54. Jahrestagung

54th Annual Meeting

27nd–28th November 2025

Aula der Med Uni Graz

Neue Stiftingtalstraße 6, 8010 Graz

www.oegtpm.at

Vorwort

Liebe Kolleginnen und Kollegen,

sehr geehrte Damen und Herren,

nach der eindrucksvollen 53. Jahrestagung im historischen Ambiente des Josephinums in Wien freut es uns in besonderer Weise, Sie in diesem Jahr wieder einmal in Graz begrüßen zu dürfen. Die 54. Jahrestagung der Österreichischen Gesellschaft für Tropenmedizin, Parasitologie und Tropenmedizin findet heuer in der Aula des neu errichteten Campus der Medizinischen Universität Graz statt – einem Ort, der für modernen Wissensaustausch, interdisziplinäre Zusammenarbeit und zukunftsweisende Forschung steht.

Die Themen unseres Faches – von der globalen Gesundheit über vektorübertragene Erkrankungen bis hin zu innovativen diagnostischen und therapeutischen Ansätzen – gewinnen in einer zunehmend vernetzten Welt weiter an Bedeutung. Klimawandel, Migration, Mobilität und geopolitische Veränderungen verdeutlichen, wie eng menschliche, tierische und ökologische Gesundheit miteinander verflochten sind. Genau hier setzt das One-Health-Konzept an, das als integrativer Ansatz längst zu einem unverzichtbaren Fundament der Tropenmedizin und Parasitologie geworden ist. Unsere Jahrestagung möchte diesen Gedanken bewusst stärken und Räume schaffen, in denen Expertinnen und Experten unterschiedlicher Disziplinen voneinander lernen und gemeinsame Lösungen entwickeln können.

Die moderne Aula am neuen Campus bietet dafür einen inspirierenden Rahmen: einen Ort, an dem wissenschaftlicher Diskurs, kritische Reflexion und persönlicher Austausch zusammenfinden.

Möge diese Tagung dazu beitragen, neue Kooperationen zu knüpfen, bestehende Netzwerke zu vertiefen und innovative Ideen zu fördern, die den One-Health-Gedanken mit Leben erfüllen. Ich wünsche Ihnen eine bereichernde, lebendige und spannende Tagung sowie viele interessante Begegnungen hier in Graz.

Mit herzlichen Grüßen

Dr. Bernhard Haas, MBA, Präsident der ÖGTPM

Priv.-Doz. Mag. Dr. Hans-Peter Fuehrer, Kongresspräsident

Wir danken unseren Sponsoren

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IDEXX

WISSENSCHAFTLICHES PROGRAMM/*SCIENTIFIC PROGRAM*

Thursday, 27 November 2025

11:00–12:00, Registrierung/*Registration*

12:00–12:15, Welcome and Introduction – Chair: Bernhard Haas and Hans-Peter Fuehrer
12:15–13:15, Dominique Moy-Wagner (Plenar) – Aktuelle Trends in der Reisemedizin
13:15–14:00, Kaffeepause/*Coffee break*

14:00–16:00, Session 1: Klinische Tropenmedizin/*Clinical Tropical Medicine* – Chair: Mirjam Groger and Bernhard Haas
14:00–14:30, Astrid Erber – TBD
14:30–14:50, Mirjam Groger – Clinical development of therapeutics against Lassa fever
***14:50–15:05, Furqan Munir –** *Coxiella burnetii* in Pakistan: A Meta-analysis
15:05–15:20, Pia Michelitsch – Activity of antifilarial drugs on microfilaremia in the treatment of loiasis: a systematic review
15:20–15:35, David Leitsch – The increasingly pressing issue of metronidazole resistance in *Giardia lamblia* and a possible causative mechanism
15:35–15:50, Hans-Peter Fuehrer – *Plasmodium ovale* spp. – Establishing clarity in naming these parasites

15:50–16:45, Kaffeepause/*Coffee break*

16:45–18:00, Session 2: Parasitologie (I)/*Parasitology (I)* – Chair: Julia Walochnik and Maria Unterköfler

16:45–17:00, Katharina Kranner – Efficacy of octenidine-containing mouthrinses on *Entamoeba* spp. in vitro and in the oral cavity
17:00–17:15, Ivana Jankovic – Molecular characterization of *Acanthamoeba* extracellular vesicle proteases and their involvement in the cytopathogenicity
17:15–17:30, Clarissa dos Santos Veloso – A mixed method design for investigating schistosomiasis in Alagoas (Brazil)
17:30–17:45, Oleg V. Shcherbakov – Parasite Fauna of Wild Carnivores as Baseline Data for Future Zoonotic Risk Assessment
17:45–18:00, Aurelia Keferstein – Antioxidant enzymes and their impact on Metronidazole and oxygen susceptibility in *Giardia lamblia*

Ab 18:00, gemütliches Get-together mit Fingerfood und Getränkeauswahl/*get together with finger food and drinks*

Friday, 28 November 2025

08:30–09:00, Registrierung/*Registration*

09:00–10:30, Session 3: Tropenmedizin/*Tropical Medicine*, Parasitologie (II)/*Parasitology (II)* – Chair: Angelika Wagner and Astrid Erber

09:00–09:25, Peter Starzengruber – Schnelldiagnostik tropischer Fiebererkrankungen bei Reiserückkehrern: Möglichkeiten moderner Multiplex–PCR

09:25–09:45, Angelika Wagner – Malariaprophylaxe in der Praxis – basierend auf einer gemeinsamen europäischen Initiative zur Harmonisierung der Empfehlungen.

09:45–10:00, Julia Walochnik – Comparative study on vector-borne blood parasites in Burkina Faso

10:00–10:15, Iuliia Nosulia – PCR detection of gastrointestinal parasites in golden jackals (*Canis aureus*) from Armenia: first molecular insights and surveillance perspectives

10:15–10:30, Aline Lamien Meda – Revealing global diversity through targeted long-read mitogenomics of *Dirofilaria* species

10:30-11:00, Kaffeepause/*Coffee break*

11:00 – 12:00, Session 4: Parasitologie (III)/*Parasitology (III)*, Prevention – Chair: Aline Lamien Meda and Martina Köhsler

11:00–11:15, Martina Köhsler – Delusional Parasitosis – Between Psychopathology and Exploitation

***11:15–11:30, Severin Schuler –** Assessment of fasciolicide efficacy using the faecal egg count reduction test in cattle herds in Tyrol, Austria

11:30–11:45, Maria Unterköfler – Phylogeny of the subgenus *Phortica* sensu stricto (Diptera: Drosophilidae) from Europe

***11:45–12:00, Furqan Munir –** A comparative in vitro anthelmintic screening of medicinal plants using dual nematode model (*Caenorhabditis elegans* and *Oscheius tipulae*)

12:00–13:00, Generalversammlung der ÖGTPM/*General assembly*
*Junior Award Candidate
13:00–14:00, Mittagspause/*Lunch break*

