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Tackling Zoonotic and Vector-Borne Parasites in a Changing Asia-Pacific

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Oral Communications

Session Track:

Companion Animals

#OC008

Anthelmintic Resistance in Canine Hookworms in Australia: Current Status and Emerging Challenges

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ABSTRACT

Anthelmintic resistance in the canine hookworm *Ancylostoma caninum* has emerged as a significant challenge for parasite control in Australia and internationally. This presentation reviews current evidence for resistance in Australian canine hookworms, drawing on molecular surveillance and longitudinal field studies. Benzimidazole resistance-associated β-tubulin single nucleotide polymorphisms (SNPs), particularly F167Y is widespread in Australian A. caninum populations and occurs at high allele frequencies associated with reduced drug susceptibility. Longitudinal monitoring of shelter dogs in Sydney has demonstrated sustained transmission of resistant genotypes, highlighting the potential for dissemination into the broader companion animal population. Surveillance of community dogs in remote central Australia, facilitated by ambient DESS preservation, is extending these observations into geographically isolated and under-sampled populations. Despite these advances, important knowledge gaps remain. Population-scale surveillance is limited, genotype-phenotype relationships require further validation and robust phenotypic assays for assessing resistance, particularly to macrocyclic lactones, remain scarce. To place these findings in a broader biological context, the presentation also considers the northern hookworm, *Uncinaria stenocephala*. Although putative resistance-associated mutations have been detected in this species, convincing evidence of phenotypic resistance is lacking. Collectively, current evidence indicates that assumptions regarding the efficacy of routine anthelmintic treatments can no longer be taken for granted. Future control strategies will require a transition from empirical treatment approaches to routine measurement through quantitative parasitological diagnostics and molecular surveillance to support sustainable hookworm control.

Keywords: *Ancylostoma caninum*; *Uncinaria stenocephala*; anthelmintic resistance; canine hookworm; molecular surveillance; Australia

#OC030

Bridging the Gap in Canine Heartworm Prevention and Management in the Philippines

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ABSTRACT

Background and Objective: Canine heartworm disease (CHD), caused by *Dirofilaria immitis*, is a highly fatal mosquito-borne disease but preventable with consistent prophylaxis. In the Philippines, climatic and environmental conditions favor year-round transmission due to high canine and mosquito populations. Yet, epidemiological data are limited, and standardized local veterinary management practices are lacking. This study integrated CHD epidemiologic data on Filipino veterinarians' diagnostic, treatment, and prevention practices to identify gaps in disease control and aid in the development of a locally adapted heartworm protocol.

Methods: A multi-site prevalence study across the Philippines was conducted, testing 700 blood samples from household and rescued stray dogs in six key areas with high dog populations between 2021 and 2023. Heartworm antigen was detected using a commercial immunochromatographic test kit reported to have 99.5% sensitivity. A separate questionnaire-based survey regarding CHD diagnostic, treatment, and prevention practices was implemented to 682 consenting licensed veterinarians from all over the Philippines.

Results: Overall CHD antigen prevalence was 5.3%, with positive dogs identified across the surveyed regions, and the highest number recorded was in Metro Manila at about 7%. These findings highlight the importance of consistent prophylaxis in reducing infection risk. Among veterinarians, antigen testing was commonly used, but microfilaria identification and differentiation using modified Knott's test was not routinely performed. Although many reported following international guidelines, most preferred slow-kill treatment. Frequently, recommended protocols were modified and late prescription of preventatives was practiced because of client budget constraints.

Conclusion: The demonstrated persistence of CHD, particularly among dogs without preventive protection, together with variability in veterinary diagnostic, treatment, and preventive practices, highlights important gaps in Philippine heartworm control. These findings support the need for an enhanced evidence-based, practical, and locally adapted national protocol to strengthen CHD control in the Philippines.

Keywords: canine heartworm disease, heartworm, epidemiology, Philippines

#OC015

Brugia Lymphatic Filariosis and Detection of Dirofilaria Sabah from Borneo, Malaysia

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ABSTRACT

Lymphatic filariasis remains a debilitating mosquito-borne infection affecting many people in North Borneo Malaysia. Across-sectional study was conducted to determine whether the companion animal host species responsible as the reservoir of *Brugia malayi* and identify *Dirofilaria* species presence in cats and dogs. Blood sampling of 528 domestic animals (292 cats and 236 dogs) was conducted across eight villages with reported human Brugian filariasis cases in Pitas and Beluran districts, Sabah. Samples underwent initial screening via conventional microscopy examination, followed by real-time and conventional PCR to verify *Brugia* & *Dirofilaria* species. Two villages demonstrated highest animal infection rates, with prevalence slightly over 30% for *Brugia* sp. indicating active transmission. Overall, cats exhibited higher odds of *B. malayi* infection, with over 5.5 times increase in risk, compared to dogs ($p < 0.05$). Microfilaraemia rates and DNA positivity reflected higher infection in cats (20.2% and 33.8%) than dogs (3.8% and 7.6%) respectively. Among the 508 samples, 209 were positive for *Dirofilaria sp*. by at least one method, giving an overall prevalence of 41.14%. Microscopy detected 37.99%, HRM-qPCR detected 34.84%, and cPCR detected 32.28% of the positive samples. cPCR, revealed that D. immitis infection was predominant in dogs (25.59%), whereas D. repens was more common in cats (7.09%). During an investigation of animals as reservoirs for the filarial parasite, two cats co-infected with *B. malayi*, Mf of a *Dirofilaria* species ('Sabah') with an average length of 299.1 μm were detected. Whole genome amplification and genome sequencing of 24 individual Mf enabled phylogenetic analysis of mitochondrial genomes, and analysis of specific mitochondrial and nuclear barcode regions. The three Mf groups formed distinct clusters and could not be identified by comparison with available reference sequences. The cluster 'Sabah' formed a monophyletic group with the zoonotic species *Dirofilaria asiatica* and *Dirofilaria* sp. 'Thailand'.

Keywords: Lymphatic Filariasis, *Brugia malayi*, *Dirofilaria* Sabah, Cats, Dogs

#OC026

Characteristics of Tick Infestation in Dogs in Indonesia: Prevalence, Species Diversity, and Pathogen Detection

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ABSTRACT

Ticks are important ectoparasites of companion animals and serve as vectors for a wide range of pathogens affecting both animal and public health. However, comprehensive information on tick infestation, species diversity, and tick-borne pathogens in pet animals in Indonesia remains limited. This study summarized findings from a single research project investigating tick prevalence, species diversity, and pathogen detection in dogs in Indonesia. Tick identification was performed using morphological characteristics, while pathogen detection was conducted using polymerase chain reaction (PCR). The results showed that *Rhipicephalus sanguineus* was the predominant tick species infesting dogs, with infestation prevalences of 67.90% in police dogs, 100% in military dogs, and 7.79% in shelter dogs. Additional tick species, including *Rhipicephalus microplus* and *Haemaphysalis wellingtoni*, were also identified in companion animals and their surrounding environment, although *R. sanguineus* remained the dominant species associated with dogs. Molecular analysis detected *Rickettsia felis* and *Anaplasma platys* in *R. sanguineus*, whereas *Borrelia* spp. were not detected. Previous blood examinations of infested dogs also demonstrated the presence of *Ehrlichia canis*, *Babesia* spp., and *Anaplasma* spp. infections. These findings demonstrate that *R. sanguineus* is the principal tick infesting pet dogs in Indonesia and acts as a potential vector for several clinically important tick-borne pathogens. This study highlights the need for continuous surveillance of tick infestation and tick-borne pathogens to support effective ectoparasite control and reduce the risk of vector-borne diseases in companion animals and humans.

Keywords: dog; tick; tick-borne pathogens; *Anaplasma*; *Rickettsia*

#OC005

Field efficacy and safety of topical esafoxolaner/eprinomectin/praziquantel against natural Lynxacarus radovskyi infestation in cats

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ABSTRACT

This open-label, uncontrolled field study evaluated the efficacy and safety of esafoxolaner in a topical formulation (NexGard Combo®) for the treatment of natural infestations with *Lynxacarus radovskyi* in 16 privately owned cats. Cats were recruited from three veterinary clinics based on inclusion criteria requiring confirmation of mite infestation and good health. Clinical assessments and mite scoring were performed on Day 0, Day 15, and Day 30 following a single topical treatment. NexGard Combo® demonstrated complete acaricidal activity, with all cats free of detectable mites by Day 30. Clinical signs such as pruritus, alopecia, and scaling improved significantly during the study period. No adverse events were reported.

Keywords: Cats; *Lynxacarus radovskyi*; esafoxolaner; efficacy

#OC022

Integrated Transcriptomic and Secretomic Analysis of Tissue-Arrested l3 of Ancylostoma ceylanicum and Their in Vitro Activation

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ABSTRACT

Tissue-arrested larvae are widespread among parasitic nematodes, and their reactivation poses a significant threat to both the livestock industry and public health. A deeper understanding of the tissue-arrested larvae development process is critical for effective management. However, current knowledge of their development remains limited. Using *Ancylostoma ceylanicum* as a model, a preliminary investigation into the morphology, transcriptomics, and secretomics of its tissue-arrested larvae (TaL3) was conducted. In this study, infective L3 (iL3) of *A. ceylanicum* were subcutaneously injected into 6-week-old female KM mice (500 larvae per mouse), and TaL3 were collected from muscle tissues 16 days post-infection. The average length of TaL3 was 681.7 ± 28.4 μm, which is significantly longer than that of iL3 (624.1 ± 22.2 μm) ($P < 0.01$). The average width of TaL3 was 27.8 ± 3.0 μm, while that of iL3 was 24.1 ± 2.5 μm. Besides, TaL3 exhibited distinct cavities, excretory orifices, and more fully developed intestinal tubes and esophageal bulbs than those of iL3. In vivo anthelmintic assays showed that high-dose ivermectin (1 mg/kg) could not completely eliminate TaL3, with a reduction rate of 81.7%. Furthermore, an in vitro culture system was established, achieving a 90% feeding rate for TaL3, which could be used for exploring TaL3 development. Finally, the transcriptomic profiling of TaL3 was sequenced, ribosomal-associated proteins, ubiquitin B, superoxide dismutase, and heat shock protein displayed higher transcription levels. Secreted proteins of TaL3 were analyzed, and a total of 609 peptides (including 526 unique peptides) and 338 proteins were identified. GO analysis showed that these proteins are mainly involved in metabolic processes, energy metabolism, and immune-related responses. KEGG pathway enrichment analysis revealed significant enrichment in the glycolysis/gluconeogenesis pathway, with multiple related enzymes identified. This study provides solid experimental evidence for elucidating diapause regulatory mechanisms.

Keywords: diapause; hookworm; morphology; nematode; transcriptome

#OC031

Looking at the Other Side: Evaluating Dog Owners' Perspective on Canine Heartworm Control in the Philippines

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ABSTRACT

Background and Objective: Canine heartworm disease (CHD), caused by Dirofilaria immitis, remains a significant but preventable threat to canine health worldwide. In the Philippines, effective prevention is particularly important given the unavailability of a registered adulticide drug. Dog owners' compliance is critical in successful CHD prevention and control. Thus, this study evaluated the knowledge, attitudes, and practices (KAP) of Filipino dog owners regarding CHD prevention and management and examined factors influencing these practices.

Methods: A cross-sectional survey was conducted among 1,087 dog owners from selected cities across Luzon, Visayas, and Mindanao. A questionnaire was prepared to obtain demographic information, and dog owners' knowledge of CHD, attitudes toward CHD management, and associated practices. The questionnaire was pre-tested and made available in multiple local languages. Ethical approval was obtained from the University of the Philippines Los Baños Research Ethics Board, and informed consent was secured from all participants.

Results: The survey demonstrated varying levels of knowledge, attitudes, and preventive practices across regions, with notable gaps in awareness and consistent implementation of heartworm prevention. Overall, the majority of respondents have poor knowledge, a good attitude, and moderate-to-good practices regarding CHD. These findings highlight challenges in translating veterinary recommendations into effective owner practices.

Conclusion: Establishing baseline KAP data on CHD provides an essential foundation for developing targeted, culturally appropriate strategies and strengthening veterinarian–owner communication. Improving owner understanding and preventive behavior may contribute significantly to reducing CHD burden and advancing responsible pet ownership in the Philippines.

Keywords: Heartworm, dog owners, KAP, Dirofilaria immitis

#OC037

Molecular Detection and Characterization of Haemoparasites in Domestic Cats from Chennai Region of Tamil Nadu

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ABSTRACT

Haemoparasitic infections in domestic cats constitute an emerging concern in small animal practice due to their non-specific clinical manifestations, potential for multisystemic involvement, and frequent underdiagnosis. This study aimed to determine the prevalence, molecular identity and phylogenetic relationships of major feline haemoparasites in Chennai region of Tamil Nadu. A total of 200 blood samples were collected from cats presented to the Madras Veterinary Teaching Hospital, chennai and from community cats in and around Chennai, with clinical signs suggestive of haemoprotozoan or rickettsial infections. Giemsa-stained peripheral blood smears demonstrated pleomorphic intra-erythrocytic forms consistent with *Cytauxzoon* spp. and piroplasms of *Babesia* spp., whereas, gamonts of *Hepatozoon felis* was not detected microscopically. PCR targeting 18S rRNA gene revealed an overall haemoparasites prevalence of 12 per cent (24/200) . Sequencing analysis confirmed the occurrence of three haemoparasite species, viz., *Cytauxzoon felis* 1.5 per cent (3/200), *Babesia gibsoni* 1.5 per cent (3/200), and *Hepatozoon felis* 1 per cent (2/200), with sequence identities ranging from 97.39 - 100 per cent relative to GenBank reference isolates. Phylogenetic analysis indicated considerable genetic heterogeneity among the detected haemoparasites. While *C. felis* isolates clustered within domestic cat, wild felid, and India-specific clades, the *B. gibsoni* isolates formed a clearly separate lineage from all earlier Indian isolates from dogs, confirming that this study forms the first documented occurrence of *B. gibsoni* infecting cats in India. *H. felis* isolates clustered with domestic cat isolates reported from European and Middle East Asian countries.

Keywords: Haemoparasites, PCR, Phylogeny, Domestic cats

#OC032

Molecular Detection of Brugia Malayi and Dirofilaria Immitis in Owned Dogs and Cats in Northern Vietnam

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ABSTRACT

Dogs and cats can serve as hosts for several filarial nematodes, including species of the genera *Dirofilaria* and *Brugia* within the family Onchocercidae. These mosquito-borne parasites are of considerable veterinary and public health importance because of their zoonotic potential. However, information on filarial infections in owned dogs and cats in northern Vietnam remains limited. This study aimed to determine the prevalence of filarial parasites in owned dogs and cats using polymerase chain reaction (PCR) and sequencing analyses. A total of 232 blood samples were collected from dogs and cats in a few provinces: Lang Son, Hai Duong, and Bac Giang in northern Vietnam using a conventional sampling method. All samples were screened for filarial infection by PCR targeting the cytochrome *c* oxidase subunit I (COI) gene. Overall, 3.45% (8/232) of the animals tested positive for filarial parasites, including 4.24% (7/165) of dogs and 1.49% (1/67) of cats. Following sequencing, five samples (3.03%) from dogs in Lang Son and Hai Duong were identified as *Brugia malayi*. Three samples (1.29%) were identified as *Dirofilaria immitis* consisting of two from dogs in Hai Duong and one sample (1.49%) from a cat in Bac Giang. In conclusion, this study provides molecular evidence of *Brugia malayi* and *Dirofilaria* immitis in owned dogs and cats in northern Vietnam. These findings provide valuable baseline information on the geographical distribution and molecular detection of filarial parasites and may contribute to assessments of their potential risks to animal and human health.

Keywords: *Dirofilaria immitis*; *Brugia malayi*; zoonotic disease; dog; cat; northern Vietnam

#OC020

Prevalence of Soil Transmitted Helminths of Zoonotic Significance Among Cats in Chennai

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ABSTRACT

Soil transmitted helminths (STHs) are important zoonotic parasites widely distributed in the environment, posing risks to both animals and human beings. Cats, due to their outdoor behavior, play a significant role in environmental contamination and transmission of these parasites. This study examined a total of 200 feline faecal samples collected from Madras Veterinary College teaching hospital as well as from animal shelters including stray and pet cats across Chennai. The collected faecal samples were examined by routine sedimentation and floatation technique. *Toxocara* spp. (23%) was the most common zoonotic parasite, followed by *Ancylostoma* spp. (9%), with a lower incidence of *Strongyloides* spp. and *Taenia* spp. Mixed infections occurred in 4 per cent of faecal samples. Other parasites such as oocysts of *Cystoisospora* spp., eggs of *Dipylidium caninum*, *Diphyllobothrium latum* and *Capillaria* spp. were also identified in the faecal samples examined. The overall prevalence of GI parasite prevalence was found to be 54.50 per cent, while zoonotic parasites accounted for 39.50 per cent. Risk factor analysis showed that kittens had the highest infection rates, followed by young and adult cats. Parasite intensities were generally mild to moderate, with heavier infections observed with *Toxocara* spp. and *Ancylostoma* spp.

