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Abstracts

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Editor: Bartłomiej Ferra

Plenary session

Session: Plenary session

55 years of parasitology at the University of Gdańsk

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Abstract

Parasitology was one of the first specializations to arise with the development of Biology at the University of Gdańsk, and research in this field has continued uninterrupted to this day. Its foundations were laid by prof. Feliks Piotrowski, one of the pioneers of Biology in Gdańsk and a founding father of the current Faculty of Biology. These origins stretch back to the Department of Zoology in 1967, part of the Gdansk University of Pedagogy, which in turn served as the foundation for the modern University, which was established in 1970. Prof. Piotrowski was involved with research on parasitic arthropod of mammals, particularly Phthiraptera. As further researchers gradually joined the team, including assistants of prof. Piotrowski, the scope of its research expanded to include new directions. This subsequent growth was driven by prof. Sławomir Kadulski, who developed a research topic on the ecology and biology of ungulates, including game and utility mammals. Then, prof. Jerzy Rokicki initiated helminthological research, which focused mainly on the subject of fish parasitofauna. This line of research was broadened to include other groups of parasites and hosts by subsequent team members, including prof. Leszek Rolbiecki and prof. Joanna N. Izdebska; from the beginning of her scientific activity, prof. Izdebska has worked with the taxonomy and biology of parasitic arthropods, particularly the skin mites of mammals. Currently, these organisms, especially the Demodecidae, constitute the flagship subject of the unit. It is worth mentioning that prof. Izdebska, together with prof. Rolbiecki and the other team members, have discovered and described 25% of the known demodecid species in the world fauna. The Laboratory of Parasitology and General Zoology currently studies a wide range of parasitic arthropods and helminths, ranging from contemporary populations of vertebrates, including humans, to archaeoparasitology, using a variety of research methods and techniques.

Keywords: 55 years of parasitology, history of parasitology, University of Gdańsk

OS – oral session

Session: Plenary session

The (almost) whole truth about ticks in forests and city parks

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Abstract

There is a widespread belief that ticks and tick-borne diseases have emerged as a health threat in recent years, and this phenomenon is mostly associated with climate change. This summary outlines the results of several projects aiming to identify the risk associated with Ixodes ricinus and Dermacentor reticulatus vector role and the environmental factors enabling their occurrence and settlement in new areas. Both species play a significant role in the transmission of viruses (TBEV), bacteria (*Rickettsia* spp. and/or *Borrelia burgdorferi* s.l.), and *Babesia* spp. Both can co-occur in natural and 'human' habitats. Among environmental factors, the availability of suitable habitats and hosts seems of highest significance. Ticks rely on biodiversity and are a part of it. There is a need for more efficient monitoring of tick diversity and density, as well as for better control (ticks) and diagnostic (tick-borne diseases) methods.

Keywords: ticks, tick-borne diseases, *Ixodes ricinus*, *Dermacentor reticulatus*

OS – oral session

[S1]

Vectors and pathogens

Session: S1 Vectors and pathogens

Vaccine and microbiota-based control strategies targeting ticks and tick-borne diseases

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Abstract

Over the past decade, the global increase in tick-borne diseases – many of them zoonotic – has underscored the urgent need for integrated strategies that safeguard both human and animal health. Advancing our understanding of the molecular interplay between ticks, pathogens, and the tick microbiome is essential to unravel the complex biology underlying vector-borne transmission. Such insights open the door to novel targets for vaccines, therapies, and vector control measures. In particular, the tick microbiome has emerged as a promising avenue for microbiota-based interventions aimed at reducing pathogen spread.

At IHMT, the research group focused on ticks and tick-borne diseases has directed its efforts toward identifying therapeutic targets that disrupt both vector competence and pathogen survival. A *Rhipicephalus–Babesia* experimental model – developed in light of the veterinary and economic impact of *Babesia* spp. – has proven to be a powerful platform for multiple investigations. This model supports a vaccinology-driven approach, complemented by transcriptomic and proteomic analyses and functionally validated through gene silencing, leading to the discovery of tick related proteins induced by *Babesia* infection towards the pathogen transmission and vector fitness.

In parallel, comparative analyses of the bacteriome in tick salivary glands and midgut tissues – both infected and uninfected with *Babesia ovis* – are shedding light on microbial shifts associated with infection, offering potential pathways for microbiota-targeted control strategies.

Keywords: *Babesia ovis*, tick-borne diseases, vaccine, microbiota, control strategies

OS – oral session

Session: S1 Vectors and pathogens

The varied rate of egg development in the tick *Dermacentor reticulatus*

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Abstract

Fully engorged adult females of the ornate dog tick *Dermacentor reticulatus* were collected from horses in the Seven Island Lake Nature Reserve in Poland. In the laboratory, the tick females were placed in an incubator at room temperature and 70–80% humidity and kept there until oviposition. Egg-laying began about two weeks after collection, and the entire process lasted from four to five weeks. Observations showed that the first larvae hatched after two to three weeks, while the female was still laying new eggs. Microscopic examination revealed that embryonic development begins shortly after the eggs are laid, resulting in clutches containing eggs at various stages of development.

Three females in the process of oviposition were subjected to histological examination. The females were fixed in 3% formalin neutralized with $CaCO_3$. Histological sections were prepared and stained with eosin and hematoxylin. The sections showed uteri filled with darkly stained, mature eggs ready for laying. Also visible were oviducts containing eggs at earlier stages of development. The intestine, filled with darkly stained remnants of food content, was pushed to the sides of the body.

Preliminary observations suggest that egg production and maturation begin immediately or shortly after the female finishes feeding. Oocytes mature unevenly, and the female's body contains eggs at different developmental stages simultaneously.

The described preliminary findings require confirmation through more detailed studies using electron microscopy techniques.

The project received funding from the MSCA4Ukraine initiative, supported by the European Union.

Keywords: *Dermacentor reticulatus*, egg, embryonic development, histological examination

OS – oral session

Session: S1 Vectors and pathogens

Transovarial transmission as a mechanism for rickettsial persistence in *Dermacentor reticulatus* populations parasitizing horses

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Abstract

While significant efforts have been made to study tick-borne *Rickettsia* spp., this public health challenge remains complicated by limited knowledge of the ecology of ticks and tick-borne rickettsiae. Equines are typically asymptomatic hosts of *Rickettsia* spp., and rickettsioses in horses are poorly documented and often underdiagnosed. The high prevalence of *Rickettsia*, including some zoonotic species, has important implications for human health, as people are increasingly in close contact with equines posing a potential risk for spread and transmission.

In this study, we assessed the likelihood of transovarial transmission of tick-borne rickettsiae from engorged adult female *D. reticulatus* ticks collected from horses in the Lake of Seven Islands Nature Reserve, Poland. In the laboratory, female ticks were maintained until oviposition. Both individual adult ticks (n=33) and pooled samples of their eggs were tested for the presence of *Rickettsia* spp. and *Anaplasma* spp. using molecular techniques. Individual blood samples were collected from horses (n=20) and analyzed using the same molecular methods.

Rickettsia spp. were detected in all surveyed *D. reticulatus* female ticks and their eggs, demonstrating the potential for vertical transmission among engorged adult females. Furthermore, seven out of twenty horses tested positive for *Rickettsia* spp., indicating a prevalence of 35%. *Anaplasma* spp. were not detected in any of the tested samples, including ticks, eggs, or horse blood.

Results provide insights into ecology of rickettsiae in horses, highlighting the role of transovarial transmission in the maintenance of *Rickettsia* spp. within the zoonotic foci of rickettsioses in natural ecosystem.

The project received funding from the MSCA4Ukraine, supported by the EU and the PAS-SAS 2024-18 project „Tick-borne pathogens of horses in Poland and Slovakia“. The views expressed are those of the authors and do not necessarily reflect those of the EU or the MSCA4Ukraine Consortium.

Keywords: *Rickettsia* spp., transovarial transmission, *Dermacentor reticulatus*, horses, natural ecosystem

OS – oral session

Session: S1 Vectors and pathogens

Vector-borne pathogen surveillance in stray animals during military conflict: A case study from Ukraine

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Abstract

The 2022 military conflict in Ukraine has triggered a humanitarian crisis, including a rise in stray dog populations due to displacement and infrastructure collapse. These animals may act as reservoirs for vector-borne pathogens, posing a growing biohazard risk, especially as climate change expands tick habitats and transmission seasons.

Vector-borne diseases caused by *Babesia, Anaplasma*, and *Borrelia* spp. are of particular concern due to their zoonotic potential. However, data on their prevalence in Ukraine's stray dogs are limited. This study aimed to assess the presence of these pathogens in stray dogs during the conflict. From March to December 2023, in collaboration with ESCCAP and Ukrainian NGOs, we conducted a parasitological survey of 247 stray dogs across Kharkiv, Sumy, Zvenyhorodka, Berdychiv, and Lviv.

Blood samples were collected and analyzed using Real-Time PCR. *Babesia canis* was detected in 39 dogs (15.8%) and *Anaplasma phagocytophilum* in 10 dogs (4.1%), while *Borrelia* spp. were not detected. Co-infections with *Babesia canis* and *Anaplasma phagocytophilum* were found in three animals (1.2%).