14:00–15:45, Session 5: Parasitologie (IV)/*Parasitology (IV)*, One Health (I), Vektor-Biologie (I)/*Vector Biology(I)* – Chair: Hans-Peter Fuehrer and Edwin Kniha
***14:00–14:15, Zoe Lindhorst –** Molecular analysis of vector-borne pathogens in red foxes (*Vulpes vulpes*) from Saxony-Anhalt (Germany)
***14:15–14:30, David Sainitzer –** Molecular Detection of Vector-Borne Pathogens in Ticks collected from Companion Animals in the Republic of Kosovo
***14:30–14:45, Seda Adamyan –** Multi-host PCR detection of *Dirofilaria* and *Leishmania* in Armenian mammals
***14:45–15:00, Katharina Platzgummer –** Phlebovirus seroprevalence in domestic dogs from Austria and Germany
***15:00–15:15, Tanto Situmorang –** Surveillance of mosquito fauna and associated pathogens in the Vienna Zoo, Austria
***15:15–15:30, Mirza Nuryady –** Phylogeography and Haplotype Characterization of *Aedes japonicus* in Austria
***15:30–15:45, Julia Reichl –** Challenges and limitations of mosquito microbiome analysis – a first insight into the microbiome of Austrian mosquitoes

15:45–16:30, Kaffeepause/*Coffee break* – Abgabe Voting Junior Awards/*junior award voting*

16:30–17:15, Session 6: One Health (II), Vektor-Biologie (II)/*Vector Biology (II)* – Chair: David Leitsch
16:30–17:00, Edwin Kniha – The One Health approach – sand fly-borne diseases as a prime example
17:00–17:15, Anna-Margarita Schötta – Austrian ticks under surveillance: current landscape of ticks and tick-borne pathogens in 2025

17:15–18:00, Preisverleihung Junior-Award und Abschluss der Tagung/*Junior award ceremony and conference closing*

*Junior Award Candidate

ABSTRACT BOOK

Plenar –Aktuelle Trends in der Reisemedizin

Dominique Moy-Wagner[1,*]

Session 1: Klinische Tropenmedizin/Clinical Tropical Medicine

Session 1-1 – TBD

Astrid Erber[1,*]

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Session 1-2 – Clinical development of therapeutics against Lassa fever

Miriam Groger[1,*]

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Lassa fever, a viral haemorrhagic disease endemic to West Africa, remains a significant public health threat due to high morbidity, mortality, and the absence of approved therapeutics or vaccines. This talk will provide an overview of the current landscape and recent advances in the clinical development of therapeutics for Lassa fever.

Despite ribavirin being the standard of care for decades, its efficacy is supported by limited and methodologically flawed evidence, prompting urgent calls for reassessment and the development of novel therapeutics. Recent systematic reviews and meta-analyses have highlighted the need for robust clinical trials and harmonized research methodologies to generate reliable evidence for both existing and new treatments. Several clinical trials recently been implemented to efficiently evaluate multiple therapeutic candidates which have shown promise in preclinical and early clinical studies.

The clinical development of Lassa fever therapeutics is driven by collaborative, regionally focused research and the advancement of new candidates into clinical trials. Continued investment in research capacity and harmonized trial frameworks will be essential to deliver effective, evidence-based treatments for Lassa fever.

Session 1-3 – *Coxiella burnetii* in Pakistan: A Meta-analysis

Furqan Munir[1,2], Amna Shakoor[3], Hans-Peter Fuehrer[2], Muhammad Danial Wazir[4], Farakh Munir[5], Zia ud Din Sindhu[1,*]

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Coxiella burnetii is a Gram-negative, intracellular, aerobic bacterium belonging to the family Coxiellaceae. It is the causative agent of Q fever in humans and coxiellosis in animals. It has been detected in various species such as rodents, birds, wildlife animals, and livestock, but the main reservoir hosts are sheep, goats, and cattle [1,2]. The pathogen is prevalent worldwide and exhibit environmental stability and a low infectious dose, therefore, occurring as an emerging pathogen. As ruminants are the main reservoirs, therefore, most human outbreaks occur because of their association with these animals [3,4].

The objective of this meta-analysis was to summarize findings from studies about *C. burnetii* in Pakistan (conducted from 1947 to 2023). The collection and evaluation of scientific literature published on *C. burnetii* in Pakistan was done in accordance with PRISMA criteria. Three internet databases - Google Scholar, PubMed, and Science Direct - were used to find published research articles.

The results showed 19 eligible studies involving small ruminants, large ruminants, camels, soil, ticks, and women from three provinces of Pakistan. The occurrence of infection was high in camels (31.3%) based on one study only, which limits its reliability, medium in goats and sheep (20.39% and 20.01% respectively), and low in women (8.41%). The maximum number of studies was conducted in Punjab (89.47%).

Because *C. burnetii* is a significant zoonotic pathogen of "One Health" importance, the current study found that published information is scarce on the prevalence and distribution of *C. burnetii* in animals, humans (including men, women, and children), and the environment in Pakistan. The high heterogeneity was also observed in the estimated pooled prevalence. Future research might be focused on addressing these limitations and filling the gaps between the veterinary and human health systems. Improving diagnostics, standardizing reporting, and conducting large-scale studies are essential for estimating the real impact of Q fever and coxiellosis on public health and animals in Pakistan.

References

1. Pexara A, Solomakos N, Govaris A. Q fever and seroprevalence of *Coxiella burnetii* in domestic ruminants. Vet Ital. 2018 Dec 31;54(4):265-279.
2. Pouquet M, Bareille N, Guatteo R, Moret L, Beaudeau F. *Coxiella burnetii* infection in humans: to what extent do cattle in infected areas free from small ruminants play a role? Epidemiol Infect. 2020 Aug 26;148:e232.
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Session 1-4 – Activity of antifilarial drugs on microfilaremia in the treatment of loiasis: a systematic review

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Loiasis, caused by the nematode/filaria *Loa loa* [1, 2], presents a major health burden in Central and West Africa. Despite the growing recognition of loiasis' medical significance, current antifilarial drugs remain inadequate in terms of efficacy and safety, particularly for individuals with hypermicrofilaremia. This systematic review aims to evaluate the efficacy of antifilarial treatment regimens for reducing *L. loa* microfilaremia and provide guidance on treatment strategies.

A systematic review was conducted to evaluate the efficacy of antifilarial treatment regimens on reducing *L. loa* microfilaremia. Data on the percent reduction of microfilaremia from baseline to nadir were extracted for each treatment regimen.

A total of 27 studies were included in the review, with treatment regimens involving albendazole (ALB), mebendazole (MBZ), ivermectin (IVM), diethylcarbamazine (DEC), levamisole, imatinib, and moxidectin, among others. ALB and MBZ showed dose- and duration-dependent efficacy, with extended treatment leading to up to a 98-100% microfilaremia reduction. IVM showed a dose-dependent effect, with single doses of 200-400 µg/kg reducing microfilaremia by 88-92%. DEC exhibited high efficacy, achieving up to a 100% microfilaremia reduction.

Antifilarial drug efficacy against *L. loa* microfilaremia varies by dosage and treatment duration, with IVM and DEC demonstrating rapid, high efficacy but presenting safety concerns for hypermicrofilaremic individuals. ALB and MBZ show efficacy with extended treatment but are slower acting. Further research is needed to optimize treatment regimens and assess clinical outcomes beyond microfilaremia reduction.

References

1. CDC. About Loiasis. Filarial Worms. https://www.cdc.gov/filarial-worms/about/loiasis.html#:~:text=to%20treat%20loiasis. Accessed 20 Mar. 2025.
2. Boussinesq M. Loiasis. Ann Trop Med Parasitol. 2006;100(8):715-31.