#OC038

The Microbiome of Fleas in Malaysia and Thailand: Detection of Novel Symbiont Strains

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ABSTRACT

Ctenocephalides felis and *Ctenocephalides orientis* fleas commonly infest cats and dogs, respectively, in Southeast Asia, whereas *Xenopsylla cheopis* is prevalent on rodents. These fleas are associated with numerous bacteria, including known pathogens such as *Rickettsia felis* and *Bartonella henselae*, or symbionts including *Wolbachia*. Our study aimed to investigate the distribution of flea pathogens and symbionts across multiple locations in Malaysia and Thailand, and determine the host or environmental factors influencing bacteria distributions. *Ctenocephalides felis* were collected from stray cats from five locations in Malaysia, whereas *C. orientis* were obtained from dogs in six villages in Nan province, Thailand. In addition, a small number of *X. cheopis* were collected from rodents in Nan province. Bacterial profiling was achieved by near full-length 16S rRNA amplicon nanopore sequencing, and the mitochondrial cytochrome oxidase I (*coi*) gene was amplified to determine flea mitochondrial haplotype. Illumina sequencing of selected specimens was performed to obtain genome assemblies from potentially novel bacteria. Preliminary analysis revealed the dominance of *Rickettsia asembonensis* in *C. orientis*. In contrast, *Rickettsia* was not detected in *C. felis* tested so far. Five *Wolbachia* strains were identified, with distinct association of symbiont strains with flea species and sex. *Bartonella clarridgeiae* was also detected in *C. felis,* but not in *C. orientis*. Metagenomic sequencing revealed a novel *Wolbachia* strain in *C. orientis* and *Candidatus* Mesenet (a close relative of *Wolbachia*) in *X. cheopis*. Bacterial profiling in additional *C. felis* and analyses of flea mitochondrial haplotypes are in progress. Our findings suggest that multiple bacteria co-exist in individual *Ctenocephalides* fleas and the distribution of the bacteria is influenced by flea species and sex. The interactions between the pathogens and symbionts, and how these might affect pathogen transmission, remain to be investigated.

Keywords: *Ctenocephalides, Xenopsylla, Wolbachia, Rickettsia, Bartonella*.

#OC034

Unmasking Dirofilaria sp. in Southern Thailand: First Molecular Identification of Canine Subcutaneous Dirofilariosis

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ABSTRACT

Dirofilaria repens (Spirurida: Onchocercidae) is a causative agent of canine subcutaneous dirofilariosis, an infection predominantly documented in Europe. Currently, the taxonomic nomenclature of the Asian *Dirofilaria* clade remains controversial, with three names having been proposed: *D. asiatica*, *D. hongkongensis*, and *D. minor*. Adult nematodes typically inhabit subcutaneous tissues and fascial planes. Although the majority of infected hosts remain asymptomatic, dermatological manifestations are occasionally reported. While autochthonous cases of adult canine subcutaneous dirofilariosis have not previously been documented in Thailand, this report describes a confirmed case of testicular localization in a dog, substantiated by molecular diagnostic techniques. Four adult filarial nematodes were surgically removed from the subcutaneous tissue of the testes during the castration of three male dogs in southern Thailand. The specimens underwent microscopic morphological examination followed by genomic DNA extraction. Conventional PCR targeting the cytochrome c oxidase subunit 1 (COX1) gene was performed on all extracted DNA samples. The resulting amplicons were sequenced using Sanger sequencing, and a phylogenetic tree of *Dirofilaria* spp. was subsequently constructed using MEGA software. All four subcutaneous nematodes were recovered from the testicular surface of the affected dogs, comprising three females and one male. Nucleotide BLAST analysis of the Sanger sequencing reads revealed 100% identity to previously deposited *Dirofilaria asiatica* sequences. Furthermore, phylogenetic analysis of the cox1 gene placed the specimens within a monophyletic clade alongside D. asiatica identified in domestic dogs from Sri Lanka and *Dirofilaria* sp. "hongkongensis" isolated from a human infection in India. Adult filarial nematodes recovered in this study were confirmed molecularly as *Dirofilaria asiatica*. These findings represent the first confirmed report of canine subcutaneous dirofilariosis in Southern Thailand. Consequently, expanded epidemiological surveillance and the routine implementation of molecular diagnostic tools are warranted. Furthermore, the taxonomic relationships among *D. asiatica*, *D. hongkongensis*, and *D. minor* require further clarification.

Keywords: *Dirofilaria spp.*; Subcutaneous; Canine; COX1 gene; Phylogenetic analysis

#OC010

Vector-Borne Pathogens in Dogs from Afghanistan: Diversity and Zoonotic Potential

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ABSTRACT

Canine vector-borne pathogens (CVBPs), especially those that are zoonotic, are becoming increasingly important due to climate change and greater animal mobility. However, data on the actual prevalence of these infections in dog populations are lacking in many Western and South-Central Asian countries, including Afghanistan. This study aimed to assess the molecular prevalence of CVBP infections among stray and owned dogs in different regions of the country. Between February 2023 and August 2025, blood DNAs from 100 dogs with outdoor lifestyles from four provinces of Afghanistan, namely Kabul, Kunduz, Mazar-i-Sharif, and Takhar, were tested and screened for *Hepatozoon* spp., *Babesia* spp., *Leishmania* spp., filarioid helminths, and *Bartonella* spp. by real-time and/or conventional PCR followed by Sanger sequencing. Overall, 81% of the dogs were positive for at least one VBP. *Hepatozoon* canis was the most common (68%, found in all provinces), followed by *Bartonella vinsonii* subsp. *berkhoffii* (18%, all provinces), *Babesia* vogeli (4%, in three provinces), *Acanthocheilonema* sp. (4%, in three provinces), *Leishmania infantum* (2%, in Kunduz), and *Babesia negevi* (1%, in Mazar-i-Sharif). Co-infections were present in 12% of the dogs. To our knowledge, this is the first epidemiological study of CVBPs in Afghanistan, revealing the co-circulation of *H. canis*, *Bartonella vinsonii berkhoffii*, L. *infantum*, *B. vogeli*, *B. negevi*, and *Acanthocheilonema* sp. These results highlight the importance of controlling endoparasites and ectoparasites in owned dogs and emphasize the need to manage feral animal populations to reduce VBP transmission.

Keywords: Babesiosis; Bartonellosis; Domestic dogs; Hepatozoonosis; Leishmaniosis; One Health; Vector-borne pathogens; Zoonosis

#OC002

Wound Myiasis-Causing Flies from Dogs and Cats in Southern China

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ABSTRACT

Wound myiasis is a parasitic infestation of vertebrate tissues by dipterous larvae, causing significant morbidity in tropical and subtropical regions. Despite its clinical importance, limited data exist on the causative fly species and their distribution in China. This study investigated the species diversity, clinical presentations, and geographic distribution of wound myiasis-causing flies in Southern China. A total of 52 wound myiasis samples were collected from dogs and cats between 2020 and 2026. All specimens were identified through integrated morphological examination and molecular analysis targeting the COI gene. Morphological and molecular identifications (>95%) showed high concordance, confirming four fly species: *Chrysomya bezziana* ((28/52, 53.8%), *Lucilia sericata* (11/52, 21.2%), *Chrysomya megacephala* (8/52, 15.4%), and *Chrysomya rufifacies* (5/52, 9.6%). Notably, different fly species were associated with distinct clinical presentations: *C. bezziana* and *C. megacephala* infestations involved deep wounds with severe tissue destruction and foul odor, indicating aggressive clinical progression, while *L. sericata* cases presented with chronic superficial ulcers and minimal inflammation. Interestingly, *C. rufifacies* was predominantly found co-occurring with *C. megacephala* (4/5). *C. bezziana* was exclusively found in dogs, while the other three species infested both dogs and cats. Phylogenetic analysis of COI sequences placed local strains within well-supported clades corresponding to each species, with some haplotypes showing close affinity to populations reported from Southeast Asia. These results provide the first comprehensive survey of wound myiasis-causing flies from dogs and cats in China, demonstrating that combined morphological-molecular identification is essential for accurate species diagnosis. All four fly species are of public health importance as they are recognized zoonotic agents capable of causing myiasis in humans. Furthermore, aside from *C. bezziana*, the remaining three species—*L. sericata*, *C. megacephala*, and *C. rufifacies*—are reported for the first time in cats and dogs in China, highlighting the potential threat these parasites pose to both companion animals and human health in the region.

Keywords: Wound myiasis; morphological identification; COI; southern China; *Chrysomya bezziana*; clinical presentation; geographic distribution

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#OC021

A Fasciola Gigantica TGF-β Ligand-Like Protein,FGTLP Mediates Host Liver Injury Through Triggering Macrophage Polarization

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ABSTRACT

Liver injury caused by the acute phase of **Fasciola gigantica** infection poses a significant threat to both human and animal health. Macrophage polarization to the M1 phenotype, via the production of pro-inflammatory components, plays a crucial role in the occurrence and development of hepatic cholangiopathy. Therefore, investigating the molecular mechanisms underlying the early triggering of M1 macrophages and subsequent liver pathology during **F. gigantica** infection is essential for elucidating **this process.** In our studies, we utilized a eukaryotic expression system to produce **recombinant** r*Fg*TLP **in vitro**, **demonstrating** its presence in the *Fg*ESP. Luciferase assay **further demonstrated** its TGF-β ligand activity. Functionally, r*Fg*TLP induced M1 polarization of the mouse-derived macrophage cell line (RAW264.7) **in vitro**, and inhibitor assays revealed that this process is **mediated by** the NF-κB signaling pathway. Furthermore, **in vivo** injection of r*Fg*TLP in mice was found to mediate hepatic injury. These findings elucidate the mechanism by which *Fg*TLP drives M1 macrophage polarization, providing crucial insights into the pathogenicity of **Fasciola gigantica** and offering a potential therapeutic target for fasciolosis.

Keywords: Functional protein; Liver injury; Trematode; TGF-β signaling pathway; Macrophage

Funding: National Natural Science Foundation of China (32660989)

#OC014

Clinical Preparedness for Severe Fever with Thrombocytopenia Syndrome in Companion Animal Practice: A Nationwide Survey from Japan

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ABSTRACT

Severe fever with thrombocytopenia syndrome (SFTS) is an emerging tick-borne zoonotic disease in East Asia. In Japan, direct transmission from companion animals to humans, including veterinary professionals, has made SFTS a practical occupational risk in small animal practice. This study aimed to describe how private companion animal clinics in Japan recognize and manage suspected SFTS cases.

An anonymous nationwide online questionnaire survey was conducted from 27 June to 15 July 2026 among veterinarians responsible for clinical policies in companion animal clinics. Descriptive statistics were calculated, and exploratory analyses examined associations between clinic size, regional SFTS occurrence, and selected clinical-management outcomes.

A total of 863 responses were obtained from all 47 prefectures. Confirmed SFTS cases had been managed by 20.6% of respondents, whereas only 15.1% reported that their clinics could provide hospitalization for suspected cases. Preparedness varied across infection-control measures: gloves and gowns were prepared or used by 83.9% and 63.2%, respectively, but eye protection was less common (eye guards or goggles, 37.7%; face shields, 37.1%). Practical training for donning and doffing personal protective equipment was not conducted in 66.3% of clinics, and only 2.8% had clear in-clinic post-exposure procedures. In exploratory multivariable analysis, the number of nursing staff, but not veterinarians, was significantly associated with hospitalization, acceptance of referral cases, and staff participation under protective measures. Clinics in prefectures with reported estimated SFTS infection areas showed higher risk perception, clinical experience, reception-based screening, and altered patient flow; however, post-exposure procedures and PPE training did not differ clearly by region.

This nationwide survey shows that SFTS is already recognized as a clinical and occupational issue in Japanese companion animal practice, but preparedness remains heterogeneous. Practical clinic-level protocols, staff training, and regional support systems are needed to connect animal health, occupational safety, and public health.

Keywords: SFTS; tick-borne zoonosis; companion animal practice; occupational exposure; questionnaire survey

#OC029

Detection of Plasmodium spp. and Brugia spp. in Free-Ranging and Captive Long-Tailed Macaques (Macaca fascicularis Raffles, 1821) from Selected Regions in the Philippines

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ABSTRACT

Long-tailed macaques (*Macaca fascicularis* Raffles, 1821) are synanthropic nonhuman primates that are widely distributed across Southeast Asia and survive in various types of habitats. Environmental changes such as deforestation, forest fragmentation, and agriculture have caused long-tailed macaques to inhabit areas near humans, bringing with them zoonotic diseases. This interaction raises concerns about potential disease transmission, particularly vector borne parasites, such as simian malaria and filarial worms. Among these are *P. knowlesi* and *Brugia* sp., which are especially known to be zoonotic and are difficult to eliminate in some countries such as Malaysia and Indonesia due to their presence in these wildlife reservoirs. This study aimed to detect the presence of *Plasmodium* sp. and *Brugia* sp. from selected regions in the Philippines where macaques are living near human settlements. Thirty-three blood spot samples from free-ranging macaques of Mindanao and forty-one samples from captive macaques in Luzon were collected. DNA extraction and real-time PCR for detection was then performed at the Malaria Research Centre, Universiti Malaysia Sarawak. Real-time PCR using the TaqMan assay with primer pairs Plasmo 1 and Plasmo 2 for *Plasmodium* detection, and Hhal repeat for the detection of *Brugia* parasites was used. For *Plasmodium* detection, a total of 12 positive samples were detected. All positive samples were from Mindanao, and samples from Luzon were all negative. Future steps for this study is to determine the specific species of the Plasmodium sp. positive samples. On the other hand, the qPCR for *Brugia* sp. detection yielded no positive results from any of the samples. Results from this study are the first records of malaria and filariosis detection in free-ranging and captive long-tailed macaques from selected regions in the Philippines.

Keywords: *Brugia* sp., filariosis, *Plasmodium* sp., simian malaria, zoonosis

#OC033

Expanding the Universe of Primate Filariosis: Potentially Novel Species of Mansonella, Dirofilaria, and Dipetalonema in Captive New World Monkeys from Thailand

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ABSTRACT

Despite the fact that primates comprise over 500 extant species and are widely distributed across the world, the species diversity and evolutionary dynamics of their filarioid parasites, particularly in New World monkeys, remain poorly explored. Here, blood samples from captive monkeys, including Tufted capuchin (*Sapajus apella*) and Mantled guereza (*Colobus guereza*), alongside adult nematode specimens discovered in the abdominal cavity of a captive spider monkey (*Ateles* sp.) were collected. Morphological examination and DNA sequencing of the *cox1* locus (843 bp) revealed monoinfections of *Mansonella* sp., *Dirofilaria* sp., and *Dipetalonema* sp., respectively. *Mansonella* sp. shared 88.36% similarity with human-infecting *Mansonella perstans* (OQ633019-OQ633019), but phylogenetically clustered with *Mansonella mariae* (KX932483) from a Weddell's saddle-back tamarin (*Saguinus* sp.) in Peru, diverging approximately 13.4 (95% HPD: 7.07-21.12) million years ago (Mya). *Dirofilaria* sp. exhibited 93.00-93.12% similarity with those Onchocercidae sp. 'Belitung I' (PX995895-PX995902) from long-tailed macaques (*Macaca fascicularis*) in Sumatra, Indonesia, forming a monophyly since the Miocene epoch (11.29, 5.22–17.67 Mya). Furthermore, *Dipetalonema* sp. had 94.87% similarity with *Dipetalonema gracile* (NC066230) from a pied tamarin (*Saguinus bicolor*) in Brazil and clustered with New World monkey-specific *Dipetalonema graciliformis*, *Dipetalonema robini*, *D. gracile*, and *Dipetalonema* spp., dating a Pliocene divergence of 5.94 (3.38-8.88) Mya. These preliminarily genetic analyses and phylogenetic hypotheses suggest all three isolates represent potentially novel filarioid species, expanding the epidemiological perspective and the universe of primate filariasis. Further investigations integrating complete mitochondrial genomes, nuclear genetic markers, and detailed parasite morphometry are currently underway to clarify their evolutionary relationships.

Keywords: primate; filariosis; *Mansonella*; *Dirofilaria*; *Dipetalonema*; Thailand

#OC004

Experimental Host Switching Reveals a Stepwise Adaptation of Sarcoptes scabiei to a Novel Host

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ABSTRACT

Background *Sarcoptes scabiei* is an obligate ectoparasite that infests more than 150 mammalian host species worldwide, yet the mechanisms underlying cross-species transmission and host adaptation remain poorly understood. To investigate this process, we established an experimental host-switching model to investigate the biological and molecular processes driving adaptation to a novel host.

Methods Rabbit-derived *S. scabiei* mites were used to establish infestation in golden hamsters under transient dexamethasone-induced immunosuppression. Clinical progression, mite burden, and horizontal transmission were monitored. Comparative transcriptomic analyses were performed between rabbit-derived mites and hamster-adapted mites to identify molecular changes associated with host adaptation.

Findings Successful and persistent infestations were achieved only in hamsters receiving moderate to high levels of immunosuppression, with severe clinical manifestations and high mite burdens observed. Following adaptation, hamster-derived mites efficiently transmitted among immunocompetent hamsters, demonstrating successful establishment in a new host species. Transcriptomic profiling identified 459 differentially expressed genes between rabbit-derived and hamster-adapted mites. Host adaptation was characterized by coordinated upregulation of membrane transport, proteolytic regulation, extracellular matrix remodeling, lipid metabolism, and detoxification pathways, accompanied by suppression of lysosomal and digestive functions. Gene set enrichment analysis further identified membrane trafficking, cell adhesion, immune-related pathways, and stress-response signalling as key adaptive processes, indicating that host-interface remodeling is a central molecular feature of *S. scabiei* adaptation to a novel host. **Interpretation** These findings provide experimental evidence for a stepwise model of *S. scabiei* host switching, in which transient immunosuppression facilitates initial colonization of a new host, enabling parasite adaptation and subsequent efficient transmission within the new host species. Our study identifies immunocompromised hosts as potential catalysts of cross-species transmission and provides mechanistic insights into the molecular basis of host adaptation in this globally important ectoparasite.