These findings provide new insights into the epidemiology of tick-borne diseases in stray dogs in Ukraine. They highlight the need for targeted surveillance and underscore the importance of a One Health approach in conflict zones. Strengthening diagnostics and timely interventions in companion animals is essential to reduce zoonotic transmission risks.

This project received funding from the MSCA4Ukraine initiative, supported by the European Union. The views expressed are those of the authors and do not necessarily reflect those of the EU or the MSCA4Ukraine Consortium.

Keywords: *Babesia* spp., *Anaplasma* spp., *Borrelia* spp., stray animals, Ukraine

OS – oral session

Session: S1 Vectors and pathogens

Ecological and genetic differentiation of *Dermacentor reticulatus* in Eastern Poland and its implications for pathogen transmission

Zbigniew Zając[1], Joanna Kulisz[1], Aneta Woźniak[1], Katarzyna Bartosik[1], Angélique Foucault-Simonin[2], Sara Moutailler[2], Dasiel Obregón[3], Alejandro Cabezas-Cruz[2]

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Abstract

The ornate cow tick (*Dermacentor reticulatus*) is a key vector of tick-borne pathogens (TBPs) in Europe, especially in the Central-Eastern region. This study presents an integrated analysis of spatial distribution, population density, genetic structure, and pathogen prevalence in adult *D. reticulatus* collected from three adjacent provinces in eastern Poland: Lublin, Świętokrzyskie, and Subcarpathian.

Fieldwork was conducted during peak seasonal activity in spring and autumn using standardized methods across 176 study sites. Tick densities varied considerably, from moderate values (3.3–5.8 ticks/100 m²) at range margins to extremely high densities (mean up to 96.8 ticks/100 m²) in lowland grassland habitats. Random forest and correlation analyses identified altitude, relative air humidity, and habitat type (e.g., ecotonal meadows) as the primary environmental factors influencing tick presence and abundance.

Molecular screening revealed a consistently high prevalence of TBPs. *Rickettsia raoultii* was the dominant pathogen (24.0–84.2%), alongside *Babesia canis*, *Anaplasma phagocytophilum*, *R. helvetica*, *R. aeschlimannii*, *Theileria* spp., and *Ehrlichia* spp. Pathogen composition varied significantly between forest and meadow biotopes, and co-infections were frequently observed.

ITS-2 sequence analyses of *D. reticulatus* revealed low genetic variability, with identified haplotypes matching those found in Central and Western Europe, suggesting a recent expansion of a genetically homogeneous lineage. The surveyed areas represent the current southern and central limits of the species' contiguous range in Poland.

These findings highlight the ecological adaptability and growing vector potential of *D. reticulatus*, emphasizing the need for continued surveillance in the context of landscape transformation and climate change.

Keywords: *Dermacentor reticulatus*, ticks, tick-borne pathogens

OS – oral session

[S2]
Modern research methods in parasitology

Session: S2 Modern research methods in parasitology

The trivalent recombinant chimeric *Toxoplasma gondii* proteins – a good diagnostic tool for detecting IgG antibodies

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Abstract

Toxoplasmosis is one of the most common and neglected parasitic diseases caused by the intracellular parasite *Toxoplasma gondii*. Although infection with *T. gondii* generally manifests in mild clinical symptoms, there are exceptions to this general pattern both between and within different host species. It is widely acknowledged that pregnant women and immunocompromised individuals are considered the main risk groups for severe complications of *T. gondii* infection. In animals, especially sheep, goats, and pigs, *T. gondii* infection can lead to abortions and congenital infections, resulting in significant economic losses for the farming industry. The parasitic invasion in humans and animals is associated with certain problems, such as the lack of effective immunoprophylaxis or a complex diagnostic algorithm, which require continuous improvement. Both problems can be overcome by the recent development of *T. gondii* proteomics, which has allowed the design of different recombinant antigens.

In this study we evaluated the potential usefulness of recombinant chimeric *T. gondii* proteins for serodiagnosis. A chimeric protein composed of the surface antigens SAG1-SAG2 was developed and used as the basis for the generation of subsequent trivalent chimeric proteins containing different immunodominant fragments of the parasite antigens. The recombinant proteins were used in an indirect enzyme-linked immunosorbent assay (ELISA) to evaluate their ability to detect specific IgG antibodies in human and animal sera. Serum samples were analyzed to assess the sensitivity and specificity of the tests. Five of the antigens tested demonstrated 100% sensitivity and specificity in the ELISA for the detection of specific IgG antibodies. These results provide an optimistic outlook for the potential replacement of the currently used native antigen mix with recombinant proteins in *T. gondii* serodiagnostics.

This research was funded by the National Science Centre, Poland (UMO-2018/31/D/NZ6/02839).

Keywords: *Toxoplasma gondii*, toxoplasmosis, recombinant chimeric protein, serum samples, ELISA, serodiagnosis, antibodies

OS – oral session

Session: S2 Modern research methods in parasitology

Parasitological diagnostics in Poland: what do medical laboratories really offer?

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In Poland, access to laboratory diagnostics at the client or patient's request has become almost unlimited. Over the past 30 years, there has been dynamic growth in corporations providing laboratory-medicine services. Private companies, driven by profit, strive to remain competitive and to reach as many clients as possible by constantly expanding their portfolios and releasing new products tailored to customer demand.

In our study, we analysed the range of parasitological laboratory tests which are available on the market, focusing on offer diversity, the prices of the tests, the types of biological material accepted, and the stability of samples prior to testing. We also examined the information provided to clients regarding the appropriate timing of tests and the limitations of the applied methods. Finally, we assessed whether the offer included tests which are inconsistent with the current state of scientific knowledge.

This work was supported by the Institute of Medical Sciences, Faculty of Medical Science. Collegium Medicum, Cardinal Stefan Wyszyński University in Warsaw.

Keywords: diagnostics, parasitology

OS – oral session

Session: S2 Modern research methods in parasitology

Circulating cell-free DNA (cfDNA) of *Toxoplasma gondii* as a diagnostic and prognostic marker of infection

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Abstract

Toxoplasmosis remains a diagnostic challenge due to the complex biology of *Toxoplasma gondii* and variable host immune responses. Current diagnostic tools include direct detection of the parasite (via microscopy or DNA amplification) and indirect serological assays detecting IgA, IgM, and IgG antibodies. However, these methods have key limitations: tissue localization of the pathogen hinders direct detection, while antibody dynamics—especially in immunocompromised individuals—complicate the interpretation. Importantly, they lack the ability to reliably distinguish between acute, chronic, and reactivated infections.

Molecular diagnostics, such as PCR, can detect *T. gondii* DNA in clinical samples but do not provide information on the parasite viability or infection stage. This highlights the need for biomarkers that are both specific and reflect active infection.

A promising candidate is circulating cell-free DNA (cfDNA)—short fragments of pathogen-derived nucleic acids, such as SAG1 gene, released into body fluids during the parasitic life cycle. cfDNA is detectable regardless of tissue localization, degrades rapidly, and is present in plasma during acute *T. gondii* infection. This makes it a potentially powerful, non-invasive marker for early diagnosis, especially in high-risk populations like immunocompromised patients, pregnant women, and newborns.

Emerging evidence suggests that *T. gondii* cfDNA could serve as a dynamic biomarker that complements or even surpasses current methods in sensitivity and clinical relevance. Its use could enable better infection staging, prognosis, and personalized therapeutic strategies.

Further research is essential to validate cfDNA's utility and standardize its clinical implementation.

Keywords: *Toxoplasma gondii*, toxoplasmosis, circulating cell-free DNA, serology diagnostic, molecular diagnostics, acute infection, chronic infection

OS – oral session

Session: S2 Modern research methods in parasitology

The potential of AI in parasitological diagnostics

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Abstract

One of the most common applications of AI in medical diagnostics is the analysis of images from computed tomography, magnetic resonance imaging or X-rays. One of the leading applications of artificial intelligence is in the area of image interpretation automation. Software can recognize and characterize objects found. These possibilities of AI applications in medicine are growing and are commonly described as "computer vision". These systems are trained on millions of images, which allows them to "learn" to recognize pathological changes – e.g. cancer tumors or atherosclerotic changes. Image analysis systems based on AI are also increasingly used in laboratory diagnostics, including: urine sediment analysis, histology and parasitology. Currently used parasitological microscopic image analysis systems offer great potential for their commercial use, but they do not allow for full automation of parasitological examination. So far, AI has found the greatest application in the examination of feces to recognize dispersive forms of parasites. The presentation aims to summarize the current advancement of AI-based systems in veterinary parasitological diagnostics.

Artificial intelligence (AI) is a hot topic in society, but increasingly also in terms of applications in medicine. Modern algorithms can learn. This learning can be supervised by a human, but unsupervised learning models are often used. However, we must still remember that computers cannot "think" in the purely human sense of the word, and yet this intrigues many of us.

