASILIENSIS* TICKS (ACARI: ARGASIDAE)

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Artificial feeding in ticks is a procedure that allows the analysis of biological aspects, evaluation of tick effectiveness as pathogen vectors, and simulation of live host utilization. This study examined natural and artificial feeding techniques in *Ornithodoros brasiliensis* ticks. To this end, the protein profiles of salivary glands were compared under different feeding protocols, utilizing live hosts and synthetic or biological membranes. The objective was to identify potential changes in protein profiles through SDS-PAGE and mass spectrometry (MS) analyses. Bioinformatics approaches relied on BLAST®, PFAM, and UniProt databases, concluding with the analysis of inorganic ion

spectra present in salivary glands using energy-dispersive X-ray fluorescence spectrometry (EDXRF). Results demonstrated differences in protein profiles among feeding methods. Furthermore, peptides involved in host inflammatory response and proteins related to neurotransmitter regulation and ATP synthesis were identified. EDXRF analysis revealed similarities in inorganic components of salivary glands regardless of feeding method. These findings suggest potential gene expression changes due to different feeding protocols, underscoring the importance of future biochemical characterizations to better understand the biological context of these ticks.

Keywords: Artificial feeding, *Ornithodoros brasiliensis*, protein, elemental composition



BEHAVIOUR, ECOLOGY & LIFE STRATEGIES

PP-14

INTERACTIONS BETWEEN MITES OF THE FAMILY OPLITIDAE (ACARI: MESOSTIGMATA) AND LASIUS UMBRATUS ANTS (NYLANDER, 1846)

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The authors present the results of observations made at two sites: in the General Henryk Dąbrowski Park in Bydgoszcz, northern Poland (52°07'13"N 17°09'21"E) and in Dąbrówka near Poznań (52°23'03"N 16°44'37"E) in two anthills of the ant species *Lasius umbratus* (Nylander, 1846). Material from the anthills was collected in 2023 and 2024. In both cases, several species of mites from the family Oplitidae were found in great abundance. These mites are relatively rare in other types of environments and microenvironments in Poland. The most abundant species was *Oplitis minutissima* (Berlese, 1903). The ratio of females to males was studied (sex ratio 1:40). Metric characteristics (body dimensions, female and male genital disc dimensions and all developmental stages) of the populations from

both anthills were compared. Phoresy was observed in the studied mite species. The carriers were workers of *L. umbratus*. The mites of the genus *Oplitis* do not produce a pedicel to attach themselves to the carrier like other Uropodina, but they attach themselves to the appendage on the ants' legs with their mouth organs located in the camerostome. This is interesting because in the case of the mites in question, only adults are phoretically transmitted, whereas in the other Uropodina species the phoretic stage is the deutonymph. The frequency of phoresis in each nest was determined as the ratio of the number of ants carrying the mite to the other ants (1:200). Preference for mite attachment sites during transport was estimated. SEM images of adults and developmental stages were prepared.



PP-15

PARENTAL INTRAGUILD PREDATION RISK AFFECTS OFFSPRING' PERSONALITY IN PHYTOSEIULUS PERSIMILIS

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Animal personality describes the consistency of behavior within individuals coupled to consistent variability among individuals over time and contexts. Typical behaviors used to characterize animal personalities are sociability, exploration, boldness, activity, and aggressiveness. Transgenerational effects on personality trajectories are poorly known. We hypothesized that the personalities of predatory mites *Phytoseiulus persimilis* are affected by early-life intraguild predation (IGP) risk experienced by their parents. For the parental generation (F0) of *P. persimilis*, eggs were placed in groups in leaf arenas harboring spider mites with or without the IG predator *Amblyseius andersoni*. Half of *P. persimilis* experienced IGP risk as larvae and protonymphs while the other half experienced no IGP risk. After becoming adult, each female (F) was paired with a male (M) that had experienced IGP risk (+) or not (-),

resulting in four parental treatments (F+M+, F+M-, F-M+, F-M-). Offspring (F1) were separately reared on spider mite-infested leaf arenas. Mated female offspring were tested for their personalities in boldness, exploration, and sociability. To this end, each female was subjected to three tests for each trait and the intraclass correlation coefficients (ICC) were calculated. The ICCs suggest that parental early-life IGP experience affects offspring' personality in boldness and exploration, but not in sociability. Offspring showed personality along the shy-bold axis only when both parents had a matching IGP experience (F+M+,F-M-), whereas offspring personality in exploration was contingent upon paternal experience. Our study highlights that transient early-life experiences by parents can have long-lasting, transgenerational impacts on offspring' personality trajectories.



PP-16

THE EFFECT OF HOST SPECIALIZATION ON THE RECOGNITION OF KAIROMONES BY THE PHYTOPHAGOUS MITE ACERIA TOSICHELLA

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Host location is crucial for passively dispersing invertebrates, as they rely mainly on dispersal agents to move through the landscape. However, dispersers do not leave their host at random; rather they rely on informed dispersal, i.e. individuals gather information before making a decision to move. For instance, herbivores can detect kairomones emitted by plants and use these to guide their dispersal. Furthermore, it is postulated that the number of kairomones that can be detected correlates with the degree of host specialization.

Here, we tested this concept using the eriophyoid mite *Aceria tosichella*, an important wheat pest with high invasive potential that is mainly dispersed by wind. Specifically, we aimed to find out whether host specialization affects kairomone recognition. We used two *A. tosichella* populations adapted to: i) a single

plant species (specialist); ii) two alternating plant species (generalist). We measured the proportion of individuals that dispersed while exposed to clean wind or wind filled with kairomones derived from familiar and unfamiliar plant species.

We found that dispersal was generally higher in generalist than in specialist, both in the absence and in the presence of kairomones. Generalist had higher dispersal rate in the presence of kairomones produced by plants to which it was adapted, whereas specialist dispersed more readily when perceiving kairomones produced by unfamiliar plant species. Our results reveal that the *A. tosichella* detects and discriminates plant kairomones, and that the degree of host-specialization strongly influences its behavioural decisions regarding dispersal.