#OC006

Full-Length Mlitochondrial ATP6 Gene-Based Genealogy of Zoonotic Echinococcus granulosus Sensu Stricto Genotypes (G1 and G3) Circulating in Small Ruminants in North India

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ABSTRACT

Cystic echinococcosis (CE) is a neglected parasitic zoonosis caused by the species complex *Echinococcus granulosus* sensu lato. Among different species under the complex, *E. granulosus* sensu stricto (s.s.) is incriminated to cause most human CE cases worldwide. The present study targeted molecular characterization, genotyping, and population structure and haplotype network analyses along with global diversity assessment of *E. granulosus* s.s. species based on the full-length mitochondrial *ATP6* gene. The vital organs (heart, lungs, liver, and spleen) of 1049 slaughtered small ruminants (sheep and goats) from North India (Haryana, Chandigarh and Himachal Pradesh), were screened for the presence of hydatid cysts. Out of 1049 animals screened, the vital organs of 85 (8.1%) exhibited the presence of hydatid cysts. However, hydatid cysts recovered from the vital organs of 33 animals were found viable. The cladistics revealed different clades of both the genotypes, G1 and G3. The population structure analysis revealed 35 haplotypes with high haplotype (0.920 ± 0.014) and low nucleotide (0.00453 ± 0.00018) diversities for 119 full-length *ATP6* gene sequences retrieved from near complete mitogenome GenBank-catalogued *E. granulosus* s.s. sequences (n = 104) along with 15 full-length sequences generated herein. The finding evinced recent population expansion, as was observed from the median-joining haplotype network, where sequences for the G1 and G3 genotypes exhibited star-shaped configuration. High genetic differentiation (F_{ST} = 0.5978) and low gene flow (Nm = 0.1681) were recorded between the populations corresponding to respective genotypes (G1 and G3). Based on the full-length *ATP6* gene, the findings of the present study suggested the expansion of *E. granulosus* s.s. (G1 and G3 genotypes) populations globally. The observations of this study also highlighted the role of small ruminants in the maintenance and circulation of the highly zoonotic *E. granulosus* s.s. population in North India.

Keywords: Cystic echinococcosis; *Echinococcus granulosus* sensu stricto; India; small ruminants; zoonosis

#OC007

Genotyping and Virulence Evaluation of a Toxoplasma gondii Strain Derived from a Squirrel Monkey (Saimiri sciureus)

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ABSTRACT
Toxoplasma gondii (T. gondii) is an obligate intracellular protozoan parasite that can infect almost all warm-blooded animals, including humans and wild animals. The isolation, genotyping and virulence evaluation of *T. gondii* wild-type from wild animals is of great significance for elucidating its transmission patterns and assessing public health risks. To clarify the biological characteristics of a *T. gondii* field strain isolated from a dead ring-tailed lemur in Sichuan, China, genotyping was performed and its virulence was evaluated. Liver tissue homogenate collected from the squirrel monkey was intraperitoneally inoculated into five BALB/c mice. PCR-RFLP based on 12 genetic markers and ROP5/ROP18 allelic genotypes was applied for genotyping. Then, the isolated tachyzoites from mice were cultured in Vero cells for proliferation and a mouse assay was carried out to evaluate the virulence of the isolate. The results showed that the wild *T. gondii* strain belongs to genotype III and exhibited the 3/3 allelic profile. In mouse assay, 3/5 mice dead during the infection and the isolate was found highest in brain (80%). However, no *T. gondii* - specific IgG antibodies were detected in any infected mice. These results demonstrate that this *T. gondii* type III isolate can cause severe infection in monkeys, especially with high brain parasitic burden and absence of detectable antibody response, underscoring the importance of close monitoring and risk assessment for primate populations.

Keywords: *Toxoplasma gondii*; squirrel monkey; genotyping; virulence evaluation

#OC024

Global Species-Level Identification of Leishmania Across Humans, Animals, and Vectors Using a Novel Portable Nanopore Sequencing Platform

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ABSTRACT

Background and aims: Leishmaniases are targeted for elimination as a public health problem by 2030 under the WHO Neglected Tropical Diseases (NTDs) road map 2021-2030. Achieving these goals requires innovative diagnostic tools to strengthen global surveillance, particularly under rapidly shifting epidemiological conditions. We developed and validated a novel long-read metabarcoding sequencing assay to accurately capture the *Leishmania* species diversity and evaluated its diagnostic performance against widely used qPCR assays.

Methods: A metabarcoding assay targeting HSP70 gene was established using portable Oxford Nanopore Technologies' MinION™ platform integrated with a curated bioinformatic pipeline and reference database for species-level identification. Optimisation used 22 cultured isolates representing 15 *Leishmania* species across four subgenera (*Leishmania*, *Viannia*, *Mundinia*, and *Sauroleishmania*), together with 26 contrived communities simulating sympatric and co-infection scenarios reported from diverse endemic regions. Diagnostic performance was benchmarked against an HSP70 qPCR using sandflies, six clinical sample type from humans and dogs (skin biopsies, saliva, lesion scarification slides, swabs, lymph node aspirates, and blood) collected from both the Old and New Worlds. Additionally, HSP70 metabarcoding was applied to evaluate the specificity of a widely employed kDNA-targeting qPCR assay in *Leishmania infantum* diagnostics.

Results: The assay accurately identified all 22 cultured isolates, both individually and in contrived communities, with 99.65–100% identity against the reference database. Field validation demonstrated weak to perfect agreement with HSP70-qPCR (Cohen's Kappa) while detecting more positives across most specimen types. Importantly, *Leishmania* species unexpected for the host or geographic setting were identified in dogs and sandflies from Europe, and multi-species co-infections were detected in humans and dogs from Brazil. Evaluation of the kDNA qPCR assay demonstrated amplification of seven phylogenetically diverse non-*L. infantum* species in both cultured isolates and clinical samples, highlighting the potential for species misidentification without confirmatory typing.

Conclusions: This metabarcoding assay enables robust species-level identification and co-infection detection across diverse sample types, outperforming conventional assays and supporting global surveillance and control targets.

Keywords: HSP70, metabarcoding, long read nanopore sequencing, specificity.

#OC016

Identification of Cestodes in Urban Bird Pest Corvus Splendens) in Seberang Perai, Penang Malaysia

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ABSTRACT

Cestodes of the genus *Raillietina* are well-known poultry parasites, posing potential veterinary risks if transmitted from wild avian reservoirs. House crows (*Corvus splendens*) may act as hosts, but *Raillietina* species diversity in urban crow populations remains poorly characterized due to limited genetic data in Genus *Raillietina* in NCBI GenBank. In July 2026, 91 house crows were sampled from Mak Mandin (Central Seberang Perai) and 10 from Bandar Tasek Mutiara (South Seberang Perai), Penang, during the Shooting Program. Dissection yielded 20 tapeworms from Mak Mandin and 17 from Bandar Tasek Mutiara. Morphological examination and molecular identification using 18S rDNA primers confirmed 7 tapeworms from Mak Mandin and 17 from Bandar Tasek Mutiara as *Raillietina* spp. Phylogenetic trees constructed using ND1 gene region primers (JB11/JB12) revealed three distinct clades within the *Raillietina tunetensis* complex. The identified clades indicate the presence of three distinct *Raillietina* species hosted by local house crows. Given that *Raillietina* species infect domestic poultry, these findings highlight a potential transmission pathway between wild crows and veterinary hosts. However, establishing exact veterinary significance requires definitive species-level identification. A critical limitation remains the scarcity of reference genetic sequences in GenBank for *Raillietina*. Future work must integrate comprehensive morphological measurements with molecular datasets and calculate pairwise genetic divergence/distance to resolve taxonomic boundaries relative to deposited sequences. House crows in Seberang Perai harbour at least three distinct clades within the *Raillietina tunetensis* complex. Updating integrated morphological and molecular databases is essential to elucidate species diversity, enable formal NCBI deposits, and evaluate the biosecurity risks posed to surrounding poultry populations.

Keywords: House crows; *Raillietina*; taxonomy; phylogenetic tree

#OC019

Molecular Characterization and Population Structure Analysis of Nematodes of the Zoonotic Ascaris lumbricoides/suum Complex: A Neglected Human Health Threat of Swine Origin in Haryana, India

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ABSTRACT

A taxonomic uncertainty exists between two very important zoonotic ascarid species, *Ascaris lumbricoides* and *A. suum.* Moreover, their interbreeding has resulted in hybrid genotypes in non-endemic regions. Thus, the present study aimed at characterization and population structure analysis of ascarids of swine origin in Haryana, India. The intestines of 265 slaughtered pigs were screened thoroughly for the presence of adult roundworms. The ascarids retrieved were characterized using PCR-RFLP based on the nuclear ribosomal internal transcribed spacer (ITS1-5.8S-ITS2) rDNA. BLASTn analysis and population structure studies were performed by targeting the mitochondrial *cox II* gene. Out of 265 pigs screened, 20 (7.54%) revealed the presence of ascarids. PCR-RFLP delineated these roundworms as *A. lumbricoides* (n = 13), *A. suum* (n = 3), and hybrid (n = 4) genotypes. Phylogenetics of the sequences generated herein with GenBank-archived sequences of *A. lumbricoides/suum* complex revealed the presence of four different clusters. In total, 48 sequences for the *cox II* gene (including 18 sequences generated herein) yielded 12 haplotypes, with high haplotype (0.818 ± 0.035) and low nucleotide (0.0173 ± 0.0013) diversities. Analysis of molecular variance revealed high genetic variation within populations (71.45%) as compared to among populations (28.54%). Our results provided novel insights into the role of pigs in the maintenance, circulation, and transmission of roundworms of *A. lumbricoides/suum* complex in Haryana, India. Population structure analysis revealed recent population expansion of *A. lumbricoides/suum* complex. Hence, the one-health approach for ascarid infections in humans in socio-economically deprived populations in India should also be targeted against the cross-transmission routes through swine hosts.

Keywords: *Ascaris lumbricoides/suum* complex; India; pigs

#OC012

Nanotherapeutic Approaches for the Treatment of Hydatid Cyst: Therapeutic Potential of Curcumin Nanocapsules in Experimental Cystic Echinococcosis

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ABSTRACT

Cystic echinococcosis remains a major zoonotic disease worldwide, and current treatment strategies rely primarily on surgery and benzimidazole derivatives, which have several limitations, including adverse effects and incomplete therapeutic efficacy. Nanotechnology has emerged as a promising strategy to enhance the delivery and bioavailability of natural compounds. Curcumin, a natural polyphenol with well-documented antiparasitic and anti-inflammatory properties, has poor aqueous solubility and limited bioavailability, which can be overcome through nanoformulation. This study evaluated the efficacy of curcumin-loaded nanomicelles against hydatid cyst infection in mice. Biocompatible oil-in-water nanomicelles containing curcumin were prepared using ethyl butyrate, sodium caprylate, and F127 in phosphate-buffered saline. For the *in vivo* experiment, hydatid cyst infection was established in BALB/c mice, and after confirmation of cyst development, experimental animals received curcumin nanomicelles at concentrations of 0.5, 0.25, or 0.125 mg/mL for 30 days, while the remaining groups received free curcumin (0.5 mg/mL), albendazole (150 mg/kg), or saline as an untreated control. Therapeutic efficacy was evaluated by comparing cyst burden, cyst weight, and maximum cyst diameter with those of free curcumin, albendazole-treated, and untreated control groups. The nanomicelles exhibited a mean zeta potential of -33.96 mV. All three nanomicelle treatments resulted in significantly fewer cysts than free curcumin, albendazole, and the untreated control groups. Total cyst weight was also significantly reduced across all nanomicelle groups compared with the free curcumin and control groups. Furthermore, the largest cysts were significantly smaller in the 0.5 and 0.25 mg/mL nanomicelle groups than in the free-curcumin, albendazole, and control groups. These findings indicate that nanoencapsulation substantially enhances curcumin's anti-hydatid activity and may serve as a safe and effective adjunct or alternative to conventional chemotherapy. Further preclinical and clinical investigations are warranted to facilitate its translation into clinical applications.

Keywords: curcumin; cystic echinococcosis; drug delivery; nanotechnology; nanotherapy

#OC028

One Health Investigation Reveals Wider Distribution of Paragonimus spp. In Sorsogon Province, the Philippines

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ABSTRACT

Paragonimiasis is a food-borne zoonotic disease caused by *Paragonimus westermani* and sustained through complex interactions among humans, freshwater intermediate hosts, paratenic hosts, and aquatic environments. Sorsogon Province is a recognized endemic area, particularly the municipality of Irosin, but the distribution and transmission of *Paragonimus* spp. in neighboring municipalities remains unknow. This study aimed to determine the distribution of *Paragonimus* spp. in Irosin and nearby municipalities using an integrated One Health approach encompassing human, animal, and environmental surveillance. Human surveillance involved 422 sputum samples from individuals suspected of pulmonary tuberculosis, with parasitological and molecular detection using ITS and cox1 markers. Intermediate host surveillance included 135 *Sundathelphusa* spp. crabs, 108 freshwater snails, and 21 Macrobrachium spp. shrimps. They were examined morphometrically and parasitologically following dissection and standardized pepsin-HCl digestion, while molecular assays were used for parasite confirmation. Environmental surveillance involved water sampling from areas selected based on flood risk, hydrological connectivity, and freshwater host occurrence. Environmental samples underwent filtration and molecular detection targeting *Paragonimus* spp. Cox1. Human surveillance demonstrated overlapping areas of paragonimiasis and tuberculosis, highlighting the potential for diagnostic misclassification especially in areas where paragonimiasis is considered not endemic. Further, high prevalence of P. *westermani* metacercariae in crabs from Irosin, Juban, and Casiguran were observed, demonstrating parasite occurrence beyond the recognized endemic municipality. Positive detections were also observed among snail hosts, whereas no P. *westermani* was detected in shrimp samples. Environmental assays successfully detected freshwater crab DNA, particularly in hydrologically connected habitats, but *Paragonimus* spp. DNA was not detected in environmental water samples. Overall, the integrated One Health approach revealed evidence of *Paragonimus* across recognized and previously underinvestigated areas of Sorsogon and provides a framework for linking human infection, host distribution, and environmental conditions in identifying transmission hotspots.

Keywords: Paragonimiasis; *Paragonimus westermani*; One Health; Freshwater hosts;

#OC027

Phylogenetic Analysis of Schistosoma Japonicum in the Philippines Using Taurocyamine Kinase Gene Intron Sequences

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ABSTRACT

Zoonotic schistosomiasis remains an overlooked public health issue in Asia. Our previous study using microsatellite markers to investigate the transmission dynamics of *Schistosoma japonicum* revealed that parasites with different host preferences are distributed across endemic regions within the Philippines. This raises the question of why the transmission dynamics of parasitic diseases differ between regions within the Philippines. We therefore conducted phylogenetic analyses of parasite populations in the Philippines using nuclear intron regions of the taurocyamine kinase (TK) gene (TkD1Int6 and TkBridInt). The sequences of the target gene, which were amplified by PCR using DNA from parasites in the provinces of Leyte and Oriental Mindoro, were analysed alongside previously reported sequences of the same gene from parasites originating in Kurume City (Japan), Hubei, Sichuan and Yunnan provinces (China), and Sorsogon and Davao Del Sur provinces (the Philippines). A haplotype network was then constructed. Consequently, seven haplotypes were identified in TkD1Int6. Parasites found in the Philippines were classified into six of these. In contrast, those found in China were classified into one haplotype, while those found in Japan were classified into two. Eight haplotypes were identified in TkBridInt. Parasites found in the Philippines were classified into five haplotypes. Conversely, parasites found in China were classified into four haplotypes, while those found in Japan were classified into one haplotype. The distribution of parasite populations with different genetic backgrounds across the Philippines suggests that these genetic differences may influence host preference. Genetic markers associated with host preference are useful for informing schistosomiasis control measures and are key to the One Health approach.

Keywords: Asian zoonotic schistosomiasis; One Health approach; Taurocyamine kinase gene

#OC025

Surveillance of Tick-Borne Pathogens in Ticks Infesting Wildlife in Indonesia

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ABSTRACT

Ticks are important vectors of a wide range of bacterial pathogens of veterinary and public health significance, including agents responsible for zoonotic diseases. Wildlife may serve as important hosts and reservoirs for ticks and tick-borne pathogens, potentially facilitating their transmission at the wildlife–livestock–human interface. This study investigated the diversity of ticks infesting wildlife in Indonesia and assessed their carriage of selected tick-borne bacterial pathogens. A total of 521 ticks were collected from various wildlife hosts, including wild boars, buffaloes, cattle, snakes, water lizards, tortoises, Sumatran tigers, armadillos, and bats, during 2018–2026. The collected ticks were morphologically identified as *Amblyomma javanense*, *Amblyomma testudinarium*, *Amblyomma varanense*, *Amblyomma* sp., *Dermacentor astrosignatus*, *Dermacentor compactus*, *Dermacentor steini*, *Haemaphysalis hystricis*, and *Rhipicephalus haemaphysaloides*. Tick DNA was extracted and screened by polymerase chain reaction (PCR) targeting partial fragments of rickettsial 17-kDa antigen and *gltA* genes, *Anaplasma groESL* gene, ehrlichial *groEL* gene, and borrelial *flaB* gene. Bacterial pathogens belonging to the genera *Anaplasma*, *Borrelia*, *Ehrlichia*, and *Rickettsia* were detected among the examined ticks. These findings demonstrate that wildlife-associated ticks in Indonesia harbor multiple bacterial pathogens of potential veterinary and zoonotic importance. The occurrence of these pathogens in ticks infesting diverse wildlife hosts highlights the potential role of wildlife–tick systems in maintaining and disseminating tick-borne pathogens and may represent a potential disease risk at the interface of wildlife, livestock, and humans.