Session 1-5 – The increasingly pressing issue of metronidazole resistance in *Giardia lamblia* and a possible causative mechanism

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The single cell parasite *Giardia lamblia* (syn: *intestinalis*, *duodenalis*) occurs worldwide and causes manifold gastrointestinal sequelae in infected persons. It can also cause malnourishment and stunting in children. As no vaccine is available, the management of the disease is limited to administration of the 5-nitroimidazole metronidazole or the benzimidazole albendazole. In most countries, however, metronidazole is the only approved treatment option. Resistance to metronidazole has been comparably rare for a long time, but in the last 15 years or so a steep increase of metronidazole-refractory *Giardia* has been reported, especially from the Indian subcontinent. In clinical practice, the treatment of *Giardia* infections has therefore become difficult.

The mechanisms causing metronidazole resistance in *Giardia* clinical isolates have remained unclear and strains isolated from refractory patients proved to be susceptible *in vitro*. In several studies over the past years, however, we found that susceptibility testing for metronidazole was probably not done properly. Some strains become clearly more tolerant to metronidazole in the presence of microaerobic concentrations of oxygen. This is also accompanied by a stronger expression of antioxidant enzymes which enable (faster) growth under these conditions. We propose that treatment failures might be caused by such strains.

This project is supported by the Austrian Science Fund [Project PAT1919524].

Session 1-6 – *Plasmodium ovale* spp. – Establishing clarity in naming these parasites

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Session 2-1 – Efficacy of octenidine-containing mouthrinses on *Entamoeba* spp. *in vitro* and in the oral cavity

Katharina Kranner[1], Martina Köhsler[1,*], Karin Riedl[2], Julia Walochnik[1]

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Entamoeba gingivalis is an amoeba inhabiting the oral cavity. Its detection in periodontitis sites significantly correlates with the diagnosis of periodontal disease, pointing towards a pathogenic potential. Proper oral hygiene is indispensable for the prevention and control of dental and periodontal problems. In that regard, antiseptic mouthrinses are widely used to support oral biofilm management, especially in otherwise inaccessible areas of the oral cavity. This study aimed to investigate the antimicrobial activity of commercially available octenidine-containing mouthrinses (octenimed®, octenident®) as well as of the wound and mucous membrane antiseptic octenisept® against *Entamoeba spp*. Octenidine-containing ready-to-use solutions have been proven in clinical trials to effectively inhibit plaque formation, gingivitis and oral microbial growth (bacteria and fungi). Moreover, octenidine itself has been recently shown *in vitro* to be highly active against amoebae of the genus *Acanthamoeba*, too. In a first step, *in vitro* assays were conducted to evaluate the effect of these octenidine-based solutions on *E. histolytica*. A 30-second exposure resulted in near-complete eradication of trophozoites with all three formulations, exhibiting a significantly stronger effect than 3 % H_2O_2, a commonly used disinfectant in dental practices. Given the limited cultivability of *E. gingivalis*, a quantitative real-time PCR approach was established in a second step to determine the organism's DNA load in oral samples of volunteers. In an ongoing clinical pilot study, *E. gingivalis* DNA will be quantified before and after twice-daily rinsing the oral cavity with octenident® over seven consecutive days. Preliminary findings already suggest a reduction of *E. gingivalis* DNA of up to 80%.
In summary, our data demonstrate a strong *in vitro* effect of octenidine-containing solutions on *E. histolytica* as well as a promising antimicrobial potential of octenident® for the reduction of *E. gingivalis* in the oral cavity.

Session 2-2 – Molecular characterization of *Acanthamoeba* extracellular vesicle proteases and their involvement in the cytopathogenicity

Ivana Jankovic[1,*], Alvie Loufouma-Mbouaka[1], Tania Martín-Pérez[2], and Julia Walochnik[1]

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Acanthamoeba spp. are opportunistic pathogens that can cause *Acanthamoeba* keratitis (AK), a severe sight-threatening eye disease affecting mainly contact lens wearers, and also other serious infections in the human host. The number of reported AK cases has been increasing worldwide in recent years, which is partly due to a growing number of contact lens wearers, but also to improved diagnostics. However, the pathogenesis of this infection is still incompletely understood. The known virulence factors of *Acanthamoeba* include surface adhesins as well as secreted molecules such as proteases. In recent years, an important role of the so-called extracellular membrane vesicles (EVs) in cell-cell interactions of many pathogenic protists has been demonstrated, and proteases carried by these vesicles may also play a key role during the infection process of *Acanthamoeba*. In the present study, the proteolytic profiles of different clinical *Acanthamoeba* strains before and upon contact with human corneal epithelial cells (HCECs) were examined by using zymography. We observed an increase in proteolytic activity of extracellular vesicles during the initial phase of interaction between the amoebae and HCECs. Our data revealed that *Acanthamoeba* EVs may play a role during *Acanthamoeba* and host cell interaction, contributing to cell adhesion and lysis.

This research is funded by the Austrian Science Fund (FWF) 10.55776/ESP5824124

Session 2-3 – A mixed method design for investigating schistosomiasis in Alagoas (Brazil)

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Schistosomiasis caused by Schistosoma mansoni is a neglected tropical disease prevalent in Brazil, primarily in southeastern and northeastern states such as Alagoas. Due to the low to medium endemicity of the disease, there has been growing awareness that the elimination of schistosomiasis in Brazil requires not only biomedical interventions but an integrated approach, prioritizing its social determinants, including sanitation services, water access, and hygiene practices [1,2].

Given this scenario, the SaneaXisto project investigates the association between different levels of access to water and sanitation services and the occurrence of schistosomiasis in Alagoas. The ongoing epidemiological study (quantitative phase) encompasses household-based sampling of 1,500 participants from 75 communities with 20 households per community and one representative from each household. Data collection includes questionnaires on socioeconomic and sanitation conditions, health status, and risk behaviors, as well as parasitological testing for schistosomiasis and other helminths. Preliminary results have shown positivity rates ranging from 5% to 20% as well as the presence of Ancylostoma, Ascaris and Trichuris trichiura. The water will be subjected to physical-chemical and microbiological analysis, as well as molecular analysis to verify the presence of DNA of Schistosoma mansoni, Biomphalaria glabrata and traces of possible hosts. The mollusks will be submitted to taxonomic analyzes for specific identification, parasitological analyzes to verify the presence of cercariae and molecular analyzes to detect Schistosoma mansoni DNA.

Here we present an explanatory sequential mixed method design in which this quantitative phase is followed by qualitative research. The epidemiological study will guide the qualitative sampling and participant observation, interviews, and focus group discussions will be used to expand on how individual and collective practices, perceptions, and constraints shape interactions with water and sanitation systems, and sustain disease transmission.

By integrating epidemiological evidence with sociocultural insights, this study aims to address how structural conditions and everyday practices interact to influence vulnerability to schistosomiasis, informing more context-sensitive approaches to disease prevention and control.

References

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Session 2-4 – Parasite Fauna of Wild Carnivores as Baseline Data for Future Zoonotic Risk Assessment

Oleg V. Shcherbakov[1,*], Sargis A. Aghayan[1,2], Ruzanna H. Gevorgyan[1], Jon A. Mkrtchyan[1], Tigran A. Abgaryan[1], Iulia V. Nosulya[1,3], Varvara V. Solovyeva[1], Emil V. Adamyan[1], Gor A. Kaloyan[1], Hasmik Sh. Gevorgyan[1]

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Wild carnivorous mammals are important reservoirs and transmitters of zoonotic diseases such as rabies, leptospirosis, alveolar and cystic echinococcosis, toxocariasis, trichinellosis, dirofilariasis, leishmaniasis, etc. Transmission occurs either through direct contact with infected wild or synanthropic animals, or indirectly via vectors and environmental contamination, thereby increasing the risk to humans. Globally, 75% of emerging infectious diseases are zoonotic, and their incidence has tripled since 1980. In Armenia, eight recent cases of alveolar echinococcosis highlight the urgent need for wildlife parasite surveillance, yet no monitoring system currently exists. The aim of this study was to document the parasite fauna of wild carnivores (Mammalia: Carnivora) in Armenia and provide initial insight into their potential zoonotic relevance. Notably, this is the first report of parasitic infections for brown bears and mustelids in the country.