Keywords: AI, diagnostics, parasitology

OS – oral session

Session: S2 Modern research methods in parasitology

A novel approach preventing spirochaetes spread in human skin models (Genoskin)

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Abstract

Lyme borreliosis is the most common TBD in Europe, affecting 650,000–850,000 people annually. Currently, no methods exist for disinfecting the site of a tick bite to prevent infection and spread of bacteria. We evaluated the effectiveness of photoinactivation using *in vitro* alive human skin model (Genoskin). Skin biopsies were intradermally inoculated with 10x5 – 10x7 *B. afzelii* followed by photoinactivation at certain time intervals. To evaluate skin infection, we set bacteria cultures from model medium (evidence of spirochate migration) and from biopsies, after 7 days of incubation. Histopathological examination of infected, treated and control biopsies was performed to assess changes caused by infection and/or treatment. Molecular methods were also used for confirmation of infection.

Results: 1) human skin models could be effectively infected with *B. afzelii*; 2) photoinactivation effectively eradicated spirochetes in treated samples, with no positive cultures in treated groups. In untreated controls, however, *B. afzelii* presence was confirmed through both culture and PCR. Histopathological examination of infected, untreated samples showed preserved tissue structure, with no substantial infection-induced damage. These findings suggest that photoinactivation may serve as a promising, non-invasive method to disinfect tick bite sites.

Study funded by UW IDUB New Ideas 2B no. IDUB-622-317/2022 (AB).

Keywords: : Lyme disease, prevention, tick bite, beam of light

OS – oral session

[S3]
Human parasitoses and environmental hazards

Session: S3 Human parasitoses and environmental hazards

Unwanted souvenirs from travel: imported parasitic skin diseases

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Abstract

Parasitic and other dermatological conditions represent a significant proportion of illnesses in travelers returning from tropical regions, accounting for approximately 20% of all diagnoses. According to data from the multicenter GeoSentinel Surveillance Network, the most common dermatological diagnoses include cutaneous larva migrans, insect bite–related conditions (including secondary bacterial infections and skin abscesses), and allergic skin reactions. Overall, arthropod-related dermatoses account for 31% of all skin disease cases in this patient population. In the Department of Tropical and Parasitic Diseases, Medical University of Gdańsk (Gdynia, Poland), the most frequently identified parasitic skin infections include cutaneous leishmaniasis, myiasis, cutaneous larva migrans, and tungiasis. The majority of patients encountered diagnostic difficulties prior to referral to our center, primarily due to limited diagnostic experience among healthcare providers in non-endemic areas. Effective prevention and timely recognition of tropical skin diseases require both appropriate pre-travel counseling and increased diagnostic awareness among healthcare professionals. Travelers should be advised to avoid direct contact with sand, soil, and animals, use insect repellents regularly, and carry a basic travel medical kit including topical antifungals, corticosteroids, and, in cases of extended or remote travel, an oral antibiotic with adequate coverage for common pyogenic bacteria.

Keywords: imported diseases, parasitosis, cutaneous leishmaniasis, myiasis, cutaneous larva migrans, tungiasis

OS – oral session

Session: S3 Human parasitoses and environmental hazards

Assessment of the risk factors in severe infections with *Acanthamoeba* spp. in humans associated with wearing contact lenses and exposure to pathogens from aquatic habitats

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Abstract

Protists from *Acanthamoeba* genus complete their life cycles in external environments as exozoic forms: active trophozoites and dormant cysts. The amoebae are ubiquitous in natural and man-made habitats worldwide; some strains can enter the human body and exist as endozoic forms; the amphizoic organisms can exist as free-living amoebae and as parasites. *Acanthamoeba* strains may pose a serious risk for human health as agents of *Acanthamoeba keratitis* (AK), which affects immunocompetent persons. Serious keratitis cases were assessed in this study. Swabs from affected eyes were tested for AK diagnosis. Slit lamp, confocal microscopy, *in vitro* cultivation under axenic conditions for the detection of Acanthamoeba spp., bacteria, and fungi, and molecular techniques were applied for amoeba species identification. In the 15 cases of serious AK detected in the wearing contact lenses (CL), symptoms of reduced visual acuity appeared with various intensity. Pathological changes in affected eyes involved corneal epithelium, with pain, excessive lacrimation, and then extended to the deeper layers progressively. From the AK referred to CL, 12 cases were connected with the exposure of humans to amoebae from water habitats: washing CL in domestic tap water, bathing in CL in chlorinated swimming pools, and seawater. In several cases, bacteria, e.g., *Pseudomonas aeruginosa*, fungi, and microfilariae were identified in contact lens users. The assessment confirmed a clear connection between serious risk of *Acanthamoeba* infections with poor hygiene during wearing contact lenses and exposure to amoebae in aquatic habitats. The progressive, sight-threatening disease is challenging in terms of diagnosis, treatment, and prevention, due to amoebae may transmit pathogenic endosymbionts, and amoeba cysts are extremely resistant to anti-microbial, anti-parasitic drugs. The ability to prevent AK is limited due to the wide range of habitats where amphizoic amoebae may occur.

Keywords: amphizoic amoebae, facultative parasites, *Acanthamoeba keratitis*, risk factors, contact lenses

OS – oral session

Session: S3 Human parasitoses and environmental hazards

Alpha-gal syndrome: from rarity to rising diagnosis – new discoveries and current knowledge review

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Abstract

Alpha-gal syndrome (AGS) is a delayed type I hypersensitivity reaction to the carbohydrate galactose-α-1,3-galactose (α-gal), recently recognized as a growing global health issue. This review summarizes current knowledge and highlights emerging insights, particularly regarding parasitic infections as potential contributors to α-gal sensitization beyond tick exposure. AGS typically presents with delayed allergic reactions (3–6 hours post-ingestion) to red meat and other mammalian-derived products, as well as immediate responses to certain drugs such as cetuximab. Clinical manifestations range from mild gastrointestinal symptoms to severe anaphylaxis. While tick bites remain the primary known trigger, recent evidence implicates helminths, including *Ascaris lumbricoides*, in the pathogenesis of AGS. We present a case of an 18-year-old woman with nocturnal anaphylaxis in the absence of tick exposure, in whom elevated anti-α-gal IgE and concurrent *Ascaris* infection were confirmed. Studies have identified α-gal epitopes in *Ascaris* glycoproteins—sometimes in higher concentrations than in ticks—and demonstrated a correlation between α-gal-specific and *Ascaris*-specific IgE. Recombinant *Ascaris* protein ABA-1 has been shown to activate basophils in AGS patients, supporting its potential causal role. These findings suggest a broader immunoparasitological perspective in which helminths may trigger or amplify allergic responses to carbohydrate antigens. Furthermore, α-gal sensitization has been associated with an increased risk of coronary artery disease, indicating potential long-term cardiovascular implications even in asymptomatic individuals. Clinically, AGS should be considered in cases of unexplained anaphylaxis or chronic gastrointestinal symptoms, regardless of tick exposure history. Parasite screening may be a useful diagnostic adjunct, and dietary recommendations should be individualized, as some patients may react to dairy products in addition to red meat.

Keywords: allergy, galactose-a-1,3-galactose, alpha-gal syndrome, *Ascaris lumbricoides*

OS – oral session

Session: S3 Human parasitoses and environmental hazards

Comparative study on oral microbiome of Polish patients from different population groups assessed in terms of threats with contagious factors

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Abstract

Human oral cavity is complex environment still requiring to enhance knowledge. In the study, intraoral microbiome of Polish patients was assessed in terms of threats with local/general infections. In 40 persons 16–26 and 42–52 year-old, parasites *Entamoeba gingivalis* and *Trichomonas tenax,* amphizoic *Acanthamoeba* spp., bacteria and fungi (Enterobacteriaceae Enterococci,and *Candida* strains) were detected by microscopic and culture methods. Concluding, because of the co-occurrence in the oral cavity the parasitic, pathogenic, the opportunistic and facultative parasitic strains including endosymbionts and bacteria and fungi, the oral cavity may act as a reservoir of infectious microorganisms. Simultaneously, it should be taken into account, although mouth microbiota may pose a threat of severe infections, interrelations between microbiome components remains rare subject of research. Pre-treatment oral microbiota species/pathogens identification, preventive elimination of potentially pathogenic strains as well as monitoring microbiome composition during therapy are highly recommended to avoid severe human health complications.

Keywords: intraoral microbiome, pathogenic factors, parasitic protists, amphizoic amoebae, opportunistic and pathogenic bacteria and fungi, threats to human health

OS – oral session

Session: S3 Human parasitoses and environmental hazards

First insights into the immunomodulatory function of phosphoglycerate kinase from *Hymenolepis diminuta*

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Abstract

Hymenolepis diminuta, a tapeworm typically residing in the small intestine of rodents, can occasionally infect humans through the ingestion of infected insects or contaminated food containing the invasive cysticercoid stage. Infections are usually asymptomatic and rarely cause significant pathological changes. To evade the host immune system, both the juvenile and adult stages of the parasite produce a variety of proteins that facilitate host invasion, modulate immune responses, and promote survival within the host's hostile environment. These proteins interact with the host immune system, altering its function and enabling long-term persistence of the parasite. One such protein with potential immunomodulatory properties is the enzyme phosphoglycerate kinase (PGK). However, its role in immune modulation within the parasite–host interaction remains largely unexplored.