Keywords: *Rickettsia, Anaplasma, Borrelia*, *Ehrlichia,* ticks, wildlife, Indonesia

#OC023

The Snail-Borne Tracheal Fluke, Tracheophylus Cymbius (Trematoda:Cyclocoelidae) of Domestic Ducks in Bangladesh: Risk Factors, Vector Snail, Phylogeny, and Anthelmintic Sensitivity

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ABSTRACT

The tracheal flukes, *Tracheophilus/Typhlocoelium* spp. (Trematoda**:**Cyclocoelidae) are the snail-borne trematodes of respiratory tract of ducks which cause obstruction of the trachea and the ducks may die of asphyxia. Here, we describe the morphological and molecular identification, prevalence, risk factors, vector snails and anthelmintic sensitivity of the tracheal flukes of domestic ducks in Bangladesh. Postmortem examination of 160 domestic ducks revealed 17.5% infection with tracheal fluke and PCR followed by sequencing of *cox1* and *nad* genes confirmed the fluke as *Tracheophilus cymbius/Typhlocoelum cymbium*. Phylogenetically, *T. cymbius* was closely related to the Indian and Chinese isolates. *T. cymbius* was detected in trachea (85.71%) and nasal passage (35.71%) of ducks. Significantly higher prevalence of *T. cymbius* infection was recorded in ducks that scavenged in low-lying water bodies (27.5%). Female ducks were more (23.33%) infected than the males (14%). Also, prevalence of infection was higher in ducks of > 1 year of age (26.67%) than in the younger ducks (20%). In summer the prevalence of infection was 12.5% while it was higher in monsoon (19.23%) and winter (20%). Experimental infection of snails of different species with *T. cymbius* miracidia revealed *Indoplanorbis exustus* as the intermediate host. *In vitro* anthelmintic sensitivity tests (death point) in RPMI medium at 37 °C with 5% CO_2 and 95% relative humidity, showed that *T. cymbius* was most sensitive to oxyclozanide (3 ± 0.88 h) followed by praziquantel (10.5 ± 5.74 h), triclabendazole (21.5 ± 3.0 h), nitroxynil (24.5 ± 4.12) and albendazole (81. ± 18 h). Notably, it remained almost unaffected to ivermectin. This study suggests that, in Bangladesh *T. cymbius* species is prevalent in ducks and *I. exustus* is the intermediate host. Age, sex, season and scavenging habitats are important risk factors and oxyclozanide may be the first choice of anthelmintics for treating tracheal fluke infections in ducks.

Keywords: *Tracheophilus cymbius*, ducks, molecular characterization, *Indoplanorbis exustus*, anthelmintic sensitivity

Oral Communications

Session Track:

Production Animals

#OC003

Molecular Epidemiology of Bovine Haemoparasitic Diseases in Sri Lanka: Prevalence, Co-infections and Risk-Based Control Strategies from Four Provinces

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ABSTRACT

Bovine haemoparasitic diseases are important tick-associated infections affecting cattle health and productivity in Sri Lanka. This plenary lecture presents molecular evidence on haemoparasitic infections in cattle from four provinces of Sri Lanka: Central, North Central, North Western and Uva. A total of 520 animal-level cattle records were analysed for *Babesia bigemina*, *Babesia bovis, Babesia ovata, Theileria orientalis* and *Anaplasma marginale*, together with selected animal-, management- and location-related risk factors.

Overall, 338 cattle were positive for at least one haemoparasite, giving an overall molecular prevalence of 65.0%. *Anaplasma marginale* showed the highest prevalence at 47.5%, followed by *Theileria orientalis* at 42.3% and *B. bigemina* at 29.2%. Any *Babesia* species was detected in 31.2% of cattle. Marked provincial variation was observed, with the highest prevalence in North Western Province at 98.2%, followed by North Central Province at 77.1%, Uva Province at 73.5% and Central Province at 12.2%. Co-infections were detected in 214 cattle, representing 41.2% of all cattle and 63.3% of haemoparasite-positive cattle.

Risk factor analysis showed that province, management system, tick infestation, acaricide use, tick fever vaccination status and clinical condition were associated with haemoparasite positivity in bivariate analysis. Cattle under semi-intensive and extensive management systems, cattle with visible tick infestation and animals showing abnormal clinical signs had higher crude infection levels. However, in the multivariable logistic regression model, acaricide use remained the strongest independent protective factor, with cattle receiving acaricide treatment showing markedly lower odds of haemoparasite positivity. Northwestern Province also remained significantly associated with higher infection odds after adjustment. These findings highlight the importance of molecular surveillance, regular tick control, strategic acaricide use and province-specific risk-based management of bovine haemoparasitic diseases in Sri Lanka.

#OC017

Redefining the Genetic Landscape of Theileria orientalis: Global MPSP Diversity, Phylogenetic Reclassification and Insights from Northern India

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Abstract

Theileria orientalis, a non-transforming *Theileria* species infecting cattle and buffaloes, is an emerging haemoparasite of economic importance. This study investigated its prevalence, genetic diversity, phylogenetic relationships, population structure and haematological impact, with emphasis on northern India. Of 1520 *T. orientalis* MPSP sequences retrieved from GenBank, 983 were analysed using DNASTAR, MEGA 11, DnaSP6, PopART and RStudio. Additionally, 1230 blood samples from cattle (n=642) and buffaloes (n=588) collected during 2022–2026 were examined by microscopy and PCR. *Theileria* was detected microscopically in 26.47% (n=170) of cattle and 2.38% (n=14) of buffaloes, while 18S rRNA PCR confirmed infection in 38% (n=244) and 5.27% (n=31), respectively. *T. orientalis*-specific PCR detected prevalence of 4.36% cattle (n=28) and 2.72% buffaloes (n=16), respectively. Mixed infections with *T. annulata* and *T. orientalis* were observed in ten cattle and four buffaloes, respectively. Phylogenetic analysis of global sequences and 15 Haryana isolates identified 12 MPSP genotypes: Types 1 (Chitose), 2 (Ikeda), 3 (Buffeli), 4, 5, 7, 8 and N1–N5. Type 6 clustered closely with *T. sinensis* (FST = 0.0015), whereas both showed strong divergence from other genotypes (Fst ranges of 0.981–0.99 and 0.78–0.97, respectively). Type 9 clustered with Type 4, supporting taxonomic reinterpretation, while reciprocal misclassification of Types 8 and 4 was evident in GenBank. Among 213 Indian isolates, eight genotypes were identified, with Types 2, N1 and N5 reported for the first time in India. Types 1 and 3 showed the widest global distribution, occurring in 21 and 20 countries, respectively, with Asia representing the major hotspot. Asia harboured all known genotypes, whereas Brazil showed the second-highest diversity with eight genotypes; Africa and Australia each had four. Gene-flow patterns varied among hosts and geographical regions, although genetic relatedness was evident between populations from neighbouring countries. The 981 isolates comprised 552 haplotypes and showed high genetic diversity (Hd = 0.988; π = 0.14). Negative Tajima's D and Fu's Fs suggested population expansion, while high FST and low Nm indicated significant differentiation and restricted gene flow. Infected animals showed reduced Hb, PCV, TEC and MCHC, with significant reductions in MCV, MCH and MCHC in buffaloes ($p<0.01$). Overall, the study highlights substantial genetic diversity, population structuring and the need for phylogenetic re-evaluation of *T. orientalis* MPSP genotypes.

Keywords: *Theileria orientalis,* MPSP gene, PCR, 18S rRNA, *Theileria annulata,* Phylogeny

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#OC018

RNASE P RNA Gene-Based Characterization of Bovine Hemoplasmas in Thai Dairy Cattle Supports Two Putative Novel Species

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ABSTRACT
Hemotropic mycoplasmas (hemoplasmas) are bacteria in the class Mollicutes that may cause hemolytic anemia in mammals. In Thailand, at least four bovine hemoplasma taxa have been detected in dairy cattle using 16S and 23S rRNA gene analyses: *Mycoplasma wenyonii*, "*Candidatus* Mycoplasma haematobovis," and two putative novel taxa. This study characterized 40 hemoplasma-positive bovine blood samples using the RNase P RNA (*rnpB*) gene to assess its discriminatory value and provide additional evidence for the two putative novel taxa. The *rnpB* gene was amplified using a modified PCR assay, and sequences were evaluated by BLASTn, phylogenetic and network analyses, and pairwise nucleotide identity. The 40 *rnpB* sequences were assigned to four groups that were congruent with the previous 23S rRNA gene-based classification: *M. wenyonii* (n = 14), "*Ca.* M. haematobovis" (n = 10), and two putative novel taxa (n = 16). The latter comprised "*Ca.* M. teganodes" (n = 13) and "*Ca.* M. geleiae" (n = 3). These findings indicate that the *rnpB* gene provides discriminatory resolution comparable to that of the 23S rRNA gene and supports the genetic distinctness of the two putative novel hemoplasma taxa. Multilocus characterization using *rnpB* and 23S rRNA genes, in addition to the 16S rRNA gene, may improve species-level identification and facilitate future investigations of pathogenicity and effects on cattle health and production.

Keywords: Bovine hemoplasmas; Dairy cattle; *rnpB* gene; Thailand

#OC011

Silent Circulation of Three Trypanosoma Species Among Domestic Animals in Northern Iran

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ABSTRACT

Members of the genus Trypanosoma infect a wide range of vertebrates globally. In Iran, cases of domestic animals infected with *Trypanosoma evansi, Trypanosoma theileri*, and *Trypanosoma vivax* are mainly reported in the central and southern regions. However, information on Trypanosoma species diversity in the Caspian Sea littoral province of Mazandaran in northern Iran—an area with a Mediterranean climate—is limited. This study offers the first epidemiological data on trypanosomoses among domestic animals in this region. Between June and December 2024, 800 blood samples were collected from apparently healthy horses, cattle, sheep, and dogs (200 from each species). Microscopically, Giemsa-stained buffy coat smears were examined for trypomastigotes, and genomic DNA was extracted from 200 randomly selected specimens (50 per host) to test for *Trypanosoma* species using group- and species-specific primers via PCR. Positive samples were sequenced and analysed phylogenetically. No trypomastigotes were observed microscopically, but PCR identified Trypanosoma infections in 59 animals (29.5%). *Trypanosoma evansi* was the most common species, infecting 43 animals (10.7%): 39 dogs (78%), 3 horses (6%), and 1 cattle (2%). *Trypanosoma vivax* DNA was detected in 34 dogs (68%) and 4 sheep (8%). *Trypanosoma theileri* infection was found in 8 cattle (16%). Phylogenetic analysis showed Iranian *T. theileri* isolates belonged to both Tth1 and Tth2 genotypes. These findings document the silent circulation of three Trypanosoma species in domestic animals in northern Iran and highlight the need for further research on prevalence, transmission, and control strategies.

Keywords: Iran; PCR; *Trypanosoma evansi; Trypanosoma vivax; Trypanosoma theileri*

#OC009

Species Identification of Fasciola spp. in Cattle from Yogyakarta Using Morphological Examination and Single-Step Duplex PCR

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ABSTRACT

Fasciolosis is a significant parasitic disease affecting ruminants, caused by the trematodes *Fasciola hepatica* and *F. gigantica*. These parasites infect the liver and bile ducts, resulting in detrimental effects on the host. Economic losses in the dairy and meat industries are attributed to factors such as emaciation, decreased milk production, mortality, infertility, and liver condemnation. This study aimed to identify *Fasciola* species using worm and egg samples collected from abattoirs and Eid al-Adha sacrificial animal slaughterhouses in the Special Region of Yogyakarta. The research was conducted from March to August 2026. The samples comprised liver organs and gallbladders from 20 cattle infected with *Fasciola* species. Examination of Fasciola worms and eggs involved organ inspection, isolation of eggs and worms, and morphological identification. Species differentiation was achieved using the Single-step Duplex PCR method. This method yielded positive identification of *F. gigantica* egg and adult worm DNA, with a band length of 615 bp, while *F. hepatica* exhibited a band length of 1031 bp. The study results indicated that all samples were of the species *F. gigantica*. The Single Duplex PCR method demonstrated efficacy in differentiating *Fasciola* species to the species level using gallbladder egg samples from Yogyakarta.

Keywords: *Fasciola gigantica*; fasciolosis; cattle; duplex PCR; Yogyakarta

#OC036

Ungulate Malaria Parasites in Thailand

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ABSTRACT

Several species of ungulate malaria parasites have been reported worldwide; however, since their discovery in 1913, they have remained poorly characterized. Among these parasites, *Plasmodium bubalis*, which infects water buffalo, and *P. caprae*, which infects goats, are malaria parasites of livestock. Since 2014, we have conducted epidemiological studies of ungulate malaria parasites in water buffalo and goats in Thailand. We have found a high prevalence of *P. bubalis* infection in water buffalo and sporadic cases of *P. caprae* infection in goats. The infected animals appeared clinically healthy, and parasitemia was very low in most animals, being detectable only by nested PCR or quantitative PCR (qPCR). Phylogenetic analyses based on mitochondrial genomes provided robust support for a clade comprising ungulate *Plasmodium* species and the bat haemosporidian parasite *Polychromophilus*, which was distinct from other *Plasmodium* species. This finding suggests that the genus *Plasmodium*, which includes species infecting diverse host groups such as ungulates, birds, reptiles, and other mammals, is not monophyletic. In addition, we attempted to isolate *P. caprae*. Experimental inoculation of blood from a *P. caprae*-positive goat into splenectomized kids successfully established infection. However, following the initial detection of parasitemia by thin blood-smear examination approximately one week after inoculation, parasite levels declined and became undetectable by qPCR within a week. Together, these findings provide new insights into the evolutionary relationship and biological characteristics of ungulate malaria parasites.

Keywords: malaria; goat; water buffalo

#OC013

Visualisation of Intracellular Oxidative Stress in Babesia bovis Merozoite Using Hyper Fluorescent Sensor Probe for H_2O_2

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ABSTRACT

Living organisms regulate various physiological functions by utilising the balance of oxidation and reduction within cells, as well as calcium oscillations. Our research focuses on cell observation and imaging experiments to investigate the oxidative stress response and calcium signalling in *Babesia* merozoites, with the aim of discovering the biological mechanisms and molecules that could lead to countermeasures against bovine babesiosis. Genetically encoded fluorescent probes have recently enabled dramatic advancements in time-lapse imaging, making it possible to investigate intracellular events in several apicomplexan parasite species. In this study, we constructed a plasmid vector to stably express a genetically encoded H_2O_2 sensor probe called HyPer in *Babesia bovis*. The HyPer-transfected parasite population was successfully developed and subjected to time-lapse imaging analysis under *in vitro* culture conditions. HyPer was capable of sensing an increasing concentration of H_2O_2 in the parasite cells, induced by the administration of paraquat as a superoxide donor. Co-staining of HyPer fluorescence with MitoTracker Red indicated that the mitochondrion was the main source of reactive oxygen species (ROS) in the parasite cell. Fluctuating ROS dynamics in parasites gliding towards, attaching to and invading target red blood cells were visualised and monitored in real time using the HyPer-expressing parasite population. HyPer-expressing parasites can be widely utilised in studies investigating the mechanisms of oxidative stress emergence and reduction, as well as signal transduction in parasite cells during host invasion and intercellular development.

Keywords: *Babesia bovis*; HyPer; Oxidative stress; Time-lapse imaging analysis

Poster Submissions

Session Track:

Companion Animals

#PC022

Comparison of the Odour and Volatile Organic Compound (VOC) Profile of Topical Feline Endectoparasiticides

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ABSTRACT

Olfaction is central to feline wellbeing and environmental interaction. Odours associated with topical endectoparasiticides may impact this and influence product acceptability and treatment compliance. This study compared the odour and volatile organic compound (VOC) profiles of five feline endectoparasiticides. A full dose suitable for a 4.5 kg cat was equilibrated with 10 L of air in a nalophan bag. Odour concentration, intensity, character and hedonic tone were assessed by trained panellists using dynamic olfactometry, while VOCs were analysed by gas chromatography-mass spectrometry. All products exhibited a chemical/solvent odour profile but differed markedly across sensory and analytical measures. Odour concentrations ranged from 185 to 2870 OU/m³, intensity scores from 4.2 to 6.0 and sum VOCs from 1.2 to 64.1 mg/tube. The esafoxolaner, eprinomectin and praziquantel formulation had the lowest odour concentration, intensity and VOC burden, together with the most favourable hedonic rating. These findings support further investigation of treatment odour as a factor influencing feline experience, owner acceptance and treatment adherence.

#PC026

Curative Efficacy and Clinical Outcome of Combined Diminazene Aceturate and Oral Secnidazole Therapy for Two Canine Trypanosomosis in Chiang Mai, Thailand

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ABSTRACT

Introduction: Canine trypanosomiasis, predominantly caused by *Trypanosoma evansi* (*T. evansi*), is an acute, fatal hemoprotozoan disease. Conventional diminazene aceturate monotherapy, whether administered as a single dose or over five consecutive days, fails to cure the infection due to resistance, toxicity, and relapses. Here, we present the first report of successful treatment using combined diminazene aceturate and secnidazole therapy.