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GENETICS & EVOLUTIONARY ACAROLOGY

PP-17

EXPLORING THE GENETIC STRUCTURE OF FEATHER MITES INHABITING THREE SPECIES OF HYDROBATES STORM-PETRELS

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Feather mites (Arachnida: Acari: Astigmata) are among the most abundant and commonly occurring bird ectosymbionts and also are interesting models for studying patterns of diversification and speciation because of their extraordinary ecological and evolutionary diversity. The aim of this study was to explore the genetic structure of feather mites inhabiting three species of *Hydrobates* storm-petrels (*H. pelagicus*, *H. castro* and *H. jabejabe*), breeding in the Atlantic Ocean and Mediterranean Sea, to test the contribution of host specificity and geography in shaping the diversity of this group. Thus, around 200 mites belonging to the three most important mite genera (*Microspalax*, *Zachvatkinia* and *Brephosceles*) were sequenced for the mitochondrial COI gene, and haplotype networks were generated using the PopART v 1.7 software. To examine the genetic structure of the feather mites, host and geographic

information was mapped onto the haplotype networks. On the three seabird hosts were found 13 feather mite species belonging to six genera (*Zachvatkinia*, *Rhinozachvatkinia*, *Microspalax*, *Brephosceles*, *Ingrassia* and *Opetiopoda*), of which four corresponded to new undescribed species. Although molecular data correlated well with morphological descriptions, some putative cryptic species were also identified. Most mite species typically exhibited strong host-associated genetic structure, whereas four mite species were shared by two hosts, *H. jabejabe* and *H. castro*. Our findings reveal the importance of host specificity in shaping the genetic structure and diversification of these ectosymbionts, and also a very weak spatial structure, almost all feather mite species sharing haplotypes among different geographical locations.



BIOGEOGRAPHY & BIODIVERSITY

PP-18

BIODIVERSITY OF SPIDER MITES IN THE PANNONIAN REGION OF SERBIA

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Biodiversity of spider mites (Acari: Tetranychidae) has been studied with emphasis on agricultural crops and ornamentals in managed habitats. On the other hand, native vegetation can act as a reservoir of species that may occur on cultivated plants. The Pannonian region of Serbia covers one third of its territory. It is predominantly a lowland region with mosaic habitat and vegetation structure. Although a large percentage of the region was turned into managed (agricultural) ecosystems, it also encompasses very diverse natural and semi-natural habitats. Sampling of spider mites in the Pannonian region was carried out over 11 growing seasons (2013-2023) on native and cultivated plants at 260 sampling locations. A total of 37 spider mite species were found on

118 plant species belonging to 33 families, among which 16 and 12 plant species from the families Asteraceae and Rosaceae had 7 and 18 mite species, respectively. The plants in natural and semi-natural habitats had 29 mite species (25 in woodland, 15 in grassland and 6 in heathland and scrub habitats), while 26 mite species were found on the plants in agricultural habitats (20 in gardens, 11 in orchards and 4 in greenhouses). A total of 18 species were found in both agricultural and natural habitats. The cosmopolitan species *Tetranychus urticae* was the most frequent, followed by *T. ludeni*, *T. turkestanii*, and *T. evansi* in agricultural habitats, and *Eotetranychus carpini* in natural and semi-natural habitats.



PP-19

MITE DIVERSITY (ACARI: PROSTIGMATA, ENDEOSTIGMATA) OF GLACIER-RELATED ECOSYSTEMS IN PYRENEES AND ALPS

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Introduction. Due to climate warming mountain glaciers are under threat of disappearing. While on one hand cold glacial microhabitats, e.g., ice surface, snow and cryoconite holes are vanishing along with shrinking glacier, on the other hand retreating ice exposes bare ground that can be colonized by small invertebrates. The aim of this study is to investigate the mite diversity in glacier-related microhabitats in Pyrenees and Alps, that changes due to glacier retreat.

Methods & results. The soil and vegetation from forefields of three glaciers in French Pyrenees and one in Italian Alps were sampled. The mites were extracted using Berlese-Tullgren funnels. Selected individuals were slide-mounted and observed under the microscope. One species new to science (Nanorchestidae) and three

species new to the fauna of France (Rhagidiidae, Tydeidae, Alicorhagiidae) were found in Pyrenees. The distribution of alicorhagiid species, up till now, was restricted to Arctic and sub-Arctic locations. At least two genera and three species (Eupodidae) recorded from Alps in this study are new to science.

Conclusions. While, among species recorded during present study, rhagidiid and tydeid are regarded cosmopolitan, the distribution of alicorhagiid seems to depend more upon microclimatic conditions (low temperatures) than climate zone (polar or subpolar). This record, along with the taxa new to science points at unexpected richness of glacier-related microhabitats and highlight their importance in shaping biodiversity of alpine regions.

The study was conducted within BiodivERsA+Call 2021 “Vanishing habitats: conservation priorities for glacier-related biodiversity threatened by climate change” financed by National Science Centre (No. UMO- 2022/04/Y/NZ8/00092).



PP-20

PLANT-INHABITING MITES FOUND ON COASTAL VEGETATION IN GREECE

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The Greek coastline is marked by diverse geomorphological features, ecosystems, and natural habitats. It includes coastal plains, river deltas, sand dunes, shingle beaches, coastal wetlands, lagoons, and salt marshes. Coastal vegetation is composed of plant species which are adapted to special conditions and severe stress (tides, wind, salinity). This study showcases some of the findings of the ongoing research whose aim is to explore the diversity of herbivorous and predatory mites found on coastal plants around the Attica region. A total of 94 plant samples collected from January 2023 till April 2024, from 6 different sites. These plants belong to 30 different families and 65 species. For the extraction of the mites Berlese-

Tullgren funnel was used. Permanent slide mounts were prepared, and all individuals were examined by using phase contrast microscope. The examination of the plant samples revealed 34 taxa belonging to two Orders (Mesostigmata and Trombidiformes) and 17 Families (Ameroseiidae, Ascidae, Laelapidae, Phytoseiidae, Anystidae, Bdellidae, Cheyletidae, Cunaxidae, Erythraeidae, Eupalopsellidae, Eupodidae, Iolinidae, Raphignathidae, Tenuipalpidae, Tetranychidae, Triophtydeidae and Tydeidae). Two species, *Hemicheyletia bakeri* (Ehara) and *Petrobia (Mesotetranychus) tunisiae* Manson, are new records for the Greek fauna.