The aim of this study was to preliminarily characterize the immunomodulatory potential of recombinant PGK. The research involved cloning of the *pgk* gene, production of recombinant protein using the *Pichia pastoris* expression system, and stimulation of human monocyte-derived dendritic cells (moDCs) with the purified protein in the presence of lipopolysaccharide (LPS). Subsequent analyses focused on pro- and anti-inflammatory cytokine secretion and surface markers associated with dendritic cell maturation and immune tolerance. The recombinant PGK was successfully expressed and its stability and enzymatic activity was assessed. *In vitro* assays revealed a subtle influence on moDC function, suggesting possible immunomodulatory effects. Further studies are warranted to elucidate PGK's precise role in host immune modulation, which could contribute to the identification of novel targets for immunodiagnostics, immunotherapy, or antiparasitic drug development.

Financial support for this study was provided by the National Science Centre Poland (project no 2019/03/X/NZ6/00672).

Keywords: *Hymenolepis diminuta*, phosphoglycerate kinase, recombinant protein, immune modulation, moDCs

OS – oral session

Session: S3 Human parasitoses and environmental hazards

Diagnostic problems in cystic echinococcosis resulting in disease progression – case report

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Abstract

Echinococcosis is a parasitic disease caused by tapeworms of the genus *Echinococcus.* The two most common forms of this disease, caused by different species of tapeworms, are cystic echinococcosis (CE) and alveolar echinococcosis (AE). In the case of CE, the etiological agents responsible for most infections in humans are *E. granulosus* sensu stricto and *E. canadensis.* Humans become infected accidentally by swallowing eggs found in contaminated water or food, or through direct contact with the definitive host, which is most often dogs. Clinically, the parasitic invasion is characterized by a prolonged asymptomatic course. The organ commonly involved in the development of primary lesions in CE is the liver. The diagnosis of CE is usually made based on epidemiological data, imaging studies, serological tests, and histopathological / PCR analyses. We present a case of a patient with the difficulties in diagnosis of CE, resulting in the progression of the parasitic disease.

Keywords: cystic echinococcosis, serological diagnostics, echinococcosis

OS – oral session

Session: S3 Human parasitoses and environmental hazards

Occurrence of *Blastocystis* in selected water reservoirs in the Tri-City (Poland) and surrounding areas

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Abstract

Blastocystis is an intestinal protozoan most frequently isolated from humans and many species of animals. Its pathogenicity has been the subject of much research and discussion for years. Infection with this protozoan can occur directly via the fecal-oral route, as well as indirectly, through consumption of contaminated water and food. *Blastocystis* is detected in various water samples worldwide, but the prevalence is not high. However, it should be noted that there are not many reports on this topic in the available literature. The aim of the study was to determinate whether *Blastocystis* occurs in water bodies in the Tri-City and adjacent areas, what is the scale of this phenomenon, and thus to indicate whether water can pose a threat of infection for people in these areas.

Water from 12 reservoirs was studied, which are places of recreational importance. Samples in each of these places were collected twice: in spring-summer season and autumn. Water samples were analyzed using the classic barcoding method: amplification of the 600 bp region of the ssu rRNA gene followed by sequencing of the PCR product.

Blastocystis was detected in three samples tested. Subtype ST2 was identified once (June, stream) and ST6 twice (November, pond and river).

Blastocystis occurs in water reservoirs in the Tri-City area and surrounding areas, so water may be a potential source of infection for humans, although this is not a significant threat. In order to assess whether the prevalence of this protozoan in particular types of water bodies depends on the season, further research should be carried out on a larger number of samples.

This work was supported by the project "Excellence Initiative – Research University" 71-01415/0004618/61/772/772/2022 „Studies on the occurrence of Blastocystis in environmental samples and in selected animals". COST European Cooperation in Science and Technology. Blastocystis under One Health (OneHealthBlastocystis) is acknowledged.

Keywords: *Blastocystis*, water, Tri-city, Poland

OS – oral session

[S4]
Experimental parasitology

Session: S4 Experimental parasitology

Antiparasitic effect of *Calendula officinalis* glucuronides on the course of *Babesia microti* infection in BALB/c mice.

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Abstract

The study investigated the antiparasitic efficacy of *Calendula officinalis* glucuronides against *Babesia microti* infection in BALB/c mice. Infected erythrocytes were incubated with glucuronides for 12, 24, 36, or 48 hours and subsequently injected into naïve mice. Parasitemia progression and chronic infection duration were monitored microscopically and via qPCR over 120 days post-infection (dpi). Mice experimentally infected with glucuronide-treated erythrocytes (SAP groups) exhibited significantly reduced parasitemia, accompanied by a 2–4 day delay in peak parasitemia compared to control mice. Hematological analysis at 12 dpi showed that SAP-treated mice had higher erythrocyte, hemoglobin, hematocrit, and platelet counts, indicating a milder course of infection. However, glucuronide treatment did not affect *B. microti* DNA persistence, as qPCR detected parasite DNA in all groups up to 120 dpi, suggesting no impact on the duration of the chronic infection. These findings demonstrate that *C. officinalis* glucuronides significantly attenuate the acute phase of *B. microti* infection but do not alter the chronic phase within the first 120 dpi. Extended monitoring to 240 or 360 dpi is ongoing to evaluate long-term effects. This study highlights the therapeutic potential of glucuronides in managing the acute stage of babesiosis. Animal use was approved by the 1st Local Ethical Committee (No. 846/2019).

Keywords: *Babesia microti*, mice, parasitemia, glucuronides

OS – oral session

Session: S4 Experimental parasitology

Determination of the effect of a homolog of macrophage migration inhibitory factor from *Dirofilaria repens* on human macrophage activity in an *in vitro* model

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Abstract

Homologs of macrophage migration inhibitory factor (MIF) have been detected in numerous parasitic nematodes. In mammals, MIF is a cytokine that is a key regulator of the pro-inflammatory immune response. The role of MIF homologs described in nematodes is not understood. Single reports indicate that these proteins have immunomodulatory properties, which could have an impact on the course of infection.

A MIF homolog has been identified in *Dirofilaria repens*, a nematode that is the etiological agent of subcutaneous dirofilariosis. This is a vector-borne disease transmitted by mosquitoes. This nematode primarily attacks dogs, which are the main reservoir of the disease. Despite the growing threat posed by this parasite to humans and animals in Europe, knowledge of its effects on the host's immune system remains limited. In this study, we examined the effect of recombinant MIF from *D. repens* (r*Dre*-MIF-1) on human macrophage activity in an *in vitro* model.

The recombinant protein was obtained using a bacterial expression system and purified by nickel affinity chromatography. THP-1 macrophages were treated with the recombinant r*Dre*-MIF-1 protein, either in the presence or absence of lipopolysaccharide (LPS). After stimulation, culture supernatants and cells were collected to assess the levels of cytokines TNF, IL-6, IL-1β, and IL-10 using ELISA, as well as selected markers associated with M1 and M2 macrophage activation phenotypes using qPCR.

r*Dre*-MIF-1 affects macrophage activity, notably by inhibiting the secretion of pro-inflammatory cytokines in macrophages pre-stimulated with LPS, indicating its anti-inflammatory properties and confirming its immunomodulatory effects.

The study was cofinanced by Science development fund of the Warsaw University of Life Sciences – SGGW.

Keywords: macrophage migration inhibitory factor, *Dirofilaria repens*, immunomodulation, recombinant proteins

OS – oral session

Session: S4 Experimental parasitology

The effect of glucuronides from marigold (*Calendula officinalis*) on the proteome of *Toxoplasma gondii* RH strain tachyzoites in *in vitro* culture

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Abstract

Toxoplasma gondii is an intracellular protozoan parasite responsible for toxoplasmosis, a disease that can cause severe complications and remains a therapeutic challenge, particularly for immunocompromised individuals and the elderly. It is especially dangerous during pregnancy, as tachyzoites can cross the placenta, leading to congenital toxoplasmosis. Although current treatments can be effective, they are often associated with significant side effects, emphasizing the need for alternative therapeutic strategies. In this study, we investigated the effect of oleanolic acid glucuronides isolated from *Calendula officinalis* (common marigold) on the proteome of *T. gondii* RH strain tachyzoites cultured *in vitro*. Parasites were treated with purified glucuronide fractions, and proteomic alterations were analyzed using SDS-PAGE, two-dimensional gel electrophoresis (2-DE), and Western blotting. 1-DE and 2-DE gels were stained with Coomassie Brilliant Blue (CBB) and silver stained (Thermo Scientific, Pierce Silver Stain Kit) to detect differentially expressed proteins.

Preliminary results demonstrate that the glucuronides significantly impair the parasite's ability to invade human fibroblast cells and alter protein expression profiles, suggesting interference with key metabolic or structural pathways.