Methods: Two cases of canine trypanosomosis, with or without concurrent *Ehrlichia canis* (*E. canis*) coinfection, received a combination of a single intramuscular dose of diminazene aceturate (3.5 mg/kg) and oral secnidazole (100 mg/kg/day for 5 consecutive days). Additionally, the dog with concurrent *E. canis* coinfection received oral doxycycline (10 mg/kg/day) concurrently with the trypanosomiasis protocol. The treatment response was monitored clinically, with parasitemia clearance tracked using the Woo technique over a 1-month follow-up period. Complete hematology, liver, and renal function tests were assessed every 1–2 weeks during this time.

Results: Rapid therapeutic response resulted in complete clearance of circulating trypanosomes within 24 hours post-treatment. Progressive clinical recovery ensued, including gradual resolution of anemia and thrombocytopenia. The protocol was well tolerated, with no both systemic toxicity and canine trypanosomiasis relapse.

Conclusions: The combination of single-dose intramuscular diminazene aceturate and a 5-day oral secnidazole course provides rapid parasitemia clearance without relapse and favorable clinical recovery. This regimen represents an effective, safe, and viable therapeutic best choice for managing canine trypanosomiasis, even in coinfected with *E. canis* patients.

Keywords: Canine, Trypanosomosis, Diminazene Aceturate, Secnidazole, Parasitemia Clearance.

#PC032

Gastrointestinal Parasites of Domestic Dogs in Bangladesh: Current Prevalence and Zoonotic Implications

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ABSTRACT

Gastrointestinal (GI) parasite infections remain an important threat to the health and welfare of domestic dogs, particularly in densely populated countries such as Bangladesh. Despite their veterinary and public health importance, recent epidemiological data on GI parasitic infections in domestic dogs in Bangladesh remain limited. This cross-sectional study was conducted from March to August 2026 to investigate the prevalence and diversity of GI parasites in domestic dogs in Bangladesh. A total of 200 fecal samples were collected and examined using simple flotation and centrifugal sedimentation techniques. Overall, 32.5% (65/200) of the dogs were positive for at least one GI parasite. Six parasite taxa were identified, with *Ancylostoma* spp. being the most prevalent (27.0%), followed by *Trichuris* spp. (5.0%), *Spirometra* spp. (1.5%), *Toxocara* spp. (1.0%), *Dipylidium caninum* (1.0%), and *Cystoisospora* spp. (0.5%). The detection of potentially zoonotic parasites, particularly *Ancylostoma* spp., *Toxocara* spp., and *Dipylidium caninum*, highlights their potential implications for public health and emphasizes the importance of a One Health approach. The findings underscore the need for regular deworming, responsible pet ownership, appropriate fecal waste management, and strengthened public health measures to reduce the burden and potential transmission of GI parasites. Further molecular studies are warranted to accurately characterize the detected parasite species, investigate genetic diversity and population structure, and identify potentially zoonotic lineages circulating among domestic dogs in Bangladesh. Integrating conventional parasitological and molecular approaches will provide a more comprehensive understanding of parasite transmission and its implications for animal and human health.

Keywords: gastrointestinal parasites; dog; prevalence; zoonotic; Bangladesh

#PC010

High Prevalence of Gastrointestinal Parasites in Shelter Dogs in Chonburi Province, Thailand: a Coprological Survey

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ABSTRACT

Background: Animal shelters represent high-density environments where overcrowding accelerates the transmission of gastrointestinal parasites (GIPs), several of which carry zoonotic potential. However, current epidemiological data regarding GIPs in Thai shelter populations remain limited. This study evaluated the prevalence, diversity, and co-infection dynamics of GIPs among shelter dogs in Chonburi Province, Thailand.

Methods: A cross-sectional survey was conducted between February and May 2026 at a rescue shelter in Chonburi Province, Thailand. Fecal samples (n = 158) were collected directly from the rectal ampulla of dogs and examined using simple flotation and formalin-ethyl acetate concentration (FEAC) techniques.

Results: Overall, GIP prevalence reached 77.8% (123/158). Helminths predominated, with hookworms exhibiting the highest detection rate (62.7%), followed by *Trichuris* spp. (42.4%) and *Toxocara* spp. (3.2%), respectively. Protozoan taxa included *Cystoisospora* spp. (9.5%) and *Giardia* spp. (7.0%). Co-infection was documented in 43.7% of examined dogs, most frequently presenting as concurrent hookworm and *Trichuris* spp. infection (34.8%).

Conclusions: The high parasite burden and extensive co-infection rate underscore critical risks to shelter animal health and potential zoonotic transmission. These findings highlight an urgent need for structured anthelmintic control programs and improved environmental hygiene in regional shelter facilities. Molecular characterization is recommended in future research to clarify species-level taxonomy and assess precise zoonotic risks.

Acknowledgements: The authors are grateful to the shelter staff and the graduate students of the Department of Parasitology, Faculty of Veterinary Medicine, Kasetsart University, for their assistance during sample collection.

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Keywords: co-infection; gastrointestinal parasites; hookworms; shelter dogs

#PC011

Imported Zoonotic Ancylostoma Ceylanicum and Ancylostoma braziliense Infections in a Cat in Romania

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ABSTRACT

Background: The international movement of companion animals may facilitate the introduction of exotic parasites into non-endemic regions. *Ancylostoma ceylanicum* is an emerging zoonotic hookworm capable of establishing patent infections in humans, while *A. braziliense* is an important causative agent of cutaneous larva migrans. Neither species is considered endemic in Europe.

Methods: A 3-year-old neutered female European shorthair cat, previously residing in Guadeloupe and subsequently relocated to Romania, was presented to a veterinary clinic in Cluj-Napoca in March 2025. Coprological examination revealed hookworm-like eggs. Fecal samples were subjected to molecular analyses in Romania and Australia, including conventional PCR targeting the ITS-2 region followed by Sanger sequencing, species-specific multiplex quantitative PCR (qPCR), and Oxford Nanopore long-read metabarcoding targeting the ITS1-5.8S-ITS2 region.

Results: Conventional PCR and sequencing identified *A. ceylanicum* with 100% nucleotide identity. Multiplex qPCR confirmed a mixed infection with *A. ceylanicum* (Cq 23.88) and *A. braziliense* (Cq 24.62). Nanopore metabarcoding further confirmed both species, generating 71,588 reads classified as *A. ceylanicum* and 30,560 reads as *A. braziliense*. Based on the travel history, the infection was most likely acquired in the Caribbean. Following treatment with milbemycin oxime and praziquantel, a subsequent coprological examination was negative.

Conclusions: This case documents the introduction of two zoonotic hookworm species into Europe through companion-animal movement. The findings highlight the limitations of morphology-based diagnosis for hookworm species identification and emphasize the importance of molecular surveillance for detecting imported parasites with zoonotic potential.

Keywords: Hookworms, *Ancylostoma ceylanicum*, *Ancylostoma braziliense*, Zoonosis, Romania, Molecular diagnosis

#PC040

Molecular Detection and Genetic Characterization of Bartonella spp. in Dogs and Cats in Northern Vietnam

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ABSTRACT

Bartonella spp. are Gram-negative, facultative intracellular bacteria of veterinary and public health importance. However, their occurrence and genetic diversity in companion animals in Vietnam remain poorly characterized. This study investigated the molecular occurrence and genetic relationships of *Bartonella* spp. detected in blood samples from dogs and cats in northern Vietnam. A total of 290 blood samples were collected from 183 dogs and 107 cats. Conventional PCR targeting the RNA polymerase beta-subunit gene (*rpoB*) was used to detect *Bartonella* DNA, and the citrate synthase gene (gltA) was analyzed for additional characterization. Positive PCR products underwent bidirectional Sanger sequencing. The resulting sequences were aligned with GenBank reference sequences, and phylogenetic analyses were performed in MEGA 12. Bartonella DNA was detected based on the *rpoB* gene in 19 of 290 animals (6.55%), with rates of 8.41% (9/107) in cats and 5.46% (10/183) in dogs. Phylogenetic analysis of the *rpoB* sequences placed the detected *Bartonella* within *B. henselae*, clustering with the Houston-I reference strain. Analysis of the available *gltA* sequences also supported this relationship. These findings document *B. henselae* DNA in both dogs and cats sampled in northern Vietnam and provide additional sequence data on *Bartonella* in companion animals. The observed clustering with Houston-I supports genetic relatedness to this reference strain, although definitive genotype assignment requires further evidence. The detection of *B. henselae* warrants further epidemiological investigation because these results alone do not establish transmission to humans or quantify zoonotic risk.

Keywords: *Bartonella henselae*, Molecular detection, Dogs, Cats, Vietnam

#PC034

Molecular Detection of Babesia gibsoni and Associated Hematological Alterations in Dogs from Selected Regions of Bangladesh

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ABSTRACT

Hemoprotozoal infections, particularly those caused by tick-borne pathogens, represent an important yet undercharacterized threat to canine health in South Asia. Diagnosis remains challenging because conventional microscopy has limited sensitivity, particularly in dogs with low parasitemia. Among these pathogens, *Babesia gibsoni* is a clinically important intraerythrocytic parasite capable of causing severe and potentially fatal disease. However, molecular evidence of *B. gibsoni* infection in Bangladesh remains limited, and its association with hematological abnormalities has not been adequately characterized. This study aimed to molecularly detect blood protozoan infections in dogs from selected regions of Bangladesh, with particular emphasis on *B. gibsoni*, and to characterize associated complete blood count (CBC) alterations. A total of 188 blood samples from pet and shelter dogs were screened by polymerase chain reaction (PCR) targeting the 18S rRNA gene. *B. gibsoni* DNA was detected in 16 dogs (8.5%). Infected dogs demonstrated pronounced alterations in erythrocyte parameters consistent with regenerative hemolytic anemia, together with significantly decreased platelet counts indicative of thrombocytopenia. Differential leukocyte profiles also showed notable alterations, suggesting a systemic inflammatory response associated with infection. By integrating molecular detection with hematological profiling across canine populations from previously understudied regions of Bangladesh, this study provides novel population-specific evidence of *B. gibsoni* infection and its associated clinicopathological manifestations. These findings highlight the value of combining molecular and hematological screening to improve early and accurate diagnosis, particularly in dogs with low parasitemia. Enhanced surveillance, molecular characterization, and targeted tick-control measures are warranted to better understand and mitigate canine blood protozoal infections in Bangladesh.

Keywords: *Babesia gibsoni*; Canine babesiosis; Canine hemoparasites; Polymerase chain reaction (PCR); Canine vector-borne diseases

#PC035

Molecular Prevalence and Clinical Associations of Hemotropic Mycoplasma spp. in Domestic Cats and Fleas in Bangladesh

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ABSTRACT

Hemotropic *Mycoplasma* spp. are globally recognized erythrocytic pathogens of cats; however, molecular epidemiological data from Bangladesh remain scarce. This study estimated the molecular prevalence of hemotropic *Mycoplasma* infection in domestic cats from Chattogram and Dhaka, investigated the presence of *Mycoplasma* DNA in fleas, and characterized the associated hematological and clinical abnormalities. Blood samples from 346 domestic cats and 130 flea samples were screened by polymerase chain reaction (PCR). Hematological indices and clinical findings were compared between PCR-positive and PCR-negative cats, while microscopy was evaluated using PCR as the reference standard. Overall, *Mycoplasma* DNA was detected in 47/346 cats, yielding a prevalence of 13.6% (95% CI: 10.4–17.6%). Prevalence did not differ between Chattogram (13.5%) and Dhaka (13.7%; $p = 1.000$). Additionally, 14/130 flea samples (10.8%; 95% CI: 6.5–17.3%) were PCR-positive. Microscopy demonstrated 85.1% sensitivity and 94.0% specificity relative to PCR. Infected cats had significantly higher median leukocyte counts (15.25 × 10^3/μL vs. 10.40 × 10^3/μL; $p = 0.006$) and monocyte percentages (3.0% vs. 2.0%; $p = 0.008$) than uninfected cats. Among PCR-positive cats, fever, anemia, and seizures were observed in 41.2%, 29.4%, and 5.9%, respectively. These findings confirm that feline hemotropic *Mycoplasma* infection is prevalent in Bangladesh and that fleas may contribute to pathogen circulation. Routine PCR-based screening, particularly for clinically ill or anemic cats, should be incorporated into veterinary practice. Integrated flea-control programs, including regular ectoparasiticide use, environmental sanitation, and management of in-contact animals, are recommended to reduce potential transmission. Cat owners should be educated regarding routine flea prevention, early recognition of clinical signs, and prompt veterinary consultation for febrile or anemic cats. Further longitudinal studies are warranted to clarify vector competence, risk factors, and the clinical impact of infection.

Keywords: Hemoplasmosis, Feline vector-borne disease, Hemotropic *Mycoplasma,* Flea-borne transmission

#PC016

Morphological and Genetic Characterization of Thelazia Callipaeda in Dogs

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ABSTRACT

Thelazia callipaeda is a vector-borne zoonotic nematode transmitted by tear-feeding flies of the genus *Phortica*. It parasitizes the conjunctival sac and lacrimal ducts of mammals, including dogs and humans, and can cause conjunctivitis, excessive lacrimation, and keratitis. Although *T. callipaeda* has historically been associated with Asia, its geographical distribution has expanded, highlighting its increasing veterinary and public health importance. In Thailand, molecular information on *T. callipaeda* remains limited despite previous reports of canine thelaziasis and sporadic human infections. This study aimed to characterize *T. callipaeda* collected from dogs in Thailand using morphological and molecular approaches and to investigate the genetic relationships of Thai specimens with previously reported isolates. Adult eyeworms were examined morphologically, followed by genomic DNA extraction and PCR amplification and sequencing of the mitochondrial 12S ribosomal RNA (12S rRNA) region. Phylogenetic analysis was performed using reference sequences to assess genetic relationships among isolates. Three Thai specimens, designated Thelazia01, Thelazia02, and Thelazia03, clustered within the established *T. callipaeda* lineage and were closely related to previously reported Chinese isolates. Thelazia02 and Thelazia03 were closely related, whereas Thelazia01 showed some genetic separation while remaining within the same lineage, suggesting preliminary intraspecific variation among the Thai specimens. These findings confirm the morphological and molecular identification of *T. callipaeda* in dogs in Thailand and provide preliminary molecular evidence of genetic variation among Thai isolates. Given the small number of specimens analyzed, broader sampling and additional genetic markers are required to characterize the population-level genetic diversity of *T. callipaeda* in Thailand. These findings provide baseline molecular information for future epidemiological and genetic studies of this zoonotic eyeworm.

Keywords: Dog, Eyeworm, Genetic diversity, Morphology, *Thelazia callipaeda*

#PC042

Preliminary Molecular Detection and Characterization of Tick-Borne Protozoa in Dogs from Southeastern Vietnam

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ABSTRACT

Introduction: Tick-borne protozoan pathogens are important infectious agents of dogs and may have veterinary and zoonotic significance. However, molecular information on *Babesia* and *Hepatozoon* infections in dogs from southeastern Vietnam remains limited. This study aimed to investigate the occurrence and molecular characteristics of *Babesia* and *Hepatozoon* in dogs from selected areas of southeastern Vietnam.

Methods: A total of 281 whole-blood samples were collected from dogs in Ho Chi Minh City, Dong Nai Province, and Tay Ninh Province. DNA was extracted from blood samples and screened using a nested PCR assay targeting the 18S rRNA gene for the detection of *Babesia* and *Hepatozoon*. Positive PCR products were subjected to sequencing for molecular identification. Further comparative molecular analyses are ongoing.

Results: Preliminary results showed that *Babesia* spp. were detected in 28 of 281 samples (10.0%), while *Hepatozoon* spp. were detected in 8 of 281 samples (2.8%). Preliminary sequence analysis identified *Babesia vogeli* among the *Babesia*-positive samples. Further molecular characterization of positive samples is ongoing.

Conclusions: These preliminary findings provide molecular evidence of the presence of *Babesia* and *Hepatozoon* in dogs from southeastern Vietnam. Further molecular characterization may provide additional insights into the genetic relationships and diversity of these canine tick-associated protozoan pathogens.