Between November 2023 and September 2025, 40 carcasses and 219 fecal samples of wild carnivores were collected from various regions across Armenia. Parasites were identified based on morphological characteristics and confirmed by molecular techniques.

Bears: Coprological analysis of 59 brown bear fecal samples showed a 52.5% positivity, with *Baylisascaris transfuga* dominating the parasitic fauna (44%). Other helminths and protozoa, including *Dicrocoelium dendriticum*, *Aonchotheca putorii*, and *Giardia duodenalis*, occurred at lower prevalence.

Foxes: Necropsy of three carcasses revealed multiple helminths, while fecal screening of 56 samples indicated 71% prevalence and high diversity (≥21 taxa). Frequent parasites included *Toxocara canis*, *Uncinaria stenocephala*, *A. putorii*, and *Alaria alata*, with protozoa such as *Giardia duodenalis* also detected.

Jackals: Among 30 carcasses, 90% were infected, harboring 17 species. *Trichinella* spp. (50%) and *Pterygodermatites petrowi* (40%) were particularly common. Fecal analysis of 11 samples confirmed 54.6% prevalence, with important zoonotic taxa such as *T. canis,* opisthorchids, hookworms, and *Mesocestoides lineatus* represented.

Otters: Three necropsied otters were parasite-free, while 51 fecal samples revealed 45% prevalence representing 15 distinct parasite species from different taxonomic groups. Frequent infections included trematodes (*Alaria alata,* opisthorchiids*, Echinochasmus perfoliatus*) and nematodes (*A. putorii, Soboliphyme baturini*), along with protozoa (*Giardia duodenalis, Isospora lutrae*), and rare detections of mites and cestodes.

Other mustelids: Necropsy of four individuals detected *Trichinella sp.* in one weasel, while 29 marten fecal samples yielded 39% prevalence. *A. putorii* was most frequent, with occasional findings of *Soboliphyme baturini*, *Baylisascaris columnaris*, and coccidia.

Wolves: Examination of 13 fecal samples revealed a prevalence of 85%, with *T. canis* and *A. putorii* (each at 31%) being the most frequently detected parasites. Other helminths (*Trichuris vulpis*, *Uncinaria stenocephala*, *Dipylidium caninum*) and Protozoa (*Cystoisospora sp., Eimeria spp.*) were recorded at lower prevalence.

According to the results of our research, out of the 47 parasite species detected, 21 species have zoonotic significance, which should be taken into account when assessing potential public health risks, and developing monitoring or prevention strategies.

The following parasites were detected for the first time in Armenia: *Spirometra erinacei-europaei* in jackals, *Macracanthorhynchus catulinus* in jackals and foxes, *E. multilocularis* in foxes, *Baylisascaris transfuga* in bears, *Baylisascaris columnaris* and *Soboliphyme baturini* in mustelids, *Capillaria hepatica* in foxes and wolves, and *Aonchotheca putorii* in different wild carnivorous mammal species.
According to current study, Armenian wild carnivores harbor a diverse range of helminths and protozoa, with prevalence varying from 39% in mustelids to over 85% in wolves. Several zoonotic parasites are widespread and occur across host species, underscoring the ecological connectivity among wildlife reservoirs. Our findings highlight the importance of integrating wildlife into One Health surveillance frameworks to better anticipate and mitigate zoonotic disease risks in Armenia.

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Session 2-5 – Antioxidant enzymes and their impact on Metronidazole and oxygen susceptibility in *Giardia lamblia*

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Giardia lamblia is an anaerobic/microaerophilic parasite, which colonizes the small intestine. It causes giardiasis, which manifests commonly in diarrhea, nausea, malabsorption but can also have post-infection symptoms. Metronidazole remains the main treatment, though resistance is increasing.

In a previous study, strains 713 and WB C6 showed differences in metronidazole and oxygen susceptibility. In 713, the strain with lower susceptibility, three proteins, oxygen-detoxifying enzymes were identified to be overexpressed (superoxide reductase (SOR), pyridoxamine 5'-phosphate oxidase (Pyridox), thioredoxin-like protein A (TlpA)). Mass spectrometry analysis found another three proteins to be overexpressed in both strains under microaerophilic conditions (high cysteine membrane protein (HCMP), flavohemoprotein (FlHb), peroxiredoxin (Prx)). However, the previous reported overexpression of SOR, Pyridox and TlpA could not be validated.

Our study aims to determine the optimal window for targeted proteomic analysis by combining protein detection by western blot with controlled microaerophilic cultivation. Candidate proteins will be tested individually or combined in tandem constructs via overexpression in the WB C6 strain to assess their effects on oxygen and metronidazole tolerance. So far, we engineered two vectors, pPac HCMP and pPac TrxR/TlpA, and introduced them into *G. lamblia*. We hypothesize that the proteomic analysis will present a set of protein associated with growth in the presence of oxygen and that several of these proteins will enhance the oxygen and metronidazole tolerance of WB C6.

Session 3-1 – Schnelldiagnostik tropischer Fiebererkrankungen bei Reiserückkehrern: Möglichkeiten moderner Multiplex–PCR

Peter Starzengruber[1,*]

Session 3-2 – Malariaprophylaxe in der Praxis – basierend auf einer gemeinsamen europäischen Initiative zur Harmonisierung der Empfehlungen

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Malaria ist nach wie vor eine schwerwiegende und potentiell lebensbedrohliche Erkrankung, sofern sie nicht prompt diagnostiziert und behandelt wird. Trotz effektiver Medikamente zur Prävention und Therapie erkranken jährlich über 250 Millionen Menschen weltweit und es werden über 500 000 Todesfälle gemeldet.

In der Reise- und Migrationsmedizin hat die Prävention von Malariaerkrankungen einen hohen Stellenwert, jedoch variieren die nationalen Empfehlungen zur Malariaprophylaxe für dieselbe Destination. Das Schweizer Expertenkomitee für Reisemedizin und die Deutsche Gesellschaft für Tropenmedizin, Reisemedizin und Globale Gesundheit arbeiten seit über 2 Jahrzenten zusammen und kürzlich haben sich auch Belgiens (Belgium Study Group of Travel Medicine), die Niederlande (National Coordination Center for Travellers Health Advice) und Österreich über die ÖGTPM angeschlossen, um gemeinsam Empfehlungen zur Malariaprophylaxe und Prävention herauszugeben. Die Empfehlungen basieren auf einer einheitlichen, publizierten Methodologie zur Risikobewertung der Malariaexposition in endemischen Gebieten. Diese Empfehlungen werden jährlich gemeinsam überarbeitet. Dadurch soll eine transparente evidenzbasierte Empfehlung der Malaria Prophylaxe in unterschiedlichen europäischen Ländern ermöglicht werden.

Im Vortrag werden die Grundprinzipien der Malariaprophylaxe in der Reisemedizin und die über die ÖGTPM verfügbaren Unterlagen (Malariakarten und Länderlisten) in der reisemedizinischen Beratung vorgestellt.