These findings provide a promising basis for further investigation into the antiparasitic potential of marigold-derived compounds as a novel therapeutic strategy against toxoplasmosis.

Keywords: *Toxoplasma gondii*, toxoplasmosis, glucuronides, antiparasitic effect, proteomics

OS – oral session

[S5]

Young Researcher Competition

Session: S5 Young Researcher Competition

Molecular diversity and taxonomic status of the genus *Australapatemon* within the family Strigeidae (Platyhelminthes, Digenea) in Central Europe

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Abstract

The genus *Australapatemon* Sudarikov, 1959 is a small group of trematodes from the family Strigeidae Railliet, 1919 that parasitizes the digestive system of waterfowl, commonly found in Europe. It was established by Sudarikov, who differentiated it from the genus *Apatemon* Szidat, 1928 by the number of flame cells in cercariae and their specificity to the second intermediate host (leeches versus fishes). The taxonomic status of these genera has been subject to debate due to subtle morphological differences, leading to misidentifications. Recent molecular analyses have revealed distinct lineages and significant hidden species diversity, highlighting the genetic variability and richness of the genus across different regions.

The aim of the study was to investigate the species diversity of the genus *Australapatemon* in Central Europe. For this purpose, phylogenetic analyses were performed of extensive material of adults and larval forms obtained respectively from birds and invertebrates from Poland, using an integrative approach. The analyses were also supplemented by material from Switzerland obtained in cooperation with the Natural History Museum of Geneva. Based on sequenced *COI* mtDNA and 28S rDNA markers, phylogenetic analyses (BI) and ASAP/ABGD analysis were performed.

Our results, based on more than 70 *COI* sequences (ca. 780 bp), provide new data on the phylogeny and biology of *Australaptemon* species, including a description of the life cycle of *A. fuhrmanii* and a determination of the taxonomic affiliation of *Apatemon fuligulae* (=*Australapatemon fuligulae*). Above that, based on the species delimitation analysis, as well as the intra- and interspecific genetic diversity, we expect the occurrence of 5–6 species lineages within the *Australapatemon* clade.

Keywords: Digenea, Strigeidae, *Australapatemon*, taxonomy

OS – oral session

Session: S5 Young Researcher Competition

Diversity of Rickettsiaceae and Anaplasmataceae bacteria within and between species in *Ixodes ricinus* ticks collected from humans in Poland

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Abstract

Ixodes ricinus is the most prevalent tick in Europe, found both in natural habitats as well as urban and rural areas. Although the most recognized tick-borne pathogen is *Borrelia burgdorferi* s.l., increasing attention is being directed towards pathogens from other groups, including spotted fever group *Rickettsia*, *Anaplasma phagocytophilum*, of which some genetic variants are pathogenic to humans, as well as *Neoehrlichia mikurensis*, a causative agent of neoehrlichiosis.

In 2021–2022, we asked participants from all over Poland to provide ticks removed from their skin and to fill out questionnaires regarding the area of tick encounter (urban or rural site). Then we screened *Ixodes ricinus* ticks for the presence of *Rickettsia* spp., *A. phagocytophilum*, and *N. mikurensis* using the PCR method based on the citrate synthase (*gltA*) gene, *16S* rRNA, and heat shock protein (*groEL*) gene, respectively. Afterwards, we sequenced randomly selected amplicons with the Sanger method, compared the obtained nucleotide sequences with the data registered in GenBank and subjected to phylogenetic analyses to identify species and/or genotypes of tested pathogens.

From a total of 1992 *Ixodes ricinus* included in our study, we obtained 342 amplicons positive for *Rickettsia*, 40 for *A. phagocytophilum*, and 55 (of 818 tested) for *N. mikurensis*. From 26 nucleotide sequences of *Rickettsia* spp., we identified 24 as *R. helvetica* and one each as *R. raoultii* and *R. monacensis*. Among the 20 sequenced amplicons of *A. phagocytophilum*, we recognized 4 genetic variants, all of which we classified as zoonotic. We identified all 21 nucleotide sequences of *N. mikurensis* identical with the European variant. Interestingly we found significantly higher prevalence of *A. phagocytophilum* in ticks from urban areas compared to rural and different distribution of genetic variants in ticks from city and the countryside.

The study was supported by the National Science Center (NCN) grant no. 2020/37/B/NZ6/01587.

Keywords: *Ixodes ricinus*, tick-borne pathogens, *Anaplasma phagocytophilum*, *Neoehrlichia mikurensis*, *Rickettsia*

OS – oral session

Session: S5 Young Researcher Competition

PPARγ, RXR, and AhR coordinate *Fasciola hepatica* FABP1-mediated immunomodulation in human dendritic cells

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Abstract

Fasciola hepatica, a helminth parasite with a complex migratory lifecycle, crosses key tissue barriers such as the intestinal wall and liver, relying on immune evasion to establish chronic infection. One of its key immunomodulators, Fatty Acid Binding Protein 1 (FABP1) can induce tolerogenic human monocyte-derived dendritic cells (moDCs), which suppress Th1 responses and promote IL-4 and IL-10 via Thrombospondin-1 (TSP-1). However, the underlying mechanisms remain poorly defined.

In this study, we examined how recombinant FABP1 influences moDC function and T cell responses. Human moDCs were stimulated with FABP1 and LPS, with or without pharmacological inhibitors of PPARγ, RXR, and AhR. Additional experiments tested the effects of retinoic acid (RA) and selected long-chain fatty acids (LCFAs). We assessed cytokine production (IL-6, CXCL11, TNF, TSP-1) and surface markers (CD40, CD80, CD86, MHC II) via spectral flow cytometry.

FABP1 suppressed IL-6 and CXCL11 and induced TSP-1 expression. RA enhanced TSP-1 induction, suggesting synergy. Inhibition experiments showed that TSP-1 induction depends on PPARγ, RXR, and AhR, while CXCL11 suppression is mediated mainly by AhR. Thus, FABP1 engages nuclear receptor pathways to exert distinct immunomodulatory effects.

To assess adaptive responses, FABP1-conditioned moDCs were co-cultured with allogenic naïve $CD4^+$ T cells. After two weeks, increased IL-4/IFNγ ratios and elevated IL-10 production upon restimulation indicated Th2 skewing and regulatory T cell polarization.

Our findings reveal that FABP1 reprograms dendritic cells via nuclear receptors to promote tolerogenic, anti-inflammatory T cell responses, facilitating parasite persistence. This mechanism offers insight into immune regulation at barrier sites and suggests potential for therapeutic modulation of inflammation using helminth-derived molecules.

Financial support for this study was provided by the National Science Center Poland, project number: 2021/43/D/NZ6/01555.

Keywords: *Fasciola hepatica*, immunomodulation, FABP1, dendritic cells

OS – oral session

Session: S5 Young Researcher Competition

Evaluation of the presence of *Toxoplasma gondii* in chicken eggs from different breeding systems – a diagnostic and epidemiological analysis trial

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Abstract

Toxoplasma gondii is a parasite with a complex life cycle, whose definitive hosts are felines, and whose intermediate hosts can be various mammals and birds. Due to the potentially severe course of the disease in pregnant women and immunocompetent individuals, and the prevalence, this parasite poses a significant threat. Although the main routes of transmission are oocysts in cat feces and consumption of raw meat with tissue cysts of the protozoan, chicken eggs – as a commonly consumed product-may be an underestimated source of infection.

Single studies around the world show the presence of protozoan DNA from 36% to 57% in free-range eggs and up to 20% in industrially raised eggs. This varied from country to country: in Australia 90% of eggs were positive, in Iraq 71%, in Ghana 64%, in Vietnam 55%, in Iran 36%, in the US about 10%. No such studies have been conducted in Poland and Europe, despite the great importance of non-thermally processed eggs in food production.

The objectives of my research are: 1) to assess the prevalence of *T. gondii* in eggs from different rearing systems in Poland, taking into account environmental conditions and risk factors; 2) to identify rearing environments particularly predisposed to transmission; 3) to develop recommendations for safe egg consumption for people in potential risk groups.

Tests for the pathogen include molecular and microscopic analysis of eggs, hen tissues and environmental samples (soil, water, feed). They are supplemented by a collected epidemiological history. They will allow identification of the most risky breeding systems. The results obtained have the potential to improve: (I) the safety of consumed eggs in Poland (especially by pregnant women and those at risk of severe toxoplasmosis) and (II) diagnostic guidelines for the poultry industry. Without them, we do not know how much the potentially high source of toxoplasmosis in eggs is a significant epidemiological factor in our country.

Keywords: *Toxoplasma gondii*, toxoplasmosis, chicken eggs, PCR, food safety, epidemiology, breeding systems

OS – oral session

Session: S5 Young Researcher Competition

The first finding of adult *Hyalomma* spp. in Poland in summer 2024: the success of citizen science project

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Abstract

Hyalomma spp. ticks play a crucial role as vectors for the Crimean-Congo haemorrhagic fever virus. *Hyalomma* spp. larvae and nymphs are transported via migratory birds to temperate regions of Europe from Africa, the Middle East, and Mediterranean areas. Recently, the emergence of adult ticks has been documented in numerous countries where they were previously not reported. This study aimed to monitor the potential occurrence of *Hyalomma* spp. ticks in Poland using a citizen science project.