Keywords: *Babesia*; *Hepatozoon*; dogs; tick-borne pathogens; Vietnam

#PC015

Prevalence of Mycoplasma Species in Community Cat in Various Villages in Sabah

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ABSTRACT

Feline mycoplasmosis, caused by haemotropic *Mycoplasma* spp., is an important blood-borne infection in cats that may lead to anaemia and compromise feline health. Limited data are available regarding its prevalence in community cats in Sabah, Malaysia. This study aimed to determine the molecular prevalence of haemoplasma infections in village community cats. Blood samples were collected from a total of 193 cats across multiple villages throughout Sabah and subjected to DNA extraction followed by conventional polymerase chain reaction (PCR) targeting 18S rDNA sequences of three distinct species of *Mycoplasma* spp. A multiplex polymerase chain reaction (PCR) was used in detection of feline haemotropic mycoplasmas which can differentiate infections of *Mycoplasma haemofelis* (Mhf), *Candidatus* Mycoplasma haemominutum (CMhm) and *Candidatus* Mycoplasma turicensis (CMtc) in feline blood simultaneously. The overall prevalence of haemoplasma infection according to species shows *Mycoplasma haemofelis* (26.42%) being the common species followed by *Candidatus* Mycoplasma haemominutum (9.33%), and *Candidatus* Mycoplasma turicensis (1.55%). Co-infections were observed in 3.1% of cats. For Mhf, outdoor cats showed elevated odds (OR = 3.51, 95% CI: 1.30–9.46, p = 0.130), suggesting that environmental exposure may play a role. Other variables were not significantly associated with Mhf infection. In contrast, CMhm infection was clearly associated with both age and sex. Cats aged 2–4 years (OR = 4.62, p = 0.026) and >4 years (OR = 12.93, p < 0.001) had markedly higher odds of infection compared to younger cats, indicating that cumulative exposure is a major risk factor. Male cats also showed significantly higher infection odds than females (OR = 0.31 for females, p = 0.046), possibly reflecting behavioural or territorial risk. Other factors, such as breed, health status, and management type, were not significant. For CMtc, the very low prevalence limited statistical power. No risk factors were significantly associated with infection. Collectively, the findings of this study contribute valuable baseline data on feline haemotropic mycoplasma infection in Sabah and provide insight into the epidemiological characteristics of haemoplasma infection in community cat populations.

Keywords: feline haemoplasma, prevalence, PCR, risk factors, community cats

#PC028

Vector-Borne Pathogens in Shelter Animals: Serological and Microscopic Evidence from Chonburi, Thailand

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ABSTRACT

Animal shelters commonly house large populations of dogs and cats in confined environments, where high population density and close animal contact may increase exposure to vectors and facilitate the transmission of vector-borne pathogens (VBPs). Important VBPs affecting companion animals include *Ehrlichia canis*, *Anaplasma platys*, and *Dirofilaria immitis*. However, epidemiological data on VBPs among shelter animal populations in Thailand remain limited. This study aimed to determine the occurrence and co-infection patterns of major vector-borne pathogens in shelter dogs and cats in Chonburi Province, Thailand, using serological and microscopic methods. A cross-sectional survey was conducted from February to May 2026 at an animal shelter in Chonburi Province, Thailand. Blood samples (n = 150) were collected from the saphenous or cephalic veins. Samples were tested using the SNAP 4Dx Plus Test and examined by light microscopy for the detection of blood-borne vector-associated pathogens. The SNAP 4Dx Plus Test revealed high positivity rates for *Ehrlichia* spp. (93.3%, 140/150) and *Anaplasma* spp. (91.3%, 137/150), while *Dirofilaria immitis* and Lyme disease were detected in 8.0% (12/150) and 0.7% (1/150) of animals, respectively. Concurrent *Anaplasma–Ehrlichia* infection was observed in 90.0% (135/150) of animals. Triple infection with *Ehrlichia*, *Anaplasma*, and *D. immitis* was detected in 8.0% (12/150), while one animal (0.7%) was positive for *Ehrlichia*, *Anaplasma*, and Lyme disease. Microscopic examination detected *Anaplasma* spp. in 2.0% (3/150) of animals and *D. immitis* microfilariae in 13.3% (20/150). This study demonstrates a high detection rate of vector-borne pathogens, particularly *Ehrlichia* spp. and *Anaplasma* spp., among shelter animals, with a high frequency of co-infections. However, both SNAP 4Dx Plus serological testing and microscopic examination have inherent diagnostic limitations related to test sensitivity, infection stage, pathogen burden, and species-level identification. Molecular assays are therefore recommended for confirmatory diagnosis and accurate characterization of the detected pathogens.

Keywords: Companion Vector-borne pathogen, Snap 4Dx plus test, microscopic examination, animal shelter

Poster Submissions

Session Track:

One Health / Wildlife

#PC037

Tick-Virus Interactions: Effects on Tick Biology

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ABSTRACT

Ticks harbor diverse microbial communities comprising bacteria, viruses, protozoa, and fungi. Although these communities include pathogens, many members are non-pathogenic, and some maternally inherited bacteria contribute to tick nutrition, development, and reproduction. In recent years, metatranscriptomic studies have revealed highly diverse tick viromes containing numerous previously undescribed viruses. Persistent viral infections suggest long-term virus–tick associations; however, these ecological patterns alone do not establish whether tick-associated viruses are mutualistic, commensal, or detrimental, and their functional effects on tick biology remain largely unknown. In this study, we examined how non-pathogenic and low-pathogenicity tick-associated viruses affect vector physiology in two tick species. Experimental infection revealed species-specific differences in viral persistence, transstadial maintenance, and post-engorgement body metrics, suggesting that viral infection may have measurable physiological effects and affect fitness-related traits in ticks. Overall, these findings contribute to a broader understanding of virus–vector dynamics by highlighting the physiological consequences of viral infection and the species-specific nature of virus–tick interactions.

Keywords: tick biology; tick-associated viruses; virus–tick interactions; vector physiology

#PC008

Hexametra Angusticaecoides (Nematoda: Ascarididae) in Chameleons in Thailand: Molecular Characterization Based on Three Genetic Markers

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ABSTRACT

The exotic pets have increased in attention and market share with the expansion of the international pet trade. For example, panther chameleons (*Furcifer pardalis*; FP) and Parson's chameleons (*Calumma parsonii*; CP) are imported to Thailand with the possibilities of carrying related foreign pathogens and parasites, including nematodes, such as *Foleyella furcata* and *Hexametra angusticaecoides*. In this study, nematodes were incidentally found in subcutaneous nodules of FP in live and necropsy cases (n = 5) and the intestine of a necropsied CP (n = 1). Nucleic acid was extracted from all individual nematodes of each case. The partial fragments of the *cox1*, 12S rRNA, and 18S rRNA genes were amplified and sequenced bidirectionally. Unfortunately, only three samples for the *cox1* gene were successfully sequenced, while the 12S and 18S rRNA genes were sequenced from all six samples and five samples, respectively. All sequences were determined percent identity using nucleotide BLAST and analyzed through phylogenetic trees. Because of available sequences for comparison, the results showed that only the *cox1* gene could reveal their actual identities as *H. angusticaecoides* (99.19–99.39%). For the 12S rDNA sequences, there is no available sequence to compare, and the closest sequence (94.34–95.21%) was *Ophidascaris* sp., a nematode genus reported from other reptile species. Lastly, the level of sequence similarity among the 18S rDNA sequences of nematodes is high, suggesting its difficulty for nematode species differentiation. To the best of our knowledge, this is the first report of the 12S and 18S rDNA sequences of *H. angusticaecoides*. The complete mitochondrial genomes (mitogenomes) of these *H. angusticaecoides* isolates should be amplified and sequenced in future studies to facilitate comparative analysis.

Keywords: Ascarididae; *Hexametra*; Panther chameleon; Parson's chameleon; Thailand

#PC004

In Vitro Evaluation of Efficacy of Six Anti-Toxoplasma Drugs Against Toxoplasma gondii Type III Strain

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ABSTRACT

A *Toxoplasma gondii* type Ⅲ wild-type was previously isolated from a monkey with acute death in Sichuan, China, suggesting a severe threat to non-human primates. Currently, effective drugs against type Ⅲ *T. gondii* are limited. Hence, this study evaluated the *in vitro* anti-*Toxoplasma* effects of six common drugs, aiming to identify candidate drugs that are effective against type Ⅲ *T. gondii* strain. In this study, cytotoxicity of the tested drugs was determined by the CCK-8 assay. Then, the proliferation and invasion of *T. gondii* tachyzoites were evaluated for the drug efficacy by quantitative real-time PCR. and the plaque assay was employed to observe the drug treatment effects for 7 days. As a result, the 50% cytotoxic concentrations (CC50) of dihydroartemisinin, pyrimethamine, and acetylspiramycin were 59.30 μM, 11.79 μM, and 138.10 μM, respectively; sulfadiazine and lincomycin showed no significant cytotoxicity within the tested concentration. In the proliferation assay, Dihydroartemisinin (5μM), azithromycin (80 μM), sulfadiazine (1000 μM), and acetylspiramycin (100 μM) work best at inhibiting the growth of *T. gondii*. The invasion of *T. gondii* were suppressed significantly by the treatment of Dihydroartemisinin, acetylspiramycin, and azithromycin (p <0.01), whereas sulfadiazine and lincomycin exhibited the limited inhibition. The plaque assay revealed that treatment with dihydroartemisinin (5 μM), azithromycin (80 μM), and lincomycin (500 μM) significantly reduced plaque area (p <0.01), whereas plaques still formed following sulfadiazine (1000 μM) treatment. In summary, dihydroartemisinin, azithromycin, and acetylspiramycin showed great inhibition in proliferation and invason against type Ⅲ *T. gondii in vitro*, with dihydroartemisinin exhibiting the best inhibitory effect.

Keywords: *Toxoplasma gondii*; type III; drug screening; *in vitro* inhibitory activity

#PC001

Molecular Detection of Spiroplasma ixodetis (Mollicutes: Spiroplasmataceae) from Ixodes Granulatus (Acari: Ixodidae) in Malaysia: A First Report

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ABSTRACT

Spiroplasma are wall-less bacteria belonging to the class Mollicutes and are commonly associated with arthropods, plants and vertebrates, with some species implicated in animal and human diseases. In Malaysia, studies on *Spiroplasma* remain limited, particularly in ticks and other ectoparasites. In this study, ticks were collected from a variety of animal hosts across Peninsular Malaysia and identified using morphological characteristics. Genomic DNA was extracted from individual ticks and screened for *Spiroplasma* using polymerase chain reaction assays targeting the 16S rRNA, *rpoB* and *gyrA* gene markers. A total of 1,465 ticks (1,229 *Rhipicephalus microplus* (n=1,229), *Rhipicephalus linnaei* (n=81), *Haemaphysalis wellingtoni* (n=58), *Ixodes granulatus* (n= 48), *Dermacentor steini* (n=25), *Haemaphysalis nadchatrami* (n= 8), *Rhipicephalus haemaphysaloides* (n=6), *Haemaphysalis bispinosa* (n=5), *Dermacentor* sp. (n=3), *Dermacentor compactus* (n=1), and *Haemaphysalis* sp. (n=1)) were collected. Twelve samples (0.82%) tested positive for *Spiroplasma*, and all positive specimens were identified as *I. granulatus*. BLAST analysis of the 16S rRNA, *rpoB*, and *gyrA* genes consistently demonstrated high similarity to *Spiroplasma ixodetis*, with sequence identities ranging from 98.89–99.86%, 97.97–99.08%, and 97.79–99.60%, respectively. This study represents the first report of *Spiroplasma* in ticks from Malaysia and the first detection of *S. ixodetis* in *I. granulatus*. Further studies are required to assess the potential risk to humans from tick associated *Spiroplasma* in Malaysia, particularly given previous reports of *S. ixodetis* in human cases.

Keywords: *Spiroplasma ixodetis*, zoonotic pathogens, tick-associated bacteria, Mollicutes

#PC018

Decadal Shifts in Bovine Haemoparasites: Temporal, Seasonal and Species-specific Trends among Cases Presented at Haryana Pashu Vigyan Kendra, Eastern Haryana, Northern India

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ABSTRACT

The decade-long analysis (2016–2026) revealed substantial temporal and seasonal variations in the occurrence of bovine haemoparasitic infections in eastern Haryana, Northern India. *Theileria annulata* was the predominant haemoparasite, with an overall positivity of 24.24% (10,390/42,858 animals). Its annual positivity showed considerable fluctuations, with the highest prevalence recorded in 2017–18 (32.50%), followed by a decline to 15.79% in 2022–23 and a subsequent increase to 25.84% in 2024–25. Seasonal analysis showed the highest positivity during the rainy season (25.33%), closely followed by summer (24.88%), spring/autumn (23.91%) and winter (18.71%), indicating greater occurrence during warm and humid periods. *Babesia bigemina* was detected at a comparatively lower overall positivity of 5.06% (2,169/42,858 animals). Its annual positivity ranged from 3.80% to 7.81%, with the highest value recorded in 2022–23, while seasonal positivity was highest during summer (6.94%). In comparison, *Anaplasma marginale* showed an overall positivity of 16.66% (7,142/42,858 animals) and exhibited a striking increase in recent years, rising from 7.98% in 2020–21 to 39.35% in 2025–26, the highest positivity recorded during the study period. Mixed infections accounted for 8.30% (3,739/42,858 animals) overall and displayed considerable annual variation, with positivity increasing markedly in the latter years to 15.42% in 2024–25 and 15.18% in 2025–26. Overall, the findings demonstrate parasite-specific temporal and seasonal patterns rather than a uniform epidemiological trend. The sustained predominance of *T. annulata*, summer predominance of *B. bigemina*, and pronounced recent increase in *A. marginale* and mixed infections indicate a changing haemoparasitic disease scenario in eastern Haryana. These findings emphasize the importance of continuous year-round surveillance, early diagnosis, and season-targeted tick and haemoparasite control strategies, particularly during periods of increased infection positivity.

Keywords: Haemoparasite, *Theileria, Babesia, Anaplasma*, Season

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#PC021

Occurrence and Spatial Distribution of Cryptosporidium spp. and Giardia spp. in the Seven Lakes of San Pablo, Philippines

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ABSTRACT
The seven lakes of San Pablo City provide aquaculture and recreational ecosystem services to the residents. However, water quality is not routinely monitored and the parameters for monitoring pathogenic parasites are lacking. *Cryptosporidium* and *Giardia* are responsible for half of the reported recreational water-associated outbreaks of parasitic protozoans worldwide. This study aims to monitor the surface water pathogens in the seven lakes of San Pablo and assess the socio-economic risk factors that contribute to their emergence. Acid-fast staining (AFS) detected *Cryptosporidium* spp. in 24.8% (N=105) of the water samples, predominantly highest in Sampaloc, and the highest mean density (0.76 ocyst/L) was recorded in Bunot. Immunofluorescence assay (IFA) detected *Cryptosporidium* spp. in 32 samples (30.48%) and *Giardia* spp. in 18 samples (17.14%). Highest percent contamination of *Cryptosporidium* spp. using IFA was recorded in Palakpakin, while highest mean density was detected in *Bunot* (0.70 oocyst/L). *Giardia* spp. was most prevalent in Calibato while highest mean density (0.70 cyst/L) was recorded in Mohicap. Sensitivity and specificity of AFS in the detection of *Cryptosporidium* spp. in water samples were 40.62% and 82.19%, respectively, with IFA as the reference test. There was a significant inverse correlation between the presence of *Cryptosporidium* spp. and total dissolved solids (TDS) (p=0.032) in Calibato. A positive correlation was found between parasite presence and TDS (p=0.023) and water or Secchi-disk transparency (SDT) (p=0.020) in Yambo. Prevalence maps were generated using Geographic Information System. Significant risk factors were: use of exclusive (OR = -0.614) or alternative toilets (OR = 0.415) and consumption of lake water products such as fish and shellfish (OR = 0.784). This report provides evidence of waterborne parasite contamination in the sampled lakes and considers these parasites as good indicators of anthropogenic impacts. The findings advocate the need to improve sanitation and waste management and the regulation of agricultural activities and residential establishments to prevent further deterioration of the lakes.

Keywords: waterborne pathogens, *Cryptosporidium, Giardia,* lake water contamination, sanitation and hygiene practices

#PC041

Molecular Detection and Genetic Characterization of Borrelia spp. in Bats and Bat-Associated Soft Ticks in Thailand

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ABSTRACT
Bats are recognized as reservoirs for numerous pathogens and host a variety of ectoparasites, including ticks, which have the potential to transmit various infectious agents. *Borrelia*, a genus of spirochete bacteria responsible for vector-borne diseases, represents a significant public health concern. However, its distribution and genetic diversity in Thailand remain scarcely documented. The aim of this study was to investigate the occurrence and genetic diversity of *Borrelia* spp. in Thai bats and bat-infesting ticks using PCR-based methods. A total of 1,031 bats were captured across nine provinces between 2018 and 2023. Morphological identification and molecular analysis confirmed 96 larval *Reticulinasus* sp. ticks infesting two bat species, *C. thonglongyai* and *E. spelaea*. Molecular screening of 48 pooled tick samples revealed four positive pools originating from three individual *C. thonglongyai* bats. Out of 814 bats, 13 individual bats (1.6%; 95% CI: 0.9–2.7), belonging to *T. melanopogon, H. gentilis*, and *C. thonglongyai*, were *Borrelia*-positive based on *flaB* genes. Additionally, one *Borrelia*-positive bat exhibited putative spirochetes on a blood smear. Multilocus sequence analysis of three concatenated genes (16S rRNA, *flaB,* and *glpQ*) revealed three distinct *Borrelia* lineages. Two lineages clustered within the relapsing fever *Borrelia* group, warranting further characterization of their biological properties. The third lineage formed a highly divergent bat-associated *Borrelia* group, pointing to potential cryptic speciation given the sequence variation across the three loci; however, formally classifying this taxon requires additional genetic markers and wider sampling. This study provides the first molecular-level evidence of *Borrelia* in Thai bats and bat-infesting ticks, suggesting the need for further investigation into the biological behavior and pathogenic potential of regional spirochetes.