Referenzen

Veit O. et al. Methodology of the joint malaria prevention recommendations of Switzerland, Germany, Belgium and The Netherlands. Journal of Travel Medicine, 2024

Link zum Download der Malariakarten und Länderlisten: www.oegtpm.at/malariakarten/

Session 3-3 – Comparative study on vector-borne parasites in Burkina Faso

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Burkina Faso has made significant progress in controlling vector-borne parasitic infections, particularly malaria and lymphatic filariasis (LF), with mass drug administration (MDA) as the main strategy against LF. However, LF remains endemic in currently 9 out of 70 health districts, and Burkina Faso still carries one of the highest malaria burdens in the world. Challenges in the elimination of these two diseases include diagnostics. LF is mainly diagnosed using the filariasis strip test, which is known to have reduced sensitivity and specificity when used in the field. Routine diagnosis of malaria relies on a rapid diagnostic test based on histidine-rich protein (HRP), which only detects *P. falciparum* and gives false negative results in case of mutations. The aim of this study was twofold, firstly to assess the effectivity of MDA in an LF-endemic region and, secondly, to assess the *Plasmodium* species composition and possible histidine-rich-protein (HRP) mutations in *Plasmodium falciparum* in a region with high malaria endemicity. Altogether, 172 blood samples of asymptomatic individuals from a region with ongoing MDA and usage of insecticide-treated bed nets were included in the study.

Of the 172 investigated blood samples, seven samples were LF-positive in serology, of which three samples were also PCR-positive for *Wuchereria* DNA. The PCR amplicons were sequenced and confirmed to be *Wuchereria bancrofti*.

Altogether, 125 samples (73%) of the 172 investigated blood samples were positive for *Plasmodium* spp. in a pan-malaria PCR, 82 samples being clearly positive and 43 being borderline-positive. The clearly positive samples were subjected to a species-specific multiplex PCR and revealed 77 *Plasmodium falciparum* and 5 *Plasmodium malariae*. The results of the multiplex PCR were confirmed by subjecting the amplicons to DNA sequencing. All *P. falciparum*-positive samples were screened for HRP mutations. Three out of the 77 samples revealed mutations (HRP2/3).

This study demonstrates that there are still hotspots where LF persists despite long-term MDA. Moreover, our study reveals possible gaps in malaria routine diagnostics.

Session 3-4 – PCR detection of gastrointestinal parasites in golden jackals (*Canis aureus*) from Armenia: first molecular insights and surveillance perspectives

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Golden jackals (*Canis aureus*) are increasingly recognized as important reservoirs and transmitters of zoonotic parasitic diseases, including echinococcosis, toxocariasis, ancylostomiasis, dirofilariasis, and leishmaniasis. Their expanding populations, facilitated by climate change, bring golden jackals into closer proximity with human settlements and domestic animals, thereby raising concerns for public health. This is particularly critical given that 75% of newly emerging infectious diseases are zoonotic and originate from wildlife, with incidence tripling since 1980. Despite this relevance, data on the parasitic fauna of golden jackals in Armenia as a corridor into European countries remain insufficient. Yet, their role as adaptable reservoirs highlights the importance of documenting their helminth fauna to better understand the risks of parasite transmission in this region. This study is conducted within the framework of the Austrian Agency for Internationalization and Education (OeAD) Academic Partnership Program for Higher Education and Research (APPEAR) project ArmBioClimate, which supports research on biodiversity, climate change, and public health in Armenia.

Gastrointestinal tracts from 30 golden jackals, obtained through road kills or legal hunting, were examined for helminths. Intestinal parasites were isolated and identified based on morphological characteristics, followed by molecular confirmation through PCR amplification using species-specific primers and sequencing.

Molecular analysis confirmed the presence of several gastrointestinal helminth species in Armenian golden jackals. Among nematodes, *Pterygodermatites sp., Physaloptera sibirica, Uncinaria stenocephala, Toxocara canis*, and *Dioctophyme renale* were identified. Cestodes included *Mesocestoides litteratus, Taenia pisiformis, Dipylidium caninum*, and *Spirometra erinaceieuropaei*, and the trematode *Alaria alata* was recorded.

Several of these species, notably *Toxocara canis, Dipylidium caninum, and Alaria alata*, are of considerable veterinary and zoonotic relevance. These results provide the first molecular confirmation of gastrointestinal helminths in golden jackals from Armenia and highlight their role in maintaining and potentially transmitting pathogens of importance for both human and animal health.

Future research will apply metagenomic approaches to fecal samples to investigate a broader parasite diversity and to enable comparative assessments of the jackal's helminth fauna in Armenia and Austria. Moreover, immune genes involved in the host response to parasitic infections will be investigated to advance understanding of host–parasite coevolution.

Session 3-5 – Revealing global diversity through targeted long-read mitogenomics of *Dirofilaria* species

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Dirofilaria species are significant zoonotic parasites whose global distribution necessitates detailed genetic characterization. This study aimed to establish a robust and efficient method for sequencing the complete mitochondrial (mt) genome to facilitate the evaluation of their genetic diversity.
We adapted six primer sets from Yilmaz and collaborators (2016) to develop a flexible approach: generating two long (8.9–10 kb) overlapping fragments via long-range PCR for high-quality DNA or using the original six overlapping fragments (~2.5 kb each) for samples with lower DNA quality. Amplicons were sequenced using Oxford Nanopore Technologies (ONT), and data were processed through a specialized bioinformatics pipeline incorporating minimap2, AGORA, and RAxML for quality assessment, annotation, and maximum likelihood phylogenetic analysis.
A total of 55 samples (adult worms, microfilariae, and extracted DNA) were collected from nine countries, including Austria, Romania, and Greece. Of these, 40 samples were successfully sequenced, yielding 34 complete mitogenomes and 6 partial sequences. The complete mitogenomes included *D. immitis* (n = 19), *D. repens* (n = 17), and *D. asiatica* (n = 4). Sequence quality was high, with mean coverage depth ranging from 107.4x to 905.6x across the reference genome. Phylogenetic analysis confirmed species-specific clustering of all newly generated sequences alongside published *Dirofilaria* and other nematode mitogenomes.
These findings demonstrate the effectiveness of targeted full mitogenome sequencing using overlapping long reads. The established method offers a powerful, high-throughput tool for generating multiple complete mitogenomes, enabling comprehensive global assessment of *Dirofilaria* genetic diversity. This approach not only enhances taxonomic resolution but also supports epidemiological tracking and control of filarial infections.

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Session 4-1 – Delusional Parasitosis – Between Psychopathology and Exploitation

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Delusional parasitosis (DP) is a neuropsychiatric disorder, characterized by a fixed, false belief of being infested with parasites such as skin mites, insects, or intestinal worms. Patients report sensations of crawling, biting, or internal movement and attribute these to intestinal or cutaneous parasites. Despite the absence of objective medical evidence, the conviction remains unshakable, leading to repetitive self-cleaning, the use of antiparasitic agents, and self-inflicted injuries. A related phenomenon is *Morgellons disease*, which was increasingly recognized during the COVID-19 pandemic.

DP may present as a primary delusional disorder or secondary to underlying psychiatric and neurological conditions. Treatment is often challenging, as patients typically reject psychiatric explanations and insist on a somatic cause. The lack of insight leads to resistance against mental health referral and poor adherence to antipsychotic therapy.