A dedicated website was created through which volunteers could submit photos of unusual ticks. Between April and November 2024, more than 500 online submissions containing tick photos were received, 11 of which were identified as *Hyalomma* spp. ticks. Additionally, we received 65 parcels containing ticks, including 4 *Hyalomma* spp. ticks (of 11 online submissions). Amplification and sequencing of the partial mitochondrial cytochrome c oxidase subunit I gene (*cox1*) was successfully performed for all received specimens.

Hyalomma spp. ticks were recorded in different regions of Poland, and most records were from Greater Poland and Silesia regions, in Western and Southwestern Poland, respectively. Two of the identified specimens were morphologically and molecularly characterized as *Hyalomma rufipes*, while another two were identified as *Hyalomma marginatum*.

The citizen science project enabled the confirmation of occurrence of adult *Hyalomma* spp. ticks in Poland, identifying a new hazard for human and animal health.

The study was funded by National Science Centre, OPUS grant no. 2022/47/B/NZ6/01610.

Keywords: *Hyalomma rufipes*, *Hyalomma marginatum*, Poland, citizen science

OS – oral session

[S6]
Zoonotic threats

Session: S6 Zoonotic threats

Prevalence and molecular characterization of *Mycoplasma* species in wild rodents from Poland

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Abstract

Mycoplasma species are cell wall–lacking bacteria that can colonize the respiratory and urogenital tracts of various mammalian hosts, including rodents, and may play a role as zoonotic pathogens. This study aimed to assess the prevalence and genetic diversity of *Mycoplasma* spp. in bank voles *Clethrionomys glareolus* in Poland.

A total of 1594 rodents were trapped in three forested areas in Mazurian Lake district in the years 1999–2022. *Mycoplasama* spp. were detected based on microscopical examination of 200 fields of vision in stained blood smears and by the PCR amplification and sequencing of *16S* rRNA gene (600 bp).

The overall prevalence of *Mycoplasma* spp. infections was 66.9%. Phylogenetic analysis revealed the presence of several *Mycoplasma* lineages, including strains closely related to *Mycoplasma* sp. from small rodent species, *Akodon montensis* from Brazil, as well as potentially novel genotypes unique to Polish rodent populations. These findings underscore the ecological diversity of *Mycoplasma* spp. in wild rodents in Poland and raise questions about their role for wildlife health and their potential zoonotic threat.

This study demonstrates a high prevalence and considerable genetic diversity of *Mycoplasma* spp. in *C. glareolus* populations across multiple years and locations in the Mazurian Lake district of Poland. The identification of both known and potentially novel *Mycoplasma* lineages highlights the ecological complexity of these bacteria in wild rodent reservoirs. These findings emphasize the need for continued surveillance and genetic characterization of *Mycoplasma* spp. in wildlife, particularly given their potential implications for animal health and zoonotic transmission.

Keywords: *Mycoplasma*, *Clethrionomys glareolus*, rodents

OS – oral session

Session: S6 Zoonotic threats

Autochthonous Asian variants of *Echinococcus multilocularis*

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Abstract

Ingestion of *Echinococcus multilocularis* Leuckart, 1863 eggs with vegetables, fruit or mushrooms can result in the development of a multilocular larva in the liver. The proliferating larva impairs liver functioning, can infiltrate surrounding tissues and metastasise. Key to the transmission of the parasite are its wild definitive hosts, responsible for contaminating the environment with eggs: the native red fox and the invasive raccoon dog (subspecies *ussuriensis*). The presence of tapeworms with Asian genetic traits in the Polish population of the red fox requires further investigation, especially in light of reports demonstrating differences in the virulence of *E. multilocularis* depending on geographical origin.

Two hundred and fifty-two adult *E. multilocularis* tapeworms were recovered from the intestines of 59 red foxes shot in the following districts of northern and northeastern Poland: Puck, Wejherowo, Kartuzy, Kościerzyna, Bartoszyce, Kętrzyn, Węgorzewo, Gołdap and Augustów. For each individual, the cytochrome c oxidase subunit I gene (*cox1*) was sequenced, and the microsatellite EmsB profile was obtained.

Eighty per cent of the tapeworms were characterised by European origin in both the nuclear and mitochondrial genomes. Six per cent of the tapeworms were of Asian origin. Haplotypes and profiles obtained for 14% of the tapeworms indicated hybridisation: interbreeding between European and Asian lineages in the small intestine of definitive hosts.

The clustering of haplotypes in networks and EmsB profiles in dendrograms, close to sequences and profiles from China, supports the hypothesis of the introduction of Asian variants of E. multilocularis into northeastern Poland by invasive raccoon dogs spreading westward from the former Soviet Union, where Soviet breeders translocated them in the early and mid-20th century from the Soviet Far East.

Keywords: alveolar echinococcosis, Asian origin, phylogeography, raccoon dog

OS – oral session

Session: S6 Zoonotic threats

Prevalence of *Echinococcus multilocularis* in household and shelter dogs from Pomeranian Voivodeship

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Abstract

Echinococcus multilocularis is the most dangerous parasite existing in Northern Hemisphere that causes alveococcosis. Humans become infected by ingestion of its eggs excreted by definitive hosts, mainly red foxes (*Vulpes vulpes*), less frequently domesticated cats. In some areas also dogs can play this role. However, in Poland data on *E. multilocilaris* infection in dogs is fragmentary. Thus, the aim of the study was to compare the prevalence of *E. multilocularis* infection in dogs living in shelters and households from Pomerania voivodeship.

In total, 517 dog faecal samples were collected with the help of owners and shelter workers along with a questionnaire describing the dog condition and investigated with the use of nested-PCR. We detected *E. multilocularis* DNA in 31 samples, with an overall prevalence of 6%. Presence of the tapeworm was confirmed in 4.63% of samples collected from shelter dogs compared to 8.29% positive of samples collected from household dogs. All samples that tested positive by nested PCR were subjected to molecular sequencing targeting the *12S* rRNA gene. Findings from this study indicate that *E. multilocularis* is present in dogs across both investigated groups. Results contribute to our understanding of the abundance of *E. multilocularis* in dogs living in Poland as well as potential role of these dogs in parasite transmission. In consequence, this study will complement knowledge about epidemiology of *E. multilocularis* infection, which is of high both local and world interest. Moreover, biomonitoring of prevalence of *E. multilocularis* infection in dogs will help to understand if, and where dogs may pose a threat for humans, especially owners and shelter workers.

This work was supported by the National Science Centre grant no.2020/37/B/NZ7/03934.

Keywords: *Echinococcus multilocularis*, alveococcosis, dogs, nested-PCR, molecular sequencing, biomonitoring

OS – oral session

Session: S6 Zoonotic threats

The first report of *Echinococcus multilocularis* in a European wildcat (*Felis silvestris*) in Poland – preliminary study on the intestinal helminth fauna of wild felids in Poland

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Abstract

Felids (Felidae) can be hosts to many species of parasites, including zoonotic ones. From the epidemiological point of view and the threat to human health, the most dangerous is the tapeworm *Echinococcus multilocularis*, which larval forms in humans lead to alveolar echinococcosis. The typical final host of this tapeworm is the fox, but it can also be other canids, and less frequently – felids. In Poland, this infection has been described in domestic cats. The aim of the study was to preliminarily determine the occurrence of intestinal helminths in wild felids in southeastern Poland, with particular emphasis on *Echinococcus* infections. For molecular testing for individual species of *Echinococcus* genus (and other selected tapeworms), faecal samples taken from the rectum were used: 7 from European wildcats (*Felis silvestris*) and 14 from Eurasian lynx (*Lynx lynx*). After DNA isolation, the material was tested using the multiplex PCR method and a set of qPCR methods. In addition, the intestines (5 wildcat and 12 lynx intestines) were examined using the SCT (sedimentation and counting technique). In one wildcat faeces sample, *E. multilocularis* DNA was detected using both the multiplex PCR and qPCR methods. In the small intestine from the same animal, mature *E. multilocularis* tapeworms were found (n=79). Species identification was confirmed by sequencing. In addition, *Mesocestoides litteratus*, *Hydatigera* sp., hookworms, *Toxocara cati* were also found in wildcats. In samples from lynxes, *Mesocestoides* spp., *Taenia serialis*, *Taenia hydatigena*, *T. cati* were found. The study showed for the first time in Poland the presence of *E. multilocularis* infection in wild felids, which should be taken into account in the analysis of the risk of human infection.

Keywords: *Echinococcus multilocularis*, European wildcat, Felidae, helminths

OS – oral session

Session: S6 Zoonotic threats

Occurrence of trichomonads in the oral cavity of domestic dogs in Lower Silesia, Poland

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Abstract

Trichomonads are protozoan parasites that can be found in a wide range of animal species, as well as in humans. They have been identified in various locations such as the oral cavity of mammals, including dogs. Previous studies indicate that *Tetratrichomonas canistomae* is one of the most frequently isolated species from the canine oral cavity, and its presence is often associated with poor oral hygiene. Other species detected in dogs include *Trichomonas tenax* and *Trichomonas brixi*, which have also been identified in humans, suggesting a potential zoonotic risk.