PP-21

PRELIMINARY STUDY OF PREDATORY MITES FOUND ON URBAN VEGETATION IN ATHENS, GREECE

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The urban vegetation within and on the perimeter of cities, which is quite diverse accounting the plants species and the range of habitats, exhibit social, aesthetic and ecological value. The city of Athens has a variety of vegetation types in its parks, roads and sidewalks which is consisted of native Mediterranean species, which have been adapted to the conditions of the Mediterranean climate, and other non-native, which were introduced in the past and have now become part of the city vegetation. The following are part of the results of an ongoing study of mite fauna on urban vegetation in the city of Athens. A total of 170 plant samples collected from March 2022 till July 2023, from 10 different

sites. The plant samples concerned species of high vegetation such as *Pinus spp.*, *Cupressus sempervirens*, *Ceratonia siliqua*, *Platanus orientalis*, *Laurus noblilis*, *Citrus aurantium* and low vegetation plants as *Nerium oleander*, *Ligustrum japonicum*, *Viburnum tinus*, *Pittosporum tobira*, *Justicia adhatoda*, *Pyracanthus coccinea*, *Cistus spp.* and others. The mites were collected by direct examination of the samples under stereoscope. The results were 21 taxa belonging to the predatory families of Phytoseiidae, Stigmaeidae, Cunaxidae, Bdellidae, Anystidae, Cheyletidae and Iolinidae. *Euseius amissibilis* Meshkov is reported for the first time from Greece.



TAXONOMY, SYSTEMATIC & PHYLOGENY

PP-22

A COMPREHENSIVE APPROACH TO TAXONOMIC IDENTIFICATION: INTEGRATING MORPHOLOGICAL AND MOLECULAR TECHNIQUES FOR EUSEIUS SPECIES IN THE WESTERN PALEARCTIC

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¹This study was funded by Scientific Research Foundation of Cukurova University, Project Number: FYL-2023-15579, ²Cukurova University, Agricultural Faculty, Department of Plant Protection, Acarology Laboratory, Adana, Turkey

There are four *Euseius* species reported in the western Palearctic realm. Among these, *E. finlandicus* stands out as a cosmopolitan species, known in over 50 countries, while *E. scutalis* and *E. stipulatus* are predominantly found in the Mediterranean basin. However, uncertainties persist regarding whether all reported populations correctly represent related species. This uncertainty arises from the reliance on morphological identification alone, or only sporadic use of molecular techniques, and the absence of integration between the two methods, except in the case of *E. amissibilis*. To address these taxonomic uncertainties, we conducted an integrative taxonomy approach, combining both techniques mentioned earlier. Initially, we measured approximately 40 key characters, commonly utilized for species delimitation, from 10 specimens of each sex per species. Subsequently, molecular analyses were

performed, with DNA isolation from each species using a non-destructive extraction method, and an ITS gene marker. Our results demonstrated a perfect of similarity between the morphological characters observed and their descriptions. Furthermore, BLAST analyses also revealed similarities between our sequences and those deposited in the GenBank database. Notably, phylogenetic analyses highlighted distinctive features of *E. scutalis*, particularly its long-narrow calyx of the spermatheca and anteriorly wider dorsal shield, clearly separated it from the other species. In conclusion, the integration of morphological and molecular data from this study enhances our understanding the systematics of *Euseius*. Specifically, we propose that the shape of the dorsal shield and spermatheca could serve as basic characteristics for the classification of *Euseius* species.



PP-23

EXPLORING THE SIGNIFICANCE OF DORSAL SOLENOSTOMES, CHELICERA DENTITION AND SPERMATHECA MORPHOLOGY IN THE FAMILY PHYTOSEIIDAE: AN INTEGRATIVE TAXONOMY APPROACH

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The systematics of the family Phytoseiidae (Acari: Mesostigmata), an important group of predators for biological pest control, primarily relies on morphological observations, with limited integration of molecular techniques. Accurate phytoseiid identification is crucial in biological control programs because some morphologically similar species may exhibit significant differences in their feeding habits. Within this family, the species identification often depends on the observation of subtle morphological differences, such as the number of teeth on cheliceral digits, the presence of dorsal solenostomes, and the presence of a neck between the atrium and the calyx of the spermatheca. During our extensive surveys in the last decade, we discovered at least two otherwise identical species, except for the aforementioned morphological characters, in each of the genera *Kampimodromus* Nesbitt,

Neoseiulus Hughes, *Paraseiulus* Muma, and *Typhlodromus* Scheuten. Therefore, we conducted molecular analyses using two gene markers, the Internal Transcribed Spacer (ITS), and/or Cytochrome c oxidase I (COX1), to determine whether these subtle differences represent intra- or inter-specific variations. Despite having arguably negligible morphological differences, each of the morphologically similar species was distinct based on ITS and COX1 sequences, showing genetic distances of at least 3-5% and over 12%, respectively. In conclusion, these values are large enough to designate each species as two separate taxa. We demonstrated and validated the taxonomic utility of chelicera dentition, the number of dorsal solenostomes, and the spermathecal neck in the systematics of the family Phytoseiidae by using an integrative approach for the first time.



PP-24

FIRST OCCURRENCE OF A MORPHOSPECIES OF THE GENUS OPLITIS BERLESE (ACARI: OPLITIDAE) IN MANURE OF HYDROCHOERUS HYDROCHAERIS (LINNAEUS, 1766), IN SOUTHEASTERN BRAZIL.

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Uropodina is a common group found on litter and soil fauna in the tropics. The genus *Oplitis* was proposed by Berlese (1884) and revised more recently by Hirschmann (1991). It is one of the most diverse genera of Uropodina with about 150 described species (Babaeian et al. 2016). Different authors considered it a member of the families Uropodidae or Trachyuropodidae. In this study, we follow Lopes et al. (2015) and the genus was included on the Family Oplitidae. The mite was collected in 2016 and the describe was based on one mite female found in capybara manure and extracted in a Berlese-Tulgreen funnel and preserved in 70% alcohol. The sample collection in the Acarological collection in Parasitology Animal Laboratory of Biological Institute of São Paulo

was reviewed and the specimen was mounted on with Hoyer's medium. Thus, this work shows some information about the diversity of uropodid mites found in capybara manure from Brazil, and also this new record of mite specie found on sampling taken from the Campinas area. In the analysis of the keys for the family Oplitidae and genus *Oplitis*, they suggest that the morphospecies found would have some similarities with the species *Oplitis apicalis*, described in Brazil by Lopes et al. (2015). The diversity of Oplitidae and others uropodid mites in Brazil should be investigated in the soil, litter and manure. More studies about these mites are needed to clarify the distribution, the role of ecosystem balance of these mites and the