In the digital era, DP-like fears have been strongly fueled by social media and alternative health markets. Influencers and commercial platforms exploit parasitic anxiety, especially fears of intestinal “worms” or “biofilms”, to promote unproven detox products and cleanses, often providing questionable scientific proof. Apart from being unethical, this reinforces delusional beliefs and delays psychiatric intervention.

Despite the fact, that our institute solely provides routine parasitological diagnostics, a growing number of inquiries of potential DP patients can be noted. A deeper insight into these cases and a closer examination of this topic demonstrates, that the disorder must be taken seriously as a genuine mental health condition, while the growing encouragement and validation of delusional beliefs through social media and alternative health networks, represent an emerging and significant public health concern.

*Session 4-2 – Assessment of fasciolicide efficacy using the faecal egg count reduction test (FECRT) in cattle herds in Tyrol, Austria

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The parasitic trematode *Fasciola hepatica* (*F. hepatica*) is of major importance in grazing ruminant livestock worldwide, as it compromises animal health and results in significant economic losses [1, 2]. The situation is further complicated by the fact that triclabendazole, the only drug effective against juvenile stages, is not permitted for use in dairy cattle, and treatment with other compounds is only effective once patency has developed. Additional challenges arise from the emergence of anthelmintic resistance and the environmental toxicity of fasciolicides [3, 4].

To determine the efficacy of fasciolicides we performed a faecal egg count reduction test (FECRT) and a coproantigen reduction test (CART) [5]. Between 2023 and 2025, we conducted the tests on 12 cattle farms in the Tyrolean region including a total of 76 individuals. Individual body weight was determined by weighing tape. Albendazole (Valbazen®, 7.5 mg/kg/bw (ABZ)), closantel oral (Flukiver®, 10 mg/kg/bw (CLO_o)), and oxyclozanide (Distocur®, 10 mg/kg/bw (OXZ)) were administered as oral suspension, while closantel pour on (closamectin®, Ivermectin 500 µg/kg/bw + Closantel 20 mg/kg/bw (CLO_p)) was given as pour on treatment. Faecal samples (rectal) were obtained at the begin of the study to identify positive individuals, and subsequently at the 28-day mark following treatment with the FLUKEFINDER® sedimentation method and the copro-antigen ELISA (Bio-X Diagnostics, Belgium).

The findings demonstrated a negative analysis in 22.2% of individuals treated with ABZ, as investigated in both the FLUKEFINDER® and the copro-antigen ELISA following treatment. The results observed from the CLO_o and CLO_p group showed a negative outcome after treatment with 100% and 71.4% of the animals tested, respectively. The OXZ group revealed a 19.0% negative rate of individuals after treatment in both tests.

The present analysis is highlights substantial differences in the reduction of *Fasciola* egg counts among four drugs commonly used in cattle. The findings support the need to strengthen this investigation by increasing the number of animals included and by implementing control groups to improve test reliability.

This study was carried out as part of the F.O.O.D. project on behalf and with financial support from the Austrian Federal Ministry of Agriculture, Forestry, Regions and Water Management.

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Session 4-3 – Phylogeny of the subgenus *Phortica* sensu stricto (Diptera: Drosophilidae) from Europe

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Drosophilid flies (Diptera: Drosophilidae) generally feed on fruits. However, within the genus *Phortica* – especially among members of the subgenus *Phortica sensu stricto* – several species are lachryphagous, feeding on mammalian tears. Through this behaviour, *Phortica okadai* and *P. variegata* act as vectors of the Oriental eyeworm *Thelazia callipaeda* (Spirurida:

Thelaziidae), which infects dogs and several other mammals including occasionally humans. While more than 80 species of the subgenus *Phortica s.s.* are known from Asia, only three species have been described in Europe: *P. variegate*, *P. semivirgo*, and *P. erinacea* (so far reported only from Bulgaria). In addition, *P. oldenbergi* (subgenus *Allophortica*) is also present. Recent studies have reported *Phortica* specimens in Austria and Italy that could not be assigned to any of these recognised known European species [1, 2].

The aim of this study was to investigate the presence and phylogenetic position of potentially unknown *Phortica* species in Europe. Over 300 specimens were analysed, originating from archived material and new collections. Samples were obtained from Albania, Austria, Bulgaria, Czechia, France, Germany, Hungary, Italy, Luxembourg, Montenegro, Portugal, Romania, Sweden, Spain, Switzerland, and the United Kingdom, while collection efforts in Bosnia and Herzegovina, Poland, Slovakia, and Ukraine were unsuccessful.

DNA barcoding of two regions of the cytochrome c oxidase subunit I (COI) gene revealed several distinct *Phortica* lineages in Austria, Czechia, Hungary, and Italy that did not correspond to any of the known European taxa. A phylogenetic analysis including both European and Asian *Phortica s.s.* sequences indicated that these lineages are genetically distinct, suggesting the presence of previously unrecognised diversity within Europe.

Future work will focus on additional markers (28S rRNA and NADH subunit 2) and detailed morphological examination of these specimens. Our results provide the first evidence for cryptic *Phortica* diversity in Europe and highlight the need for integrative taxonomic approaches. Such knowledge is essential to assess the potential vector competence of European *Phortica* species beyond *P. variegata*.

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*Session 4-4 – A comparative *in vitro* anthelmintic screening of medicinal plants using dual nematode model (*Caenorhabditis elegans* and *Oscheius tipulae*)

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Caenorhabditis (*C.*) *elegans* is a model organism that is being used for the screening of medicinal plants to evaluate their anthelmintic activity [1]. Comparably, *Oscheius* (*O.*) *tipulae* might also be used to screen the anthelmintic potential of plant extracts [2]. Secondly, the Subcontinent region is naturally enriched with medicinal flora, and researchers in this region explore the nematocidal properties of natural products using non-model organisms such as *Haemonchus contortus* because of the lack of a suitable environment for the growth of *C. elegans* [3,4].

We hypothesize that *O. tipulae* may possess the same potential as *C. elegans* and serve as the best alternative to *C. elegans* for screening compounds in tropical regions. The *in vitro* tests of plant extracts were carried out against the L_1 stage larvae of the worms.

The results indicated that there was no variation in the dose-dependent response of ivermectin against both strains, and all ten plant extracts possess nematocidal potential. Based on the LC_{50} values (CI 95%) in the case of *Leucas aspera*, there was a non-significant difference between CEW1 0.049 (0.043 – 0.058) and N2 strains 0.046 (0.041 – 0.052). This statistical non-significant difference indicates the usefulness of both strains for the screening of plant extracts. The LC_{50} values suggest that a slightly higher dose of plant extracts was required for the mortality of the 50% population of CEW1 than N2.

This led to the conclusion that those plant extracts that were effective against CEW1 must also have their activity against N2. Therefore, *O. tipulae* could be used as a model organism for the screening of plant extracts or natural products.

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*Session 5-1 – Molecular analysis of vector-borne pathogens in red foxes (*Vulpes vulpes*) from Saxony-Anhalt (Germany)

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Vector-borne pathogens (VBPs) are becoming increasingly important in veterinary medicine and public health, with wildlife potentially playing a key role in their transmission. The objective of the current study was to investigate the occurrence of vector-borne pathogens in red foxes (*Vulpes vulpes*). Spleen samples from 277 legally hunted foxes were collected over a period of twelve months (May 2020 to April 2021) in Saxony-Anhalt, Germany. VBPs were identified by performing PCR analysis on the samples, followed by Sanger sequencing, and a phylogenetic analysis was performed on *Mycoplasma* spp. A total of 94% of the samples showed a positive result. The pathogens identified were *Hepatozoon canis* (77%), *Babesia vulpes* (68%), *Mycoplasma haemocanis* (5%), *Mycoplasma* spp. (5%), and *Trypanosoma pestanai* (0.4%). None of the examined samples tested positive for filarioid helminths, *Bartonella* spp., *Rickettsia* spp., and Anaplasmataceae. This study highlights the role of foxes as reservoirs for pathogens that may affect domestic animals and humans, potentially contributing to the spread of these pathogens through shared environments and vectors.