The aim of the study was to determine the frequency and genetic diversity of trichomonads isolated from the oral cavities of domestic dogs in the Lower Silesia region.

Oral swabs were collected from household dogs living in Lower Silesia between July 2024 and June 2025. Before sample collection, the condition of the oral cavity was assessed. The material was transported in Amies medium and delivered within 24 hours after collection. It was subsequently inoculated into culture medium supplemented with rice starch and horse serum. Samples were evaluated and passaged three times at 48-hour intervals. Genetic material was isolated from the samples, from which protozoan growth was confirmed microscopically. PCR amplification was performed using primers T1 and T2 specific for the ITS1–5.8S rRNA–ITS2 region. PCR products were sequenced, and the obtained sequences were compared to those deposited in the GenBank database.

In some of the examined samples, the presence of trichomonads was confirmed microscopically. Sequencing allowed for the identification of species such as *Trichomonas brixi*.

Keywords: protozoa, trichomonads, dogs

OS – oral session

Session: S6 Zoonotic threats

Wild boars as a reservoir of the zoonotic parasite *Toxoplasma gondii* in Poland

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Abstract

Wild boars may constitute a significant reservoir of the parasite *Toxoplasma gondii*. The high rate of *T. gondii* infection in wild boars may be due to the frequent feeding of these animals near human settlements and contact with *T. gondii* oocysts excreted by cats. The aim of the study was to assess *T. gondii* infection in wild boar population in Poland based on the serological tests and detection of parasite DNA in tissues.

Serum and tissue samples from 500 and 400 wild boars, respectively, were collected during hunts in 2024. A commercial ELISA test was used to detect specific IgG antibodies. Tissue samples were digested with pepsin/HCL solution and DNA was extracted using a commercial kit. To identify *T. gondii* DNA, nested and Real time PCR (B1 gene) were performed. The amplification products were subjected to sequence analysis to confirm the *T. gondii* species.

In total, among 500 wild boars 39.2% positive results in serological tests was found. The highest percentages were found in the

Mazowieckie (67.9%) and Lubuskie (58%) regions and the lowest in Warmińsko-Mazurskie (6.9%) region. In PCR, *T. gondii* DNA was detected in tissue samples of 7% of tested wild boars, which came from: Podkarpackie (23.1% of animals positive in PCR), Wielkopolskie (17.2%), Pomorskie (12.2%), Lubelskie (10.9%), Dolnośląskie (8.3%), Podlaskie (7.1%) and Zachodniopomorskie (4.6%) regions.

The high percentage of seropositive results (39.2%) and the detection of DNA parasite in 7% of the tested animals, indicate a high rate of *T. gondii* infection in the wild boar population in Poland, which is important from the point of view of the potential health risk for consumers.

Keywords: *Toxoplasma gondii*, wild boars, serology, PCR

OS – oral session

[S7]

Alien and invasive species of hosts and parasites

Session: S7 Alien and invasive species of hosts and parasites

Biological invasions in Poland: molluscs and trematodes

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Abstract

Alien species, including molluscs, have been considered key drivers of ecosystem changes, including biodiversity loss. Their success in colonization of new areas is strongly connected with human activity, characteristics of new habitats and biological traits of the species. Interspecific interactions also play a crucial role. There is extensive literature on predation or competition between native and alien taxa, while the data on parasitism are still insufficient. It may be due to several reasons, among which the complexity of the life cycles of many parasites and the lack of comparative parasitological data from native areas of exotic hosts are essential.

Our study aimed to check whether alien in Poland species of molluscs, including *Potamopyrgus antipodarum*, *Physella acuta*, *Menetus dilatatus*, *Dreissena polymorpha*, *Dreissena rostriformis bugensis*, *Sinanodonta woodiana* and *Corbicula* spp. can act as first or second intermediate hosts for digenean trematodes, or can be final hosts for aspidogastrean trematodes.

We found one species of aspidogastrean (*Aspidogaster conchicola*), and three species of digeneans (*Phyllodistomum* sp., *Rhipidocotyle campanula* and *Sanguinicola* sp.) in collected molluscs. Moreover, echinostome metacercariae and xiphidiometacercariae were also observed. Only *Corbicula* spp. had no parasites. In most cases, alien molluscs played the role of the second intermediate hosts for echinostome metacercariae instead of the first intermediate hosts. Further research will allow us to assess whether exotic for Poland molluscs infected with trematodes can decrease the prevalence in native molluscan host populations and cause the 'dilution effect'.

Keywords: biological invasions, snails, mussels, trematodes, lakes, prevalence

OS – oral session

Session: S7 Alien and invasive species of hosts and parasites

Thelazia spp. in European bison (*Bison bonasus*) in Poland: epidemiology, morphological, and molecular data

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Abstract

Nematodes of the genus *Thelazia* pose an increasing threat for wild and domestic ruminants.

To investigate the prevalence, species composition, and associated ocular pathology in European bison populations in Poland, eyes and swabs of 223 European bison from Lowland and Lowland-Caucasian line were collected in years 2020–2024.

Eyes were subjected to parasitological examination by rinsing the conjunctival sac, tear ducts, and surface of the cornea in tap water. Nematodes of the genus *Thelazia* were isolated from the decantated eye sediment, preserved in 70% ethanol, and subjected to morphometrical and molecular analysis of a 689 bp fragment of the mitochondrial cytochrome c oxidase subunit 1 (*cox1*) gene. Genetic material was isolated from swabs and examined using a commercial Real-Time PCR tests for the presence of *Mycoplasma* spp., *Moraxella bovis*, *Moraxella bovoculi*, and *Chlamydia* spp.

Epidemiological analysis of *Thelazia* infection in relation to age, sex, genetic line of European bison as well as severity of ocular changes, bacterial infections, habitat, and season was performed.

Nematodes of the genus *Thelazia* were detected in 61.9% (CI 95%: 55.4%, 68.0%) of the examined animals, with *T. skrjabini* significantly more prevalent than *T. gulosa* (56.5% vs. 14.8%; $p<0.001$).

Presence of ocular changes, including conjunctivitis, keratitis, and corneal ulcers was significantly positively associated with infection of *T. skrjabini* (odds ratio: 3.8; CI 95%: 1.7, 8.7; $p=0.001$).

No significant associations between the occurrence of eyeworms and sex or age of animals, as well as bacterial infections, habitat, or season, were found, supporting the hypothesis that *Thelazia* is endemic in the studied European bison populations.

These findings underscore the widespread presence of *Thelazia* spp. in the European bison population of Poland, and indicate potential clinical significance and impact on animal welfare exerted by *Thelazia*, especially *T. skrjabini*, infection.

Keywords: *Thelazia* nematodes, wild ruminants, eye diseases

OS – oral session

Session: S7 Alien and invasive species of hosts and parasites

From North America to Europe: raccoons, parasites, and public health implications

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Abstract

The presence of invasive species, globally and locally, poses a major threat to biodiversity. The spread of the raccoon, native to North America, and its documented impact on native fauna are now undeniable concerns. With no natural predators, raccoon populations are growing rapidly, making effective control difficult. This expansion also raises questions about the role of invasive species in the spread of parasites and pathogens. An attempt to answer this question was the aim of our long-term study. Parasitological surveys of helminths were conducted on material obtained between 2008 and 2019. Over 300 raccoons were examined post-mortem, including individuals from Poland (mainly), Germany, and the Czech Republic. The overall prevalence was 59.8%, and in total, 13 taxa of helminths from Digenea, Cestoda, Nematoda, and Acanthocephala were identified. Additionally, environmental studies were carried out in selected urban areas to assess soil contamination with eggs of *Baylisascaris procyonis.*

At the same time, faecal and tissue samples were collected for molecular detection of intestinal microparasites and vector-borne pathogens.

Molecular analysis revealed the presence of *Cryptosporidium* skunk genotype, which appears to be the predominant genotype in non-native areas. The *Enterocytozoon bieneusi* NCF2 and D genotypes were also identified. Both Cryptosporidium skunk genotype and *E. bieneusi* genotype D are considered zoonotic. Additionally, the obtained sequences showed significant consistency with representatives of the Eimeriidae isolated from rodents, birds, and reptiles from North America. This result may indicate importation during the expansion.

In total, close to 400 tissue samples (spleen, liver, and ear biopsies) were examined. The presence of the DNA of vector-borne pathogens was screened by amplifying different genes. As a result, the occurrence of *Babesia*, *Theileria*, *Hepatozoon*, *Anaplasma*, *Neoehrlichia, Bartonella*, *Borrelia*, *and Rickettsia* was confirmed.