PP-25

FIRST REPORT OF *EUTETRANYCHUS AFRICANUS* (TETRANYCHIDAE) IN THE AMERICAS

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The spider mite *Eutetranychus africanus* (Tucker), first described in South Africa about a century ago, can damage agricultural and ornamental crops. It is widespread in Africa, Asia, and Oceania, affecting plants from 21 families (Migeon et al. 2024). Recently, it was also reported in Europe, specifically on Madeira Island, Portugal (Naves et al. 2024). In this study, surveys of phytophagous mites on fruit trees in Alagoas State, Northeastern Brazil, were conducted in October 2022. Spider mites from the genus *Eutetranychus* were collected on carambola (*Averrhoa carambola*, Oxalidaceae) in Arapiraca (97° 00' 19.20"S, -36° 68' 64.69"W). Significant leaf damage and high infestation levels were observed. It was initially assumed the mites were *Eutetranychus banksi*

(McGregor), the most common *Eutetranychus* species in Brazil and the Neotropical region. For identification confirmation, specimens were slide-mounted and examined under phase-contrast and DIC optical microscopes, using criteria from Kamran et al. (2018) and Naves et al. (2024). Unexpectedly, the specimens were identified as *E. africanus*. This is the first report of *E. africanus* in Brazil and the Americas, and also the first report of this mite on carambola and an Oxalidaceae host plant. The recent findings in the Americas and Europe suggest the species range is expanding. Considering the invasive pest status of *E. orientalis* (Klein) and *E. banksi* (McGregor) in Europe, this report highlights the potential phytosanitary risk *E. africanus* may pose.



PP-26

GENETIC DIVERSIFICATION OF ACERIA SPECIES INHABITING JUGLANS REGIA IN SERBIA

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Introduction

The Persian walnut (*Juglans regia* L., Juglandaceae), grows naturally in mesic, mixed, or deciduous forests across the Balkans, northern Turkey, southern Caspian region, Caucasus, and Central Asia (Zohary & Hopf, 2000). Various eriophyid mite species of the genus *Aceria* induce gall formations on different *Juglans* species, leading to significant economic losses (Khan & Kundoo, 2018). To date, *Aceria tristriata* (Nalepa) and *A. erinea* (Nalepa) are the exclusive species commonly observed on *J. regia* in Serbia (Petanović & Stanković, 1999). Recently, *A. brachytarsus* (Keifer), an invasive species from the USA, was identified on *J. regia* and *J. nigra* in Hungary (Ripka et al. 2018). This prompted a more comprehensive survey of *Aceria* spp. on walnut trees, and initial results are presented herein.

Methods and results

Mites were collected from leaf galls of *J. regia* in 8 locations in Serbia. The barcode region of mtCOI gene was amplified from individual mite specimens. Pairwise comparison of the COI distances showed presence of three species, with the ingroup genetic distance between 11.7% and 17.5% (uncorrected). BLAST analyses of two known species revealed a 100% identity with *A. erinea* and *A. tristriata*, while the third species remains unidentified, yet.

Conclusions

Molecular analyses based on mtCOI barcode region showed clear separation between three *Aceria* species on *J. regia*. Two of them, *A. erinea* and *A. tristriata* were already well-established in Serbia (Petanović & Stanković, 1999). However, the status of the third species remains unknown, and ongoing taxonomic characterization combining molecular and morphometric analyses is underway.



PP-27

IS ACULUS CORNUTUS (Banks) SEPARATE SPECIES, OR JUST SYNONYM OF A. FOCKEUI (Nal. & Trt.) – MORPHOMETRIC AND MOLECULAR APPROACH

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Introduction

Aculus fockeui (Nalepa & Trouessart, 1891) (Acari, Eriophyoidea) was described from European plum (*Prunus domestica*) and to date has been recorded on about 17 wild and cultivated *Prunus* spp. (Schlieske, 1977). *Aculus cornutus* (Banks, 1905) was described from peach (*Prunus persica*) in North America. It has been long disputed whether these species, which originate from different hosts, are conspecific or distinct ones, since it was difficult to find morphological differences between them. However, Oldfield (1984) experimentally established that *Aculus* sp. associated with plum and peach could interbreed, so *A. cornutus* was received the status of a synonym. The aim of this study is to verify the true status of *Aculus* sp. found on peaches using morphometric and molecular methods.

Methods and results

Populations of *Aculus* mites have been collected from plums and peaches. For morphometric

analysis, 23 morphological characters were measured on 30 protogynous females per sample. MANOVA and CVA were used to determine differences between populations at the morphological level. The barcode region of mtCOI gene was amplified by PCR. Results of morphometric analyses clearly separated plum and peach populations according to the first canonical axis (79.12%). Phylogenetic tree inferred by ML analyses of the mtCOI gene resulted in two clearly defined lineages of *Aculus* sp., corresponding to the *P. domestica* and *P. persica* populations.

Conclusions

Taxonomic characterization, combining molecular and morphometric analyses, showed clear separation between populations inhabiting plums and peaches, indicating that these are two cryptic species within *A. fockeui* complex of species.



PP-28

UNRAVELING PHENETIC AND PHYLOGENETIC RELATIONSHIPS AMONG CECIDOPHYES MITES (ACARI: ERIOPHYOIDEA)

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Introduction

The genus *Cecidophyes* is widespread and is considered one of the largest genera in the eriophyoid subfamily Cecidophyinae (Oldfield, 1996), encompassing 43 species (Amrine et al., 2003). However, this number is constantly changing as new species are described. In the last decade, numerous comprehensive studies have been conducted to understand the phylogeny and evolution of the Eriophyoidea. Despite this, research specifically addressing the taxonomy, phylogeny, and morphological variability of the *Cecidophyes* is scarce. Therefore, the aim of this study is to clarify the phylogenetic relationships among seven species (*C. galii*, *C. rouhollahi*, *C. glaber*, *C. gymnaspis*, *C. nudus*, *C. psilonotus*, and *C. lauri*) based on molecular data and to investigate their morphological variability and phenetic relationships using linear morphometrics.

Methods and results

Thirty-five morphological characters were measured for statistical analyses. The morphological variability and phenetic relationships among the studied species were analyzed using MANOVA, CVA, and UPGMA analyses. Phylogenetic relationships were investigated using the D1-D2 region of the 28S rDNA gene sequences. The ML phylogenetic tree revealed species separation into three groups, indicating that *Cecidophyes* is paraphyletic. The MANOVA showed statistically significant interspecific differences. Both the CVA and UPGMA analyses yielded identical results, notably the clear distinction of *C. psilonotus* and two clusters: one comprising *C. gymnaspis* and *C. lauri* and the other composed of the remaining four species.

Conclusions

Our findings highlight the complexity of *Cecidophyes* taxonomy and the need for further research in this area.