*Session 5-2 – Molecular Detection of Vector-Borne Pathogens in Ticks collected from Companion Animals in the Republic of Kosovo

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Tick-borne diseases pose an increasing threat to animal and human health, particularly in areas with frequent vector–host interactions. This study presents the first molecular investigation of tick-borne pathogens in ticks collected directly from companion animals during veterinary visits in Prishtina, Kosovo. Companion animals can act as sentinels for zoonotic transmission, providing valuable insights into local pathogen circulation.

During summer 2024, 304 ticks were collected from 120 dogs and 20 cats presented for routine veterinary care. Ticks were morphologically identified and subjected to DNA extraction for barcoding and PCR screening targeting *Anaplasma*, *Borrelia*, Piroplasmida, and *Rickettsia*. Barcoding results were compared with morphological identifications for quality control.

Five different tick species were identified. Preliminary PCR screening detected *Rickettsia* DNA in several samples. Barcoding confirmed morphological identifications. Sequencing of positive samples and screening for other pathogens are ongoing.

Veterinary-clinic–based sampling is a practical, noninvasive approach for tick-borne pathogen surveillance. The detection of *Rickettsia* highlights the zoonotic potential of local tick populations and underscores the importance of preventive measures and awareness among veterinarians and pet owners. Continued analyses will clarify the diversity and public health significance of tick-borne pathogens in Kosovo.

*Session 5-3 – Multi-host PCR detection of *Dirofilaria* and *Leishmania* in Armenian mammals

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Vector-borne parasites such as *Dirofilaria* spp. and *Leishmania* spp. pose significant zoonotic risks and their distribution is significantly affected by climate change, however, data on their prevalence in many countries is still very limited. Armenia plays a special role in this context as it is on one of the main migratory routes for wildlife, including important reservoir hosts, between Asia and Europe. In 2024, we conducted a countrywide study of domestic and wild mammals to evaluate the prevalence of these parasites among various host species. Tissue samples were collected from 30 golden jackals (*Canis aureus*) and two foxes (*Vulpes vulpes*), and blood samples were collected from 69 domestic dogs and 3 brown bears (*Ursus arctos*). All samples were preserved in ethanol and DNA/RNA shield respectively, for transport. The samples were then screened using PCR for *Dirofilaria* spp. and *Leishmania* spp. *Dirofilaria immitis* was detected in 7 out of 30 (23.33%) Golden jackals (4 females and 3 males, 5 from Armash in Armavir and two from Ararat), 35 out of 73 (47.94%) dogs (13 females and 25 males, 32 from Yerevan, 2 from Ararat and 1 from Shirak), 2 out of 3 cats (3 male from Yeravan) and 2 out of the 3 bears (one female and one male from Yerevan region). One male dog from Yerevan tested positive for *Leishmania*. Notably, spatial overlap of *Dirofilaria*-positive hosts was observed between jackals and dogs in Ararat and between dogs, cats and bears in Yerevan, indicating the co-occurrence of infections in both, domestic and wildlife populations. Male dogs showed a higher prevalence of infection, whereas infections in wildlife hosts were more evenly distributed between the sexes. These findings emphasize the widespread circulation of *Dirofilaria* in Armenian mammals and highlight the importance of integrated One Health approaches for monitoring zoonotic parasites in both domestic and wild species.

*Session 5-4 – Phlebovirus seroprevalence in domestic dogs from Austria and Germany

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Sand fly-borne phleboviruses are of high medical importance by causing sand fly fever (e.g. sandfly fever Sicilian virus, SFSV), or even meningitis and meningoencephalitis (e.g. Toscana virus, TOSV). *Phlebotomus mascittii* is the regionally predominant sand fly species in Austria and Germany, however, knowledge about its role in phlebovirus transmission and about potential vertebrate reservoirs for phleboviruses remains limited. While it is well known that dogs are reservoirs for the protozoan parasites *Leishmania*, the role of dogs in phlebovirus transmission remains unclear, although studies frequently report exposure. The aim of this study was to shed light on phlebovirus exposure in dogs in two understudied Central European countries. Overall, 760 Austrian and 760 German dog sera, collected between November and February 2023/24 and 2024/25, were tested for antibodies against SFSV and TOSV using seroneutralization assays. Our results show that dogs living in Austria and Germany have been exposed to SFSV and TOSV, with some dogs showing co-exposure to *Leishmania infantum*. An initial assessment of the positive dogs' import and travel history suggests that exposure is only partially attributable to exposure in endemic countries. Analysis of transmission cycles is crucial to determine the extent to which Austrian and German dogs come into contact with sand flies and sand fly-borne pathogens and to closely monitor potential endemicity of phleboviruses in so far non-endemic countries, especially since the distribution range of sand flies and sand fly-borne pathogens is expected to increase due to global warming.

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*Session 5-5 – Surveillance of mosquito fauna and associated pathogens in the Vienna Zoo, Austria

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The Vienna Zoo is the world's oldest zoo still in operation and is also a UNESCO World Heritage Site. With over 500 animal species in captive, it provides unique configurations of exotic and endemic animals and plants. It also creates a wide variety of breeding habitats and potential blood sources for local mosquito populations. A thorough understanding of mosquito ecology and host-feeding behaviour is therefore essential to improve mosquito control and to prevent pathogen transmission within these settings.

725 adult mosquitoes were collected during the summer of 2024 and 2025. Morphological and molecular analyses showed that *Culex pipiens/torrentium* (664/725; 91.6 %) was by far the dominant species. Besides that, 13 other mosquito species (from five genera) were found in lower numbers. No potentially invasive species were found. 15 mosquitoes (from four different genera) were found to be bloodfed and therewith to be subjected to bloodmeal analysis.

Also, 453 mosquito eggs were collected with ovitraps during the same period and were pooled in 21 samples. Multiplex PCR detected parasite DNA of two potentially invasive mosquitoes, the Asian Tiger Mosquito (*Aedes albopictus*) and the Asian Bush Mosquito (*Aedes japonicus*). These two mosquito species are known to be capable to transmitting Dengue, Chikungunya, and Zika viruses [1]. From the side catches, we found 222 biting midges (*Culicoides*) and 150 black flies (*Simulidae*), which are known vectors for bluetongue viruses and filarioid nematodes, respectively [2,3].

Touchdown PCR detected parasite DNA of filarioid helminths and nested PCR detected parasite DNA of *Plasmodium spp.* and trypanosomes. These are done in pooled adult mosquito samples (n = 191). The results of the pathogen detections are still being finalised.

This study is the first report of mosquito identification and parasites detection in the Vienna Zoo.

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*Session 5-6 – Phylogeography and Haplotype Characterization of *Aedes japonicus* in Austria

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Aedes japonicus, a mosquito species originating from East Asia, is a known vector for various viruses and has successfully established populations across Europe and North America. The presence of *Ae. japonicus* is confirmed in Austria, but there is limited data on its haplotype distribution in connection with global genetic analysis of *Ae. japonicus* populations. This study aims to provide a comprehensive picture of the current dispersal and genetic structure of *Ae. japonicus* haplotypes in Austria.