Keywords: *Borrelia*; bats; soft ticks; *Reticulinasus* sp.; Thailand

#PC027

Molecular Identification of Caparinia sp. and Notoedres cati Mites from African Pygmy Hedgehogs (Atelerix Albiventris) in Thailand

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ABSTRACT

The African pygmy hedgehog (*Atelerix albiventris*) (Mammalia: Erinaceidae) is a widely kept exotic pet prone to mite infestations, such as genus *Sarcoptes, Otodectes*, *Chorioptes*, *Demodex*, *Caparinia*, and *Notoedres*. Of these, *Caparinia* and *Notoedres* mites cause significant dermatological diseases, including pruritus and inflammation. While *Caparinia* infestations are documented in Asia, there are currently no published reports of *Caparinia* and *Notoedres* co-infestation in hedgehogs globally, nor any documented cases of either mammalian species. Thus, in this study, five affected hedgehogs were sampled from a private veterinary hospital in Bangkok Province, central Thailand. Skin lesions were scraped and collected for microscopic examination of mites and DNA sequencing of the partial cytochrome c oxidase subunit 1 (*cox1*) genes. Results revealed that two hedgehogs were infested exclusively with *Caparinia* sp., one with *Notoedres cati*, and two exhibited a co-infestation of both species. Genetic analysis demonstrated that all *Caparinia* sequences shared an identical haplotype with 100% similarity to *Caparinia* sp. AD1647 (KF891934) infesting an African pygmy hedgehog in South Korea. In the meantime, *Notoedres* sequences contained two haplotypes, sharing 99.24-100% similarity with *Notoedres cati* M23-14 (PV933848) from a raccoon (*Procyon lotor*) in Florida, USA. To our knowledge, this represents the first confirmed report of *Caparinia* sp. and *N. cati* co-infestation in hedgehogs in Thailand. Importantly, although *N. cati* has zoonotic potential, human infestation is uncommon and typically causes transient, self-limiting pruritic dermatitis. Accurate identification of this mite is therefore essential for appropriate veterinary treatment and for minimizing health risks to affected animals and people in close contact with them.

Keywords: African pygmy hedgehog; mite; *Caparinia*; *Notoedres cati*; Thailand

#PC039

Morphological and Molecular Characterization of Lipoptena axis from Captive Eld's Deer at Khao Kheow Open Zoo, Thailand

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ABSTRACT

Deer keds (*Lipoptena* spp.) are hematophagous ectoparasitic flies of the family Hippoboscidae. Although L. axis has been reported in Thailand, additional data are needed to characterize deer keds in captive cervid populations. This study aimed to identify deer keds from captive Eld's deer at Khao Kheow Open Zoo, Thailand, using morphological and molecular analyses and to describe their COI sequence variation.

A total of 37 keds (14 males and 23 females) were collected and morphologically identified as *Lipoptena axis*. The mitochondrial cytochrome c oxidase subunit I (COI) gene was amplified and sequenced for all 37 specimens. BLASTn comparisons yielded 100% nucleotide identity to GenBank sequences labeled as *L. axis* (PQ428974; 80% query coverage), *L. fortisetosa* (OL850869; 93% query coverage), and *Lipoptena* sp. (OP451897; 93% query coverage), and 92.4% identity to *L. cervi* (KR362255; 100% query coverage). These identities apply to the aligned regions, and the matches to multiple species labels limit species-level interpretation of the BLAST results. Sequence analysis in DnaSP identified two nucleotide sequence types (ntSTs). Maximum likelihood phylogenetic analysis in IQ-TREE placed the two ntSTs in a cluster with reference sequences identified as *L. axis* from Khon Kaen Zoo and *Lipoptena* spp. previously reported from Khao Kheow Open Zoo.

Morphological identification supported the occurrence of *L. axis* on captive Eld's deer at Khao Kheow Open Zoo, while COI analysis documented two ntSTs and their relationships with previously reported Thai sequences. These findings add molecular data for deer keds at this site. However, the BLAST matches to sequences carrying different species labels highlight the need for cautious interpretation of COI-based species identification alongside morphological evidence.

Keywords: *Lipoptena axis*, COI, Eld's deer, Thailand

#PC031

Mosquito Community Composition and Diversity in Ranong and Bangkok, Thailand, with Molecular Screening for Avian Malaria

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ABSTRACT

Mosquitoes are ecologically important insects and vectors of pathogens that cause diseases in humans, birds, and other vertebrate hosts. Understanding mosquito community composition and diversity is therefore essential for ecological assessment, vector surveillance, and disease monitoring. However, information on mosquito diversity and the potential occurrence of avian malaria parasites in mosquitoes in Thailand remains limited and fragmented, partly because mosquito communities and population dynamics are influenced by environmental conditions. This study aimed to characterize and compare mosquito community composition and diversity between Ranong, representing a coastal habitat, and Bangkok, representing an urban habitat, and to investigate the occurrence of *Plasmodium* spp. in *Culex* mosquitoes. Adult mosquitoes were collected using CDC light traps during three sampling rounds from December 2024 to June 2026, yielding 14,147 specimens, including 1,683 from Ranong and 12,464 from Bangkok. Collections were dominated by *Culex*, particularly *Culex sitiens* in Ranong and the *Cx. vishnui* subgroup in Bangkok. Ten taxa were recorded in Ranong and 13 in Bangkok. Based on taxon-level abundance, Ranong showed slightly higher Shannon diversity ($H' = 0.507$) and Pielou's evenness ($J' = 0.220$) than Bangkok ($H' = 0.469$ and $J' = 0.183$, respectively), whereas Simpson diversity was comparable between the two areas ($1 - D = 0.205$ and 0.204, respectively). For molecular analyses, 170 *Culex* mosquitoes from Ranong were examined by PCR targeting the mitochondrial *cox1* gene and screened for *Plasmodium* spp. using the mitochondrial cytochrome *b* (*cytb*) gene. Twenty mosquitoes from the first collection, morphologically identified as 18 *Cx. sitiens* and two *Cx. gelidus*, were selected for *cox1* sequencing to confirm species identification, while no *Plasmodium*-positive samples were detected. These findings provide baseline information on mosquito community composition and diversity in coastal and urban settings in Thailand and establish a foundation for vector surveillance and monitoring of avian malaria parasites.

Keywords: avian malaria; mosquito diversity; parasite; Thailand; vector

#PC020

Multilocus Sequence Analysis of the Spotted Fever Group Rickettsiae in Amblyomma varanense Ticks from Varanids in Thailand

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ABSTRACT

Reptiles are increasingly recognized as hosts or reservoirs of diverse microorganisms; however, the diversity of rickettsiae in their associated ticks remains poorly investigated. The present study aimed to characterize *Rickettsia* species circulating within *Amblyomma varanense* ticks parasitizing Asian water monitors (*Varanus salvator*) from Western Thailand. We utilized a comprehensive multi-locus sequence analysis targeting a robust 6-gene panel (*gltA*, *17-kDa*, 16S rRNA, *ompA*, *ompB*, and *sca4*) to accurately resolve the taxonomic position of these bacteria. Phylogenetic hypotheses and genetic analyses demonstrated two distinct clades (A and B) within the spotted fever group (SFG) rickettsiae. Of these, clade B was identified as *Candidatus* Rickettsia ranongensis. Meanwhile, clade A showed genetic divergence that is highly consistent with established criteria for the recognition of a putative novel *Rickettsia* species compared to clade B or the other relatives *Rickettsia monacensis* IrR/Munich (LN794217) and *Rickettsia tamurae* subsp. *buchneri* PalLab (CP113531). For this taxon, we propose the name "*Candidatus* Rickettsia varanensis". Interestingly, these two species exhibited identical *gltA* sequences but diverged significantly in the *ompA* and *ompB* sequences, suggesting cryptic lineages. These findings emphasize the necessity of multilocus analysis for accurate rickettsial taxonomy and underscore the extensive, hidden microbial diversity.

Keywords: Tick; *Amblyomma varanense*; *Rickettsia*; Spotted fever group; Thailand

#PC014

Practice-Based Risk Management for Severe Fever with Thrombocytopenia Syndrome in Companion Animal Clinics: Field Experience from Yamaguchi, Japan

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ABSTRACT

Severe fever with thrombocytopenia syndrome (SFTS) is an emerging tick-borne zoonotic disease in East Asia. In Japan, SFTS has become a practical concern in companion animal practice because direct transmission from infected animals to humans, including veterinary professionals, has been reported. Yamaguchi Prefecture, which has accumulated early clinical, virological, and regional veterinary experience with SFTS, provides a relevant field context for sharing clinic-level preparedness.

This practice-based report summarizes field experience from a companion animal clinic in Yamaguchi and regional veterinary association activities aimed at raising awareness and preparedness for suspected SFTS cases. Key points were organized from the viewpoint of first-contact companion animal practice.

Practical risk management begins before close contact with the animal. Reception-based screening should include outdoor access, tick exposure or prevention status, fever, depression, anorexia, jaundice, thrombocytopenia, and leukopenia. Suspected cases can be managed through time and space separation, such as car waiting, modified appointment timing, and limited patient flow. Personal protective equipment should protect against bites, scratches, blood, body fluids, and mucosal exposure while remaining practical for safe cat handling. Sample handling, including blood collection, smear preparation, centrifugation, packaging, and referral testing, should be treated as a potential exposure point. Staff involvement should be minimized and roles should be defined in advance. Post-exposure procedures and communication pathways with medical and public health sectors should be prepared before an incident occurs.

Unlike well-recognized zoonoses such as rabies, SFTS may pose an unrecognized occupational risk during routine examination, restraint, treatment, and sample handling before the disease is suspected. Field experience from endemic areas can help translate scientific knowledge into practical clinic-level protocols connecting animal health, occupational safety, and public health.

Keywords: SFTS; tick-borne zoonosis; companion animal practice; occupational exposure; One Health

#PC025

Prevalence of Leishmania Infection in Cattle in Thailand Using Direct Agglutination Test (DAT), ELISA, and Nested ITS1-PCR

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ABTSRACT

Leishmaniasis is a zoonotic disease caused by protozoan parasites of the genus *Leishmania*, and identifying competent reservoir hosts is key to understanding its transmission. In Thailand, rising numbers of autochthonous human cases have raised concerns over domestic and peridomestic animals, particularly cattle, as potential reservoir hosts. This study aimed to investigate the occurrence of *Leishmania* infection in beef and dairy cattle across the four major regions of Thailand. A total of 316 blood and serum samples were collected from beef and dairy cattle in 14 provinces. Samples were examined for anti-*Leishmania* antibodies using the Direct Agglutination Test (DAT; *L. donovani* antigen) and enzyme-linked immunosorbent assay (ELISA; crude soluble antigen of *L. martiniquensis*), while *Leishmania* DNA was detected using nested ITS1-PCR. Among the 316 samples, 109 (34.5%) had DAT titers >1:100, with three samples (0.95%) reaching the endemic-area cutoff (≥1:3200). ELISA identified 233 seropositive samples (73.7%), whereas nested ITS1-PCR detected *Leishmania* DNA in 47 samples (14.9%). The overall agreement between DAT and ELISA was 27.2%. These findings indicate widespread serological evidence of *Leishmania* exposure in cattle, though their epidemiological role as reservoirs remains unclear. Further longitudinal and vector-based studies are needed to clarify cattle's contribution to *Leishmania* transmission. This study provides baseline data for future surveillance and supports One Health strategies for leishmaniasis control in Thailand.

Keywords: *Leishmania*; cattle; DAT; ELISA; Nested ITS1-PCR

#PC019

Protozoan Parasites of Rodents in the West of Iran with a Focus on Their Zoonotic Potential

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ABSTRACT

Rodents play a significant role in transmitting zoonotic protozoan diseases, including leishmaniasis, babesiosis, giardiasis, cryptosporidiosis, and microsporidiosis. Although scattered reports of rodent parasitic infections exist across Iran, no comprehensive study has examined the diversity of rodent parasites in Nahavand County, Hamadan Province. This study aimed to examine the occurrence of blood and intestinal zoonotic protozoan parasites in rodents in Nahavand County, Western Iran.

From May to October 2022, a total of 61 rodents from seven species were captured in rural areas, and blood (*n*=48) and fecal (*n*=57) specimens were examined using conventional PCR (cPCR). Genomic DNA was extracted, blood DNA was tested for *Leishmania*, *Trypanosoma*, *Hepatozoon*, and *Babesia*, and fecal samples were tested for *Giardia*, *Cryptosporidium*, *Enterocytozoon*, and *Encephalitozoon*. Positives were Sanger-sequenced. In addition, thin smears of rodent blood were prepared, stained with Giemsa, and examined microscopically.

In total, 54.4% (31/57) of rodents were infected with at least one intestinal protozoan, with the infection rate highest in males (31.6%) than in females (22.8%). Fecal specimens tested were positive for *Cryptosporidium* spp. 31.6% (*n*=18), *Encephalitozoon* spp. 19.3% (*n*=11), *Enterocytozoon* spp. 14% (*n*=8), mix *Enc.+Ent.* 5.3% (*n*=3), and *Giardia* spp. 10.5% (*n*=6). Infection was highest in *Arvicola amphibius* (*n*=19, 33.3%), followed by *Microtus socialis* (*n*=5, 8.8%), *Mus musculus* (*n*=5, 8.8%), and *Talpa davidiana* (*n*=2, 3.5%). The other rodent species, i.e., *Rattus norvegicus*, *Apodemus sylvaticus*, and *Apodemus witherbyi*, were free of intestinal protozoa. *Cryptosporidium parvum*, *Enterocytozoon bieneusi*, *Encephalitozoon intestinalis*, *Cryptosporidium* sp., and *Giardia* sp. were confirmed by Sanger sequencing. No positive blood protozoa were observed in thin blood smears or by cPCR.

This study reveals a high prevalence of zoonotic intestinal protozoa in rodents in western Iran. The results highlight the need for continuous monitoring and risk assessment of the transmission of these parasites to humans and animals in the region.

Keywords: Rodent; *Cryptosporidium*; *Giardia*; *Enterocytozoon*; *Encephalitozoon*; Iran

#PC033

Spatio-Temporal Distribution of Avian Haemosporidian Parasites Infecting Captive Avians in Thailand Zoological Parks

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ABSTRACT

Zoos play an important role in ex-situ conservations. The health of captive animals is essential to guarantee success of such programmes. However, zoo birds frequently suffer from vector-borne parasitic infections, which are often caused by avian haemosporidian parasites (Phylum: Apicomplexa) of the genera *Haemoproteus*, *Plasmodium*, and *Leucocytozoon*. Unfortunately, studies determining the occurrence and diversity of these parasites in zoo avians in Thailand are limited and fragmented. In this study, the prevalence and genetic lineage of avian haemosporidians (*Haemoproteus*, *Leucocytozoon* and *Plasmodium*) infecting avians in various zoological parks in Thailand were investigated. A total of 505 birds, comprising 49 species across 13 orders, were collected randomly as a part of routine health checks in three different seasons (summer, rainy, and winter) between 2023 and 2026. Thin blood smear microscopy and PCR targeting the cytochrome b (*cytb*) gene were used to detect and identify infections. PCR products were subsequently subjected to DNA sequencing, and the resulting sequences were queried against the GenBank and MalAvi public databases for parasite identification. In total, 129 birds (25.5%) were PCR-positive, comprising of 15 (2.9%) infected with *Haemoproteus* spp. across 6 different lineages and 64 (12.7%) with Plasmodium spp. in 11 different lineages. The highest rates of *Plasmodium* infection were detected in the Galliformes order (21/64; 32.8%) and Sphenisciformes (19/64; 29.7%). Temporal analysis revealed that the majority of cases occurred during the winter season, with possible explanations including climatic effects on parasite development or spatial variation in vector abundance.

Keywords: Bird; haemosporidian; *Plasmodium*; spatio-temporal distribution; zoo

#PC036

Zoonotic Protozoan Contamination in the Seven Lakes of San Pablo, Laguna: A One Health Approach for Ecosystem and Community Health

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ABSTRACT

Freshwater lake ecosystems sustain food sources, recreational activities, and community livelihoods, yet they remain vulnerable to contamination from zoonotic pathogens such as *Cryptosporidium* spp. and *Giardia* spp. These pathogens pose significant public health risks, particularly in areas where human, animal, and environmental interfaces overlap. The ongoing study investigates the prevalence and potential sources of these enteric protozoans in lake waters and tributaries, and surrounding animal populations in the Seven Lakes of San Pablo. Fecal samples were collected from companion animals (dogs and cats), livestock, and poultry within a 200-meter radius of the lakes, concurrent with 10-L water samples from lake bodies and tributaries. Using immunofluorescence assay (IFA), initial findings revealed high prevalence rates of *Cryptosporidium* and *Giardia* across multiple hosts. For *Cryptosporidium*, infection rates reached 63.0% (dogs) and 71.0% (cats), 78.2% in poultry, and 50.0% in livestock. *Giardia* was similarly widespread, detected in 18.3% of companion animals, 63.3% of poultry, and 60.0% of livestock. Water samples, specifically in Sampaloc Lake, likewise showed contamination, with *Cryptosporidium* in over 70.0% of the sites and *Giardia* at 40.0%. Knowledge, Attitude, and Practices (KAP) surveys among households highlighted gaps between awareness and hygiene behaviours among animal owners and lake communities, indicating that anthropogenic activity, and poor sanitation practices exacerbate contaminations risks. These preliminary findings emphasize the need for integrated surveillance, source tracking, and community education within a One Health framework. Coordinated efforts are essential to mitigate protozoan contamination, safeguard ecosystem integrity and protect human health.