PP-29

THREE NEW FEATHER MITE SPECIES OF THE GENUS *PROTEROTHRIX* GAUD, 1968 (ANALGOIDEA: PROCTOPHYLLODIDAE: PTERODECTINAE) FROM BIRDS OF PARADISE (PASSERIFORMES: PARADISAEIDAE)

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Introduction

Feather mites (Astigmata: Anaigoidea and Pterolichoidea) are common and diverse ectosymbionts of birds that spend their entire lives on their hosts. Four bird of paradise specimens of Lesser Bird-of-paradise *Paradisaea minor* Shaw, 1809 and one of Crinkle-collared Manucode *Manucodia chalybata* (Pennant, 1781), which are deposited in Bird Collection of “Grigore Antipa” National Museum of Natural History (Bucharest, Romania), have been examined to collect feather mites. In this acarological material, three new species of feather mites belonging to the genus *Proterothrix* were identified and described. In the past, six proctophyllodid species belonging to the genus *Proterothrix* have been described on birds of paradise (Paradisaeidae) (Trouessart 1885, 1899).

Methods and results

Mite samples were collected by the scraping technique (Gaud & Atyeo 1996) and placed in 96% ethanol. Later, mite specimens were cleared in 90% lactic acid for 24 hours and mounted on microscope slides in Hoyer’s medium.

The newly discovered and described species of feather mites are: *Proterothrix* sp. n. A and *Proterothrix* sp. n. B from the host *Manucodia chalybatus*, and *Proterothrix* sp. n. C from *Paradisaea minor*.

Conclusions

The diversity of feather mite genus *Proterothrix* is unusually high on this hosts; on the 4 species of birds of paradise that have been investigated so far, 9 different species of mites have been identified (3 of them described in this paper). Two species of birds of paradise (*Manucodia chalybatus* and *Manucodia ater*) are known now to carry three different *Proterothrix* species.



PP-44

AN INSIGHT INTO HOST-PARASITE RELATIONSHIPS OF SYRINGOPHILID MITES ASSOCIATED WITH SUNBIRDS

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Quill mites of the Syringophilidae family (Acariformes: Prostigmata) are obligate parasites living in bird feather quills. This study focuses on those associated with Sunbirds (Passeriformes: Nectariniidae). Nectarinidae includes 154 species across 16 genera, and they are distributed from sub-Saharan Africa to northern Australia, with the highest diversity in equatorial regions.

Specimens from all previously described syringophilid species parasitising nectariniids were examined alongside new mite material collected from dry bird skins at the Bavarian State Collection of Zoology in Munich, Germany. We used parasite prevalence as a quantitative index and employed the 'bipartite' package in R to analyse the parasite-host ecological web.

Our findings reveal 12 syringophilid species spanning five genera and two subfamilies,

exclusively associating with Sunbirds as mono- or oligoparasites. The prevalence of infestation varied from 1.4% to 75%. The bipartite network between syringophilid mites and Sunbirds showed low connectance (Con = 0.10), indicating limited interactions among potential host-parasite pairings. Our results also demonstrated high specialisation (H2' index = 0.94), supported by significant divergence from null model expectations (mean H2' for null model = 0.060; $t = -360.2$, $p < 0.001$). The network's temperature of nestedness was 13.49, showing notable internal organisation, and the normalised specialisation level (d') ranged from 0.60 to 1, illustrating unique interactions within the network. Additionally, high modularity (likelihood = 0.80) was observed, identifying nine distinct modules within the network.

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BIOLOGICAL CONTROL & INTEGRATED PEST MANAGEMENT

PP-30

ACAROPATHOGENIC FUNGI AGAINST THE HAZELNUT BIG BUD MITE: PRELIMINARY LABORATORY TESTS

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Hazelnut is gaining higher economic importance in the Mediterranean basin and, particularly, in Turkey and Italy, where most of the world's hazelnut production is concentrated. *Phytoptus avellanae* is increasingly involved in severe infestations with disturbance in plant growth and reduction in nut yield. This work explores low-impact control strategies for hazelnut mites. Laboratory bioassays were conducted on mites using fungal-control products (or commercial mycopesticides) containing *Beauveria bassiana* and *Lecanicillium muscarium*.

Phytoptus avellanae infested buds during plant vegetative growth abnormally enlarged in winter. According to Kanagaratnam et al. (1981) protocol, mite infested big buds were cut into two halves and dipped in conidia suspension for 10 seconds. Products concentrations were obtained according to label notes. The buds

were dried on filter paper and incubated at controlled temperature and humidity. Bioassays were replicated and conducted in two different laboratories under same experimental conditions on 8-16 bud replicas for each commercial formulation and untreated (using sterilized water).

Acaropathogenicity on mites was assessed by quantifying live mites in buds at 7th incubation day.

No survival mites were observed on *B. bassiana* treated buds compared to control 38-50% survived mites. Some mites from inoculation experiments showed on microscope typical fungi infection hyphae and phialides by *B. bassiana*.

This first result gives insight into a sustainable eriophyoid control strategy for organic farming as well.

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PP-31

COMPETITIVE AND PREDACIOUS INTERACTIONS OF *AMBLYSEIUS SWIRSKII* ATHIAS-HENRIOT AND *IPHISEIUS DEGENERANS* (BERLESE) (MESOSTIGMATA: PHYTOSEIIDAE)

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Amblyseius swirskii Athias-Henriot and *Iphiseius degenerans* (Berlese) are two commercially available phytoseiid species. They are commonly used for the control of thrips and often in combination. We tested under experimental conditions ($25 \pm 1^\circ\text{C}$, $65 \pm 10\%$ relative humidity, and a photoperiod of 16:8 [L:D] h) the consumption of adult females (1 and 2 females) of each predatory species separately and in combination (1 female *A. swirskii* and 1 female *I. degenerans*) to increasing densities of *Thrips tabaci* Lindeman (Thysanoptera: Thripidae) larvae. We also tested the preference of the two

phytoseiids in attacking conspecific and heterospecific larvae (ratio 1:1) in the absence of prey. *I. degenerans* females consumed significant lower number of thrips larvae than *A. swirskii*. The consumption of the 2 females of *A. swirskii* did not differ from that of the combination of two phytoseiid species. *I. degenerans* showed no preference in attacking conspecific or heterospecific larvae, while *A. swirskii* preferred attacking larvae of *I. degenerans*. The results indicate that *A. swirskii* is more efficient predator of *T. tabaci* and more competitive than *I. degenerans*.