Mosquito eggs were sampled using ovitraps from 382 sampling points across Austria between 2020 and 2021. From these, 343 confirmed *Aedes japonicus* samples were analysed. DNA sequences of the Cytochrome Oxidase subunit I (COX1) gene were aligned using MEGA, subjected to BLAST analysis against NCBI references, and utilized for Maximum Likelihood phylogenetic analysis. Furthermore, haplotype diversity and population structure within Austria were calculated, and a Haplotype Network was constructed using PopArt.

The COX1 sequences of the 343 Austrian samples showed high similarity to 33 sequences deposited in NCBI, predominantly originating from Germany, Italy, and the Netherlands. Phylogenetic analysis revealed at least 12 distinct clades, with three clades confirmed as monophyletic (specifically from Tyrol and Styria). Population density analysis showed the highest number of samples in Tyrol (99 samples), while Carinthia exhibited the highest haplotype diversity (78%). Population structure analysis indicated low, with FST values consistently below <0.1. Network analysis highlighted the presence of two major haplotypes, suggesting that, *Ae. japonicus* colonization of Austria occurred through multiple introduction events, followed by subsequent geographical evolution. Comparative *insilico* analysis of the global COX1 database revealed only 11 distinct haplotypes, with Haplotype 3 being the most widespread globally including the Austrian population of *Ae. japonicus*.

In conclusion, *Ae. japonicus* populations are established in Austria due to multiple introductions, most likely originating from neighbouring countries such as Italy and Germany within the regions of Carinthia and Tyrol. Additionally, the genetic structure of *Ae. japonicus* in Austria is currently categorized as low, indicating recent or extensive gene flow among local populations.

*Session 5-7 – Challenges and limitations of mosquito microbiome analysis – a first insight into the microbiome of Austrian mosquitoes

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In recent years, it has been shown that the microbiome composition of mosquitoes can have a huge impact on various aspects including development, survival, and vector competence. Therefore, microbiome manipulation has been suggested as a new tool to control and combat vectors and their associated pathogens. However, knowledge on microbiome composition of mosquitoes in different geographical areas is still limited. In this study, we aim to get a first insight into the microbiome of Austrian mosquitoes while also evaluating challenges and limitations in mosquito microbiome analyses.

For this purpose, 44 mosquito samples, which were collected with BG-Sentinel traps at the Vienna International Airport between May and September 2023, were identified morphologically and afterwards subjected to microbiome analyses. The mosquitoes were homogenized, and half of the homogenate was subjected to DNA extraction and subsequent 16S amplicon sequencing. Additionally, the rest of the homogenate was used for a microbiological approach (inoculation of liquid broths, culture on different agar plates and identification with MALDI-TOF MS).

The preliminary results show that the 44 adult mosquito samples either consisted of a single individual (n=16) or pools of up to 20 mosquitoes of the same species (n=28). The majority of the samples were identified as *Ae. vexans* (n=30). *Aedes sticticus* was present in 13 samples, while one sample was classified as *Ae. cinereus/geminus*. The top bacterial genera identified in the samples included *Asaia, Cutibacterium, Enterococcus* and *Pantoea*.

Results of this study help to provide more data on mosquito microbiome composition in different species and geographical areas, which can contribute to the development of new vector and pathogen control techniques. Moreover, the challenges and limitations of different methods for mosquito microbiome analyses can be evaluated, which can help to design future studies more effectively.

Session 6-1 – The One Health approach – sand fly-borne diseases as a prime example

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The One Health approach recognizes the interconnectedness between health of humans and animals as well as ecosystems, requiring interdisciplinary collaboration to effectively address emerging infectious diseases.

For vector-borne diseases, this concept is particularly relevant as environmental changes, animal reservoirs, and human activities jointly shape disease dynamics. Sand fly-borne pathogens exemplify these complex interactions in Europe, as *Leishmania* parasites circulate between sand flies and mammalian hosts, including dogs and wildlife, causing zoonotic leishmaniasis in humans. Or similarly, phleboviruses such as Toscana virus and Sandfly fever Sicilian virus are maintained in enzootic cycles involving sand flies and vertebrate hosts, occasionally spilling over to humans. Recent environmental and climatic changes may facilitate the expansion of vectors into new areas, leading to the emergence and establishment of both leishmaniasis and phlebovirus infections in southern and central Europe.

Implementing a *One Health* framework enables integrated surveillance systems that combine entomological monitoring, veterinary screening, and human diagnostics to improve early detection and control. Strengthened cross-sectoral collaboration supports targeted vector control, public awareness, and habitat management strategies. Furthermore, the integration of genomic, ecological, and environmental data – such as vector competence studies and environmental DNA (eDNA) monitoring – enhances understanding of pathogen transmission dynamics. Adopting a comprehensive *One Health* approach is essential for anticipating, preventing, and managing sand fly-borne diseases in an evolving European landscape.

Session 6-2 – Austrian ticks under surveillance: current landscape of ticks and tick-borne pathogens in 2025

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In 2024 a nationwide tick monitoring programme was launched at the Austrian Agency for Health and Food Safety (AGES). In this citizen science project people are encouraged to submit ticks that were found in Austria as well as photographs of specimens that could potentially belong to the genus *Hyalomma*. Received ticks are morphologically identified and subsequently screened for several tick-borne pathogens.

Endemic ticks of Austria are investigated for the presence of *Borrelia burgdorferi* sensu lato (Bbsl), the relapsing fever spirochete *Borrelia miyamotoi*, *Anaplasma phagocytophilum*, *Neoehrlichia mikurensis*, *Spiroplasma ixodetis*, *Rickettsia* spp., and *Francisella tularensis*.

As of beginning of September, more than 5000 ticks from all over Austria were obtained for this year. Most ticks belonged to the genus *Ixodes* (96.7%), followed by *Dermacentor* (2.6%) and *Haemaphysalis* (0.6%). Within these genera we found the following tick species: *I. ricinus*, *I. hexagonus*, *I. acuminatus*, *D. reticulatus*, *D. marginatus* and *Ha. concinna*. The most frequently found pathogens are spirochetes of the Bbsl complex with approximately 25% of all ticks being positive. But also, other tick-borne pathogens were found with *Rickettsia* spp. being the second most frequent organisms in ticks (14.6%), followed by *S. ixodetis* (8.8%), *A. phagocytophilum* (7.6%), *N. mikurensis* (3.8%) and *B. miyamotoi* (1.9%). The infection rates varied between different NUTS3 regions and whether ticks were already attached to hosts or still caught questing for their next bloodmeal.

This year nine *Hyalomma* ticks were already reported to AGES of which some were associated with travel abroad. Findings of this "giant tick" species are increasing and could potentially lead to new threats and diseases like Crimean-Congo Haemorrhagic fever (CCHF) caused by the CCHF virus or spotted fever disease caused by more virulent *Rickettsia* spp. such as *R. aeschlimannii*. So far, none of the investigated *Hyalomma* ticks were positive for CCHF virus, however, in two out of six available *H. marginatum* ticks *R. aeschlimannii* was detected.

Thanks to the contributions of citizen scientists this continuous tick monitoring project provides valuable insights into the tick vector landscape in Austria. Additionally, vector surveillance combined with investigation for associated pathogens can help to identify emerging threats for humans and animals.

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