Keywords: One health, Seven Lakes, protozoans, *Cryptosporidium*, *Giardia*

#PC005

Uncovering Hidden Strongyle Diversity in Captive Asian Elephants and White Rhinoceroses Using ITS-2 DNA Metabarcoding

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ABSTRACT

Gastrointestinal strongyle nematodes are among the most prevalent parasites affecting captive megaherbivores, yet their taxonomic diversity and host specificity remain inadequately characterized due to the limited resolution of conventional morphological diagnostic methods. This study employed high-throughput internal transcribed spacer-2 (ITS-2) rDNA metabarcoding to characterize the gastrointestinal strongyle communities of captive Asian elephants *(Elephas maximus)* and white rhinoceroses *(Ceratotherium simum)* maintained in a private zoo in Thailand. Fecal samples collected from four elephants and six rhinoceroses were subjected to Illumina MiSeq amplicon sequencing, followed by sequence denoising using the DADA2 pipeline and taxonomic assignment against the NCBI/GenBank database. Metabarcoding analysis identified *Murshidia* spp. in both host species, whereas *Kiluluma ceratotherii* was detected exclusively in rhinoceroses. Phylogenetic reconstruction based on ITS-2 sequences revealed distinct host-associated clades and provided evidence of potential cryptic diversity within the *Murshidia* and *Kiluluma* lineages, suggesting evolutionary divergence linked to host adaptation. To our knowledge, this is among the first studies in Southeast Asia to apply ITS-2 metabarcoding for the molecular characterization of strongyle communities in captive elephants and rhinoceroses. These findings demonstrate the utility of DNA metabarcoding as a sensitive, non-invasive approach for comprehensive parasite surveillance, improve our understanding of strongyle biodiversity and host specificity, and underscore the importance of expanding curated molecular reference databases to enhance taxonomic resolution and support conservation-oriented health management of endangered wildlife.

Keywords: DNA metabarcoding, ITS-2 rDNA, Strongyle nematodes, Wildlife parasitology

Poster Submissions

Session Track:

Production Animals

#PC017

Host miRNA Signatures in Bovine Theileriosis: Insights from Peripheral Blood Mononuclear Cells

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ABSTRACT
Bovine theileriosis is an economically important haemoparasitic disease associated with alterations in host immune responses. MicroRNAs (miRNAs) are important post-transcriptional regulators and may serve as molecular biomarkers of infection. This study characterized miRNA expression in peripheral blood mononuclear cells (PBMCs) from healthy and diseased cattle and identified candidate biomarkers of bovine theileriosis. PBMC samples from healthy (n=4) and diseased (n=5) cattle were subjected to small RNA sequencing using the Illumina platform. Following quality filtering and removal of adapters, non-coding RNA and repetitive sequences, reads of 18–30 nucleotides were mapped to the *Bos taurus* reference genome. Known and novel miRNAs were identified and quantified using miRDeep2, while differential expression was assessed using DESeq2, with $p<0.05$ considered statistically significant. A total of 471–539 known and 64–84 novel miRNAs were identified across individual samples. Comparative analysis identified 541 miRNAs in the differential-expression dataset, of which 77 were significantly differentially expressed, comprising 46 upregulated and 31 downregulated miRNAs in diseased cattle. Several miRNAs showed consistent upregulation, including bta-miR-155, bta-miR-34a, bta-miR-143, bta-miR-222, bta-miR-10225a, bta-miR-3432a, bta-miR-122, bta-miR-147, bta-miR-877, bta-miR-7857-5p and bta-miR-144. Among the most strongly upregulated miRNAs were bta-miR-10225b, bta-miR-10225a, bta-miR-2285u, bta-miR-3533 and bta-miR-2357, whereas bta-miR-11986b, bta-miR-130a, bta-miR-2425-5p, bta-miR-7861 and bta-miR-135b were among the most strongly downregulated. Several miRNAs also exhibited consistent downregulation across diseased animals, including bta-miR-181a, bta-miR-494, bta-miR-125a, bta-miR-130a, bta-miR-340, bta-miR-375, bta-miR-99b and novel-miR-1372. Heat map analysis clearly separated healthy and diseased samples, indicating a distinct disease-associated miRNA signature, while volcano plot analysis highlighted significantly differentially expressed miRNAs based on fold change and statistical significance. Target gene enrichment suggested involvement of these miRNAs in immune regulation and infection-related signalling pathways. Target-gene enrichment suggested involvement of differentially expressed miRNAs in immune regulation and infection-related pathways. The distinct miRNA profile in diseased cattle identified promising candidate biomarkers of bovine theileriosis. Selected miRNAs were further validated by RT-qPCR, with analysis currently underway to assess their diagnostic potential.

Keywords: miRNA, Theileriosis, Bovine, Biomarker, PBMC

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#PC030

Philometrid Nematode Infecting the Ovaries of Japanese Threadfin Bream Nemipterus japonicus (BLOCH, 1791): Prevalence, Histopathology, and Effect on Reproductive Potential

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ABSTRACT

A philometrid nematode was observed infecting the ovaries of female Japanese threadfin bream *(Nemipterus japonicus)*, locally known as "bisugo," collected from Manila Bay, Philippines. A total of 817 female *N. japonicus* were systematically examined from August 2018 to January 2019. The overall prevalence of infection was 56.1%, with intensity ranging from 1 to 14 nematodes per infected host. The highest prevalence was recorded in Bataan (69.3%), followed by Cavite (62.8%) and Bulacan (37.8%). Moreover, infection rates were significantly higher during the wet season (66.7%) compared to the dry season (44.4%) ($p \leq 0.05$). Histopathological examination of infected mature ovaries revealed severe tissue alterations, including oocyte follicle displacement, tissue fibrosis, necrosis, and host inflammatory responses marked by granuloma formation, macrophages, and lymphocytic infiltration around viable and degenerated worms. Furthermore, infection significantly impaired host reproductive fitness, with mean fecundity being significantly higher in uninfected individuals (121,490.81 ± 9,442.58 eggs per ovary) than in infected fish (73,818.58 ± 3,456.40 eggs per ovary; $p = 0.0001$), accompanied by a significant negative correlation between infection intensity and egg count ($r = -0.118$, $p = 0.037$). These findings demonstrate the high occurrence of gonad-infecting philometrids in Manila Bay and highlight their direct pathological damage and adverse impact on host reproductive potential.

Keywords: *Nemipterus japonicus*, Philometridae, histopathology, fecundity, Manila Bay

#PC002

Diagnosis of Immature Paramphistomosis in Cattle: Moving Beyond Egg Detection Towards Stage-Specific Diagnosis

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ABSTRACT

Paramphistomosis, or rumen fluke infection, is an important snail-borne trematode disease of cattle and other ruminants. Adult *Paramphistomum* spp. are commonly found in the rumen and reticulum, but they are generally of low pathogenic significance. The major clinical disease is caused by immature flukes that colonise and damage the small intestinal mucosa, particularly the duodenum and anterior jejunum. Heavy immature burdens can result in enteritis, foul-smelling diarrhoea, dehydration, loss of electrolytes and proteins, loss of condition, reduced productivity and mortality.

Routine diagnosis is commonly based on faecal sedimentation for detection of paramphistome eggs. This method is useful for identifying patent adult infection, but it has important limitations in acute immature paramphistomosis because immature flukes do not yet produce eggs. Literature from snail-borne disease mapping also emphasizes that prepatent infections are not detectable by egg detection and that eggs per gram is not a reliable direct measure of adult fluke numbers. Therefore, diagnosis of the pathogenic immature stage requires a stage-specific approach.

This lecture will discuss a practical diagnostic framework combining routine egg sedimentation, dissecting microscopic examination of diarrhoeic faeces, total sediment count of immature flukes, and post-mortem recovery of immature paramphistomes from the proximal small intestine.

#PC003

Epidemiological Investigation of Five Zoonotic Intestinal Protozoa from Yaks and Sheep on the Qinghai-Tibet Plateau

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ABSTRACT

Yaks and Tibetan sheep are endemic livestock species on the Qinghai-Tibet Plateau. Infections with intestinal protozoa in these animals not only affect their health but also pose potential threats to public health safety. In this study, fecal samples were collected from Sichuan, Qinghai, and Ningxia, and a total of 265 samples were subjected to PCR and nested PCR assays for the identification of five zoonotic protozoa (*Blastocystis* sp., *Entamoeba* spp., *Cryptosporidium* spp., *Enterocytozoon bieneusi*, and *Buxtonella sulcata*). *Blastocystis* sp.-positive samples were further selected for 18s RNA high-throughput sequencing. Based on sequence alignment and phylogenetic analyses, the molecular epidemiological characteristics of these five zoonotic intestinal protozoa in yaks and Tibetan sheep were elucidated. The results showed that the overall positive rate of the five protozoan species reached 92.83%, with mixed infections being prevalent, among which dual infections accounted for 58.13%. The infection rate of *Blastocystis* was 75.85%, and a total of ten subtypes (ST1, ST5, ST10, etc.) and one potential novel subtype were identified. The infection rate of *Entamoeba* was 89.43%, with nine species (including *E. bovis*, *E. cf. bovis*, *E. marina*, etc.) and three potential novel genotypes being detected. The infection rate of *Cryptosporidium* was relatively low (0.75%) identified as *Cryptosporidium parvum*. The infection rate of *Enterocytozoon bieneusi* was 12.45%, with a significantly higher rate in Tibetan sheep (18.56%) than in yaks (8.93%) ($p < 0.05$). The infection rate of *B. sulcate* was 7.55%, with a significantly higher rate in yaks (11.31%) than in Tibetan sheep (1.03%) ($p < 0.05$), and the infection in diarrheic samples was significantly higher than that in healthy samples ($p < 0.05$). This study provides the prevalence of five zoonotic intestinal protozoa in yaks and Tibetan sheep on the Qinghai-Tibet Plateau, confirming the widespread occurrence of zoonotic genotypes. Thereby, it provides a basic data for risk assessment and control of those parasites in this region.

Keywords: Yak; Tibetan sheep; zoonotic protozoa; molecular epidemiology

#PC007

Molecular Identification of Anaplasma spp. in Cattle, Thailand: The Role of MSP-4 in Understanding Phylogenetic Relationships

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ABSTRACT

Although *Anaplasma marginale* is the most frequently reported *Anaplasma* species infecting cattle in Thailand, relatively little is known about the occurrence and genetic diversity of other *Anaplasma* spp. in the country. Previous studies have documented *A. marginale* infections in several regions of Thailand, including the northeastern, central, northern, and southern regions. In the present study, we investigated *Anaplasma* infection in cattle from Nan and Phatthalung provinces using an *msp4*-specific primer. The aligned regions of the *msp4* gene were approximately 849 bp for *A. marginale* and 682 bp for other *Anaplasma* sp. sequences. Phylogenetic analysis based on *msp4* sequences revealed five distinct clades. Four *Anaplasma* sequences obtained in this study clustered within clade 1 and were closely related to *A. centrale* sequences from South Africa and Israel and Uncultured *Anaplasma* sequences from Sudan and Kenya. In contrast, two sequences obtained in this study were clustered with *A. marginale* sequences previously reported from Thailand, Colombia, and India within clade 3. Notably, the close phylogenetic relationship between the four sequences and *A. centrale* suggests the presence of an *A. centrale*-related *Anaplasma* lineage in cattle in Thailand. Overall, these findings indicate that genetically diverse *Anaplasma* lineages may circulate among cattle in Thailand, including lineages related to *A. centrale* in addition to the widely reported *A. marginale*. Further studies using additional molecular markers and epidemiological approaches are warranted to confirm the taxonomic identity, distribution, and epidemiological significance of these *Anaplasma* lineages.

Keywords: *Anaplasma* sp., *msp4* gene, cattle, Phylogenetic analysis, Thailand

#PC038

Development of Transient Transfection System in Theileria orientalis

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ABSTRACT

Theileria orientalis is a tick-borne hemoprotozoan parasite that infects cattle and causes oriental theileriosis. Several outbreaks associated with substantial economic losses have been reported throughout the Asia–Pacific region, including Australia and Japan. A better understanding of this parasite's biology is essential for developing effective control strategies. To facilitate functional studies, genetic manipulation has become an indispensable tool in apicomplexan parasites. Transfection system established for *Plasmodium* spp. and *Babesia* spp. have greatly advanced our understanding of parasite biology and host–parasite interactions while accelerating vaccine and drug development. However, despite the availability of the whole-genome sequence of *T. orientalis*, functional studies of this parasite have not been performed because no transfection method has been established. Therefore, this study aimed to develop a transient transfection system for *T. orientalis* as the first step in transfection system development. The parasites were maintained in bovinized mice, in which circulating blood had been replaced with bovine red blood cells (RBCs), and parasitemia reached approximately 30% at 4 weeks post-infection. Plasmids containing the *T. orientalis elongation factor 1* α 5′ untranslated region (UTR), *NanoLuc luciferase* or *gfp* as a reporter gene, and the *thioredoxin peroxidase 1* 3′ UTR were constructed. The plasmid was transfected into parasite-infected RBCs collected from bovinized mice using the Amaxa 4D-Nucleofector system. NanoLuc luminescence activity was subsequently measured. Six electroporation programs were tested, most of which had previously been reported for use with *Plasmodium* and *Babesia* species. Among these, transfection with FP115 showed the highest luminescence activity. Furthermore, GFP-expressing parasites were detected by fluorescence microscopy 24 h after transfection with the GFP expression plasmid using the FP115 program. In summary, this study successfully achieved transient transfection in *T. orientalis* for the first time.

Keywords: *Theileria orientalis*; tick borne disease; transfection

#PC024

Identification of Etoposide as a Lead Repurposed Anticancer Agent Against Trypanosoma evansi Through Integrated In Vitro, In Vivo, and Molecular Analyses

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Abstract

The *Trypanosoma evansi* is the most pathogenic animal trypanosome, which leads to annual economic loss of US $ 671.1 million in India. Limited drug availability, high toxicity, severe side effects and emerging drug resistance necessitate the investigation of novel and safer chemotherapeutic agent. Therefore, in the present study, a total of three anti-cancer drug molecules (etoposide, gemcitabine and β-lapachone) were evaluated for their anti-trypanosomal activity against *T. evansi* and cytotoxicity against mammalian cells. The IC_{50} value of etoposide, gemcitabine and β-lapachone were calculated as 4.856 μM, 32.35 μM and 684.7 nM, respectively. Likewise, the specific selectivity index (SSI) of drugs against Vero cell line was recorded as 5.98, 5.01 and 7.44, respectively. Similarly, the specific selectivity index (SSI) of drugs against equine PBMCs was recorded as 5.34, 6.55 and 39.0, respectively indicating substantial margin of safety of the drugs in mammalian cells. Thereafter, all the drugs with more than five specific selectivity index (SSI) were evaluated for therapeutic efficacy in the mice model. In mice experimentation, significant reduction in parasitaemia and increased longevity of *T. evansi* infected mice was observed after administration of etoposide. Further, these drugs were investigated for their mode of action by studying the mRNA expression of 13 drug target genes using qPCR. In mRNA expression analyses, there is significant down-regulation of trans-sialidase, topoisomerase II and calcium ATPase 1 after exposure of *T. evansi* with IC_{50} concentration of etoposide indicating the effect of drug on calcium homeostasis, cellular uptake of macromolecules and production of replication intermediates. The data generated will be of immense use in future drug development strategies for curtailment of *Surra* in animals.

Keywords: Anti-cancer drugs, Cytotoxicity, qPCR, mice experimentation, *Trypanosoma evansi*

#PC006

Comparative Efficacy of Anthelmintics Against Equid Gastrointestinal Nematodes and Molecular Identification of Cyathostomins in Bahtoo Area, Myanmar

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ABSTRACT

In equids, gastrointestinal nematodes cause health complications ranging from nutrient loss, anemia, and diarrhea to life-threatening colic. Monitoring anthelmintic efficacy is essential for sustainable parasite control and preventing treatment failure. In Myanmar, there was limited information and this study aimed to evaluate anthelmintic efficacy, and identification of GI nematodes. Faecal samples prior to administration of any anthelmintics were collected and examined for the presence of GI nematode eggs by using McMaster counting method to count eggs per gram (EPG). The 80 horses, 80 donkeys and 80 mules with EPG ≥ 50 were selected and divided into four groups; one group was 20 equids; Group A (Ivermectin treated group), Group B (Albendazole treated group), Group C (Combination of Ivermectin and Albendazole (CombIA) treated group), Group D (untreated group). On day 14 post treatment, EPG and faecal egg count reduction percentage (FECR%) were calculated. The results demonstrated highly significant reduction in mean EPG for all treated groups across all three equids. Untreated groups showed a statistically significant increase in mean EPG. In horses, FECR% showed 99.41% in CombIA, 91.54% in ivermectin and 83.51% in albendazole. In donkeys, FECR% showed 99.99% in CombIA, 95.35% in ivermectin and 93.30% in albendazole. In mules, FECR% showed 99.29% in CombIA, 85.50% in ivermectin and 82.87% in albendazole. Across all three equids, albendazole showed the lowest reduction rates and CombIA indicated a highly effective synergistic action. Therefore, utilizing a combination strategy may achieve optimal clinical efficacy and delay the development of drug resistance. In faecal examination, strongyle eggs were predominantly observed and species identification was performed. DNA was extracted from Cyathostomins and PCR targeting 5.8S rRNA gene and ITS-2 region was proceeded. Cyathostomin species were confirmed by sequencing analysis. The nucleotide sequence was identical to *Cylicocyclus nassatus* and allows precise monitoring of anthelmintic resistance.

Keywords: Equids; Gastrointestinal nematode; Ivermectin; Albendazole; CombIA