PP-32

EFFECT OF RELEASING THE PREDATORY MITES *AMBLYDROMALUS LIMONICUS* AND *TYPHLODROMUS TRANSVAALENSIS* ON PHYTOPHAGOUS AND PREDATORY MITES IN A CITRUS ORCHARD IN SÃO PAULO

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Euseius concordis (Chant), *Euseius citrifolius* (Denmark and Muma) and *Iphiseiodes zuluagai* Denmark &

Muma are the species of predatory mites of Phytoseiidae family most abundant in Brazilian citrus orchards. Among the phytophagous mites, the most abundant are those from the families Tetranychidae (e.g. *Panonychus citri* (McGregor), *Tetranychus* spp.), Eriophyidae (e.g. *Phyllocoptruta oleivora* (Ashmead)) and Tenuipalpidae (e.g. *Brevipalpus* spp.). The objective of the present study was to evaluate the impact of the release of the predatory mites *Amblydromalus limonicus* (Garman & McGregor) and *Typhlodromus transvaalensis* (Nesbitt) (Acari: Phytoseiidae) on the diversity and abundance of phytophagous and predatory mites in organic citrus (Tahiti lime) orchard in the municipality of Mogi Mirim, state of São

Paulo, Brazil. The experiment was conducted from February to November 2023. Monthly releases of approximately 500 predatory mites per plant were carried out, for each species and release date. Initial results indicated influence of the two predator species on the population reduction of *P. oleivora* and *Brevipalpus* spp. In the case of predatory mites, a population reduction of *E. concordis* was observed, however, with an increase in the abundance of *I. zuluagai*. The largest populations of *I. zuluagai* were detected in leaf samples with low population densities of *E. concordis*. An increase in the number of *A. limonicus* mites found on citrus plants was observed throughout the release period, indicating the potential use of this predator to control arthropod pests in citrus orchards in São Paulo.



PP-33

EFFECTS OF DIFFERENT TOMATO GENOTYPES ON SPIDER MITES AND PHYTOSEIID PREDATOR PERFORMANCE

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Tomato crops are a vital component of global agriculture. However, they are susceptible to various pests, which can cause significant yield losses. Among these pests, the two-spotted spider mite *Tetranychus urticae*, can inflict severe damage on tomato plants. Given the impact of mite infestations on crop production, identifying, and utilizing resistant tomato cultivars is an important strategy in integrated pest management.

The present study aims to evaluate a series of non-commercial tomato accessions from the national genebank for their resistance to *T.urticae*. We assessed the effect of the tomato genotypes on the development and dispersal of the mites. To determine the effect of these genotypes on mite biology, life table parameters of *T.urticae* were assessed on tomato leaflets in Petri dishes. Also, we recorded all

developmental stages of the mites on four-weeks whole plants after the initial infestation with young adult spider mite females. Moreover, the number of glandular and no glandular trichomes on the plant stems were counted for each tomato genotype.

Results show that the tomato genotypes significantly impact the development and dispersal of *T. urticae*. Significant differences on the numbers of mites were observed suggesting that certain tomato genotypes can be resistant to the establishment of mites. Moreover, the fitness of biological control agents, such as the phytoseiid *Typhlodromus reckii* across tomato genotypes is also examined. Implementing pest-resistant cultivars and biological control agents will improve IPM strategies for tomato crop, leading to sustainable crop production.

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PP-34

EVALUATION OF *MENTHA PULEGIUM* AND *OCIMUM BASILICUM* ESSENTIAL OILS AGAINST *TETRANYCHUS URTICAE*

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Introduction and the aim of the study

The aim of our study was to evaluate the toxic and repellent effects of pennyroyal (*Mentha pulegium* L.) and basil (*Ocimum basilicum* L.) essential oil (EO) as well as their encapsulation products in β -cyclodextrin (β -CD) nanosystem carrier against *Tetranychus urticae* in dishes and tomato plants. The main components of the pennyroyal EO were pulegone (66.5%), isomenthone (22.6%) and limonene (3.8%), in case of the basil EO were linalool (49.8%), eucalyptol (14.6%) and estragole (11.2%).

Methods and results

Tetranychus urticae nymphs and adults were sprayed by the EO emulsions or the encapsulated EOs and placed on a similarly treated bean leaf in a dish. Repellency was investigated through the leaf-dipping method. Mortality rate was further searched in larger

scale (tomato plants) by spraying. Phytotoxicity tests were conducted in separated experiments. In Petri dishes, encapsulation of *M. pulegium* EO and *O. basilicum* EO in β -CD significantly increased nymphal (88% and 76% vs 58% and 46%) and adult mortality (84% and 86% vs 66% and 65%, respectively). Encapsulated EOs on plants showed reduced adult mortality in comparison to dishes which was almost 2-fold higher (51% and 50%) than free EOs (25% and 31%, respectively). In both EOs, mortality was recorded for a longer period in comparison to that of the free emulsions (up to 5d vs 3d). No phytotoxicity was recorded.

Conclusions

Encapsulation in β -CD improved and extended efficacy of the tested EOs and for this reason their evaluation under field conditions should be performed.



PP-35

NATURAL BIOLOGICAL CONTROL OF *TETRANYCHUS URTICAE* KOCH (ACARIFORMES, TETRANYCHIDAE) ON ORGANIC STRAWBERRIES IN GREENHOUSE

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A case of biological control of *Tetranychus urticae* Koch by the native *Phytoseiulus persimilis* Athias-Henriot and the alien *Neoseiulus idaeus* Denmark & Muma naturally occurred, has been observed in organic strawberries in greenhouse in Sicily during the winter period (December-January). The initial strong infestation of *T. urticae* (79% of sampled leaves), was reduced to 3% of infested leaves after 4 weeks. During this period, phytoseiids were constantly present on 75.1% of infested leaves (66.7 - 88.9%), but also on 16.4% (4.1 –

28.6%) of the uninfested ones. *P. persimilis* occupied the 49.2% (27.8-66.7%) of infested leaves whereas *N. idaeus* the 57.4% (37.4-66.7%) of them; on 31.5% (13.9-44.4%) of infested leaves both phytoseiids have been recorded.

These data showed that the con-presence of the highly specific on *T. urticae*, *P. persimilis* with the selective on tetranychids *N. idaeus* did not hamper the predation activity of both species resulting in an effective control of *T. urticae* within a short time period.



PP-36

MANAGEMENT OF *TETRANYCHUS URTICAE* KOCK (ACARI: TETRANYCHIDAE) IN COMMERCIAL HOP CULTIVATION: THE PREDATORY MITE *PHYTOSEIULIS MACROPILIS* (ACARI: PHYTOSEIIDAE) X ORGANIC SILICON ADJUVANT PRODUCT (96%)

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Hops, *Humulus lupulus* (Rosales: Cannabaceae), contain secondary metabolites, flavonoids, oils and polyphenols, a key part in building the characteristic aspects of beer. Severe attacks by *T. urticae* damage the quality of the cones, where lupulin is present, in addition to other compounds of great importance. The culture has been gaining prominence in Brazil's industrial and economic sectors, with the support of the national beer industry. The objective of this research was to evaluate the efficiency of the predatory mite *P. macropilis* and the adjuvant product Organic Silicon (96%), non-selective, in controlling *T. urticae* in hop crops. The experiments were carried out in a greenhouse (Figure 1), at the headquarters of the company Van de Bergen (Campinas, SP, Brazil). Hop

seedlings with the same number of leaves were used, with the same number of adult females of *T. urticae* on each leaf. The treatments were: T1) release of adult females of *P. macropilis*; T2) periodic applications of the adjuvant; 3) control. The average number of live pest mites decreased over time for the T1 treatment. T2 caused high mortality on the day of application. In the control treatment, there was a rapid increase in the pest population (Graph 1). By analyzing the results, it was found that the adjuvant product, in addition to being a non-selective product, only provides an immediate effect, as it has no residual effect. On the other hand, predatory mites can establish themselves in the crop and promote better control in the long term.



PP-37

IN VITRO EVALUATION OF THE PATHOGENIC ACTION OF THE ASSOCIATION OF TWO ISOLATES *STEINERNEMA RARUM* (PAM 25) AND *HETERORHABDITIS BACTERIOPHORA* (HB EN01) ON THE *RHIPICEPHALUS (BOOPHILUS) MICROPLUS* TICK

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Bovine livestock plays a crucial role in Brazil's economic growth but faces significant challenges due to the Rhipicephalus (*Boophilus*) microplus tick, an ectoparasite causing annual losses estimated at US\$ 3.24 billion. Conventional control with acaricides has led to resistance development, driving the search for alternative methods such as fungi, bacteria, and nematodes. This study evaluated the pathogenic action in vitro of the association of two isolates, *Steinernema rarum* (PAM 25) and *Heterorhabditis bacteriophora* (HB EN01), on female *R. microplus* ticks. Each experimental unit consisted of a Petri dish, with fifteen previously weighed females placed on a piece of

filter paper covering the dish's internal surface. In each dish, 1 ml of nematode suspension was applied at concentrations of 100, 200, and 300 JIs/female, with 10 repetitions for each concentration and for the control group, to which 1 ml of distilled water was added to each experimental unit. Efficacy results of the nematode association were calculated using female weight, egg weight, and larval hatching data. The mean efficacy percentages at the respective concentrations (100, 200, and 300) were 51.1%, 69.3%, and 73.6%. These results indicate the potential use of entomopathogenic nematodes in controlling *R. microplus* ticks.



PP-38

TRANSCRIPTOMIC RESPONSE OF THE PREDATORY MITE *AMBLYSEIUS ANDERSONI* CHANT (ACARI: PHYTOSEIIDAE) TO THE SECONDARY METABOLITES OF THE TOMATO TRICHOMES.

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Phytoseiidae, are key agents in augmentative biological control of pests on various vegetable crops. However, on tomato crops, phytoseiid mites are ineffective at controlling pests, because of the detrimental effect of the glandular trichomes. Glandular trichomes produce a variety of secondary metabolites with antibiotic and antixenotic effects that act against arthropods.

Searching for tomato-adapted predatory mites, phytoseiids were collected from tomato crops in Greece and *Amblyseius andersoni* Chant (Acari: Phytoseiidae) was identified. The toxicity of the trichome secondary metabolites was assessed on the tomato population of *A. andersoni*. Solutions of tomato trichome metabolites were tested for their effect on adult mite survival. Moreover, in order to explore the gene response of *A. andersoni* to the secondary metabolites of

the tomato trichomes, an RNA-seq approach was employed. The total RNA of mites exposed to trichome metabolites was isolated and sequenced, and the genes differentially expressed after exposure to these metabolites were identified. Also, mites were reared for multiple generations on tomato plants and their gene expression was compared to the initial population. Four biological replicates per condition were sequenced by Illumina platform, generating 480 million paired-end 150bp reads. Our results indicate that the tomato trichome metabolites have a lethal effect on these predatory mites, which cannot be overcome by their transcriptomic responses. The genes potentially involved in the response to the phytotoxins indicate whether the predatory mites have evolved or not mechanisms to overcome the tomato trichome defenses.

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PP-39

SPONTANEOUS VEGETATION AS A STRATEGY FOR THE CONSERVATION OF PREDATORY MITES IN APPLE ORCHARDS

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This study aims to recognize the acarofauna present in the spontaneous vegetation associated with apple orchards, defining the plant species with the greatest potential as a reservoir of predatory mites of economic importance. The studies were carried out in the 2020-21, in three organic orchards (Eva, Fuji and Gala), in Antônio Prado, two conventional (Fuji and Gala), in Muitos Capões, state of Rio Grande do Sul and two of regenerative agriculture (Fuji and Gala), in São Joaquim, state of Santa Catarina. Monthly collections were made of the five spontaneous plants present in the greatest quantity in the sampled apple orchards. The collected plant material was transported to the laboratory where were identified and sorted. Sixty-seven species/morphospecies belonging to 26 botanical families associated with apple

orchards did sample, with plants from eight plant families hosting mites. The botanical families that presented the greatest abundance were Asteraceae (33%), followed by Plantaginaceae (33%), Poaceae (19%) and the other families (15%). *Plantago australis* Lam. (Plantaginaceae) showed greater mite abundance (32.7%), with 41.7% being predators. The second plant was *Vernonanthura tweediana* (Baker) H. Rob. (Asteraceae) (16.9%), with 51.9% predators. The greatest richness was found associated with the spontaneous vegetation of organic orchards, with greater diversity presented by phytoseiid mites. *Plantago australis* and *V. tweediana* prove to be the most suitable plant species for maintaining native natural enemies in apple orchards.



CHEMICAL CONTROL, RESISTANCE AND TOXICOLOGY

PP-40

EVALUATION OF TOXICITY OF *ACMELLA OLERACEA* EXTRACT AGAINST *TETRANYCHUS URTICAE* IN LABORATORY TESTS

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Tetranychus urticae Koch is a polyphagous pest causing serious damage to crops. The uncontrolled use of synthetic acaricides have caused the development of resistant strains of the tetranychid making its control tricky. Research on botanical pesticides showed that these products could be valid alternatives to synthetic ones in IPM programs. Herein, the toxicity of *Acmella oleracea* (L) R.K. Jansen (Asteraceae) extract was assessed on *T. urticae* in laboratory tests.

Acmella extract was prepared by Soxhlet extraction using n-hexane as solvent and it was characterized by N-alkylamides, being spilanthol the major constituent, as determined by HPLC-DAD-MS analysis. The extract was tested on young adult females of *T. urticae* at concentrations of 312.5, 625, 1250, 2500, and 5000 $\mu\text{L/L}$. The extract showed high toxicity on

T. urticae females at all concentrations. All females died within 4 days after the treatment with the two highest concentrations, whereas 22 and 20% of females remained alive at the end of the tests (8th day) with the two lowest concentrations. It is noteworthy that, in tests with the two lowest concentrations (312.5 and 625 $\mu\text{L/L}$), alive females oviposited at low levels within the first 4 days. Afterwards, their oviposition did not differ from that registered in the control.

Acmella extract showed high toxicity against *T. urticae* females and a considerable rapidity of action at the highest concentrations. The short persistence of the extract on treated leaves should be considered an advantage within IPM strategy because of the short-time effects on natural enemies.



PP-41

INSECTICIDE RESISTANCE STATUS AND TARGET SITE RESISTANCE MONITORING OF CITRUS RED MITE *PANONYCHUS CITRI* (ACARI: TETRANYCHIDAE) FROM GREECE

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The citrus red mite *Panonychus citri* (McGregor) (Acari: Tetranychidae) is a major mite pest in citrus groves. It is distributed worldwide and attacks deciduous fruit trees and ornamental trees as well as citrus trees. The species due to its short life cycle, and high reproductive capacity combined with repeated acaricide applications, has acquired resistance to most pesticides

The aim of the study was the evaluation of toxicity status and the presence and frequency of insecticide target site resistance mutations in Greek populations of citrus red mite from different localities of the country.

Resistance status of Greek populations was assessed via toxicity single dose bioassays at the recommended field rate of five registered pesticides (abamectin, cyflumetofen, fenpyroximate, acequinocyl and hexythiazox) belonging to five different modes of actions, frequently applied for pest control. A suite of six

ddPCR assays was developed to assay validated target site resistance mutations in pooled samples with high sensitivity (limit of detection for mutant allele frequency: 0.2%) [mutations: H110R in PSST subunit associated with resistance to mitochondrial electron transport inhibitors F1538I in voltage gated sodium channel (VGSC), associated with resistance to pyrethroids, I1017F in chitin synthase 1 (CHS1), associated with resistance to mite growth inhibitors, G126S/A133T in cytochrome b (cytb), associated with mitochondrial electron transport inhibitors, T752C in β -2R adrenergic-like octopamine receptor (β -2R OctR)], associated with amitraz resistance.

The molecular and phenotypic resistance screening may provide useful knowledge and could prove a valuable tool for pesticide resistance management of this important mite species.

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PP-42

THE EFFECTS OF MICROEMULSION FORMULATIONS OF SOME BOTANICAL ACARICIDES ON LIFE TABLE PARAMETERS OF *AMBLYSEIUS SWIRSKII*

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The microemulsion formulations of terpenoids, orange and neem oils produced by Nanomik company result in high mortality and deter egg laying in *Tetranychus urticae* (Koch) (Acari: Tetranychidae). This innovative formulation enhances botanical acaricide persistence. Despite biological control agents show promise for *T. urticae* control in IPM, the compatibility of these acaricides with the effective predatory mite *Amblyseius swirskii* Athias-Henriot (Acari: Phytoseiidae) remains unstudied. To examine the relative fitness of these formulations on *A. swirskii*, its life table parameters were observed under controlled conditions. Biological properties were observed 7 days post-application of effective doses of the botanical and the synthetic acaricides (milbemectin) on eggplant leaves. After seven days waiting

period, the development duration was not affected by both botanical and synthetic acaricides compared with control. The mean fecundity, oviposition duration and longevity of *A. swirskii* females treated with botanical acaricides were not affected compared the control. Nevertheless, milbemectin treatment reduced these parameters. The intrinsic rate of increase ($r_m=0.172$; 0.158 ; 0.146 d⁻¹), the net reproductive rate ($R_0=10.04$; 8.58 ; 8.45 offspring), the mean generation time ($T=13.44$; 13.62 ; 14.65 d) and the finite rate of increase ($\lambda=1.19$; 1.17 ; 1.16 d⁻¹) of *A. swirskii* females treated with orange and neem oils and terpenoid blend, respectively, were found similar with those of control ($r_m=0.150$ d⁻¹; $R_0=8.67$ offspring; $T=14.36$ d; $\lambda=1.16$ d⁻¹).

The study suggested that the botanical acaricides can be combined with realising *A. swirskii* after 7 days waiting. The research as PhD thesis of the first author was funded by TAGEM under grant number 5807.



PP-43

MOLECULAR DIAGNOSTICS FOR RATIONAL USE OF ACARICIDES AND RESISTANCE MANAGEMENT OF AGRICULTURAL PESTS

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Acaricide resistant agricultural pests become increasingly difficult to control, among others due to the dramatic reduction in the availability of active ingredients. It is crucial to make rational decisions on acaricide use to ensure effective and sustainable pest control. However, resistance monitoring programs that inform on pest susceptibility and resistance are not yet common practice in agriculture. Several molecular diagnostic platforms have been developed for the detection of genetic traits and biomarkers, at very low cost. However, several factors determine the strength of a biomarker, while the significance and the interpretation of molecular diagnostic applications are critical for insecticide

resistance management. Functional approaches for elucidating pesticide resistance mechanisms at the molecular level, including in vivo validation of the role of genetic traits when present alone or in combination in a pest using CRISPR/Cas9 methods, not only improve our understanding for the genetic basis of resistance, but also determine the diagnostic value of the genetic biomarkers in field populations. This research provides new opportunities for decision making in an operational meaningful way, for evidence base rational use of pesticides, within the frame of the EU Green Deal and integrated pest management strategies.

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Keywords: pesticide, acaricide resistance, molecular diagnostics, IPM