Keywords: raccoon, invasive species, parasites, pathogens

OS – oral session

Session: S7 Alien and invasive species of hosts and parasites

Data on the biodiversity and biology of skin mites from the family Demodecidae (Acariformes: Prostigmata) in the Eurasian beaver *Castor fiber*

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Abstract

Parasitic arthropods are relatively rare in mammals associated with the aquatic environment, due to the restricted possibility for transfer caused by the biology and ecology of the host, and the fact that it is an unusual environment for these mainly terrestrial ectoparasites. A specific and unique example of the parasitic arthropod fauna occurs in the Eurasian beaver *Castor fiber*, which is the largest European rodent with an amphibious lifestyle. Its parasitofauna has been found to lack the Phthiraptera or Siphnonaptera; two species of tick, *Ixodes apronophorus* and *I. hexagonus*, the beetle *Platypsyllus castoris*, typical of beavers, and 44 species of fur mites from the genus *Schizocarpus* have been reported. Among the skin mites, *Demodex castoris* has been found only once in the nasal area (Izdebska et al.2016).

Currently, the skins of six beavers obtained from the Masurian Lake District in 2011 have been subjected to intensive research based on the digestion and decantation method. It was found that *D. castoris* can inhabit the entire hairy skin of the body and is the dominant species in terms of numbers, with 100% prevalence. No pathological changes associated with its infestation were observed. Two new species to science were discovered, with different locations and limited microhabitats, and mites from the related family Psorergatidae. One, *D.oviportans*, presents an interesting biology: the females transfer the egg and even larvae on the dorsal side of the podosoma. This is the first observation of care for offspring in Demodecidae and one of the few in the context of mites. The Demodecidae in the Eurasian beaver demonstrate an analogous infestation pattern to that in other mammals, with a dominant species inhabiting the hairy skin of the body (hair follicles) with co-occurring species characterised by limited microhabitats. However, the discovery of a species with a biology previously unknown in the Demodecidae indicates a certain uniqueness to this parasitofauna.

Keywords: Acari, Demodecidae, skin mites, *Castor fiber*, host-parasite interaction

OS – oral session

Session: S7 Alien and invasive species of hosts and parasites

Assessment of the degree of helminth infection of the raccoon (*Procyon lotor*) population in Lubusz Voivodeship, Poland

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Abstract

In Poland, raccoon is most abundant in the northern and western parts of the country. Potentially zoonotic parasites for which raccoons can be a reservoir include *Toxoplasma gondii*, *Trichinella spiralis*, *Toxocara* spp., *Baylisascaris procyonis*, *Dirofilaria* spp., and cestodes of the family Taenidae. Because humans can become infected with these parasites, there is a need for monitoring of the spread of raccoon populations and for parasitological studies taking into account qualitative and quantitative analyses of helminth communities as well as the role that raccoons play in the life cycle of specific species of parasites.

The aim of the study was to determine the degree of helminth infection of raccoons in Gorzów County and Sulęcin County in Lubusz Voivodeship.

Raccoon carcasses were obtained in the years 2021–2023 from hunters belonging to the Ostęp Hunting Club and from representatives of the Regional Board of the Polish Hunting Association in Gorzów Wielkopolski. The raccoons were from the vicinity of Witnica, Lake Marwicko, Bogdaniec, and Rudna. Parasitological necropsy was performed on 95 raccoons, of which 75% were infected with helminths. The most commonly isolated helminths were cestodes (Cestoda, prevalence 55.8%, intensity of infection 53, range from 1 to 200) and trematodes (Digenea, prevalence 40.0%, intensity of infection 31, range from 1 to 220). The prevalence of nematodes (Nematoda) was only 3.16% (intensity of infection 2, range from 1 to 3), and the prevalence of acanthocephalans (Acanthocephala) was 5.26% (intensity of infection 2, range from 1 to 3).

The nematodes isolated from the intestines were in the larval stage (probably L3). They were preliminarily identified as belonging to the family Ascarididae. Further identification of the helminths by microscopic and molecular biology techniques was planned.

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Keywords: raccoon *Procyon lotor*, helminth infection, Nematoda, Cestoda, Digenea, Acanthocephala

OS – oral session

[S8]

Helminths in terrestrial and aquatic environments

Session: S8 Helminths in terrestrial and aquatic environments

Helminths of common crane (*Grus grus*) wintering in the South of Ukraine

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Abstract

The common crane (*Grus grus*) is a migratory bird, with a distinct population that winters in southern Ukraine. This study presents the first report on helminths of the crane in Ukraine, based on the examinations of 50 carcasses collected from the Kherson region between January and March 2021. A total of 2,176 specimens of gastrointestinal helminths were recovered. Nematodes were the most prevalent, with a prevalence (P) of 100%, whereas trematodes were found in 54% of cranes and cestodes in 14%. In total, nine helminth species were identified – five nematodes, three trematodes, and one cestode species. The nematodes *Tetrameres paradisea* (P = 86%, intensity (I) = 1–142), *Porrocaecum ardea* (P = 70%, I = 1–31), and *Eucoleus obtusiuscula* (P = 62%, I = 1–53), together with the trematode *Strigea gruis* (P = 50%, 1–96), were predominant. These are all considered typical helminths of cranes. Other species found – *Strongyloides* sp. (P= 26%, I = 1–13), *Gruitaenia lattissima* (P = 14%, I = 1–5), and *Bilharziella polonica* (P = 10%, I = 1) are rarely encountered in cranes. The crane is a new host for nematode *Physocephalus sexalatus* (P = 18%, I = 1–6) and trematode *Strigea sphaerula* (P = 4%, I = 2–8). The crane-specific cestode *G. lattissima* differed slightly from american species *Gruitaenia gruis* in the size of rostellar hooks. Analysis of helminth species co-occurrence within infracommunities revealed no significant associations. Regression models indicated no effect of host sex on intensity, species richness, or infracommunities composition. Within the helminth sample, *T. paradisea* was the most abundant parasite (916 specimens, 42.1 % of all helminths), followed by *S. gruis* (28.4%), *E. obtusiuscula* (16.0%), *P. ardea* (9.70%), and *Strongyloides* sp. (2.1%); the remaining species together accounted for only 1.8% of all helminth specimens.

This study was supported by the National Research Foundation of Ukraine (project number 2023.03/0068).

Keywords: *Grus grus*, helminths, communities, Ukraine

OS – oral session

Session: S8 Helminths in terrestrial and aquatic environments

What are the main parasites of salmon (*Salmo salar*) from the southern Baltic Sea?

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Abstract

Despide of the fact that Atlantic salmon (*Salmo salar*) is important fish species, popular in human consumption, the information related to the presence of parasites in wild fish from the southern Baltic Sea is scarce. That area is a feeding ground where mixing of the populations from different rivers around the Baltic was reported. The aim of our studies was to analyse the presence of liver and intestines parasites in salmon sampled in Polish marine waters during in recent years. During standard ichthyological analyses liver and intestines have been collected and frozen. Thawed livers were digested in artificial gastric juice. The cross section of intestines was conducted. Parasites have been rinced out and the surface of the digestive tract was carefully examined to detect parasites. Parasites were collected and identified to the lowest possible taxonomic level based on anatomical and morphological features. All analysed fish have been found infected with intestinal parasite *Eubothrium* sp. Presence of Anisakidae nematodes *Contracaecum* sp. and *Pseudoterranova* sp. were detected in livers of salmon. Presence of parasites may negatively affected the condition of the fish. Zoonotic Anisakidae nematodes pose a human health risk.

Funding: EU Multiannual Programme for Fisheries Data Collection; statutory research fund of National Marine Fisheries Research Institute: DOT ParaSalmon.

Keywords: salmon, *Contracaecum* sp., *Eubothrium* sp.

OS – oral session

Session: S8 Helminths in terrestrial and aquatic environments

How heavely are the European flounder (*Platichthys flesus*) from the southern Baltic Sea infected with Anisakidae nematodes?

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Abstract

Anisakidae nematodes (such as *Anisakis* sp. and *Contracaecum* sp.) are zoonotic and pose a risk to human health. Surprisingly, the information related to the presence of these nematodes in European flounder (*Platichthys flesus*) is scarce, even though this flatfish is popular in human consumption. The aims of our study was to evaluate the level of European flounder infection with Anisakidae parasite in fish sampled in the Polish waters, southern Baltic Sea. Liver samples were collected in spring 2025 in two sampling areas located in the Polish marine waters. Visual inspection of 250 livers per area was conducted and revealed the presence of nematodes. Furthermore, subsamples of 50 livers per area were collected and digested in artificial gastric juice to reveal the presence of the nematodes. Identification of collected larvae was conducted based on anathomo-morphological features. Prevalence and intensity of infection were calculated and analysed in relation to the biological parameters of fish. In the Gdańsk Basin, the prevalence of nematode infection detected during visual inspection of livers was 0.8 %, and after digestion 8 % (intensity of infection 1–4); in the case of fish caught in the area south of Bornholm island these numbers were 2.8 % and 10 %, respectively, with the intensity of infection ranging 1–9. This indicates that using only visual inspection of livers leads to the underestimation of the infection rates. The presence of *Anisakis* sp., *Contracaecum* sp. and *Hysterothylacium* sp. in the liver of flounder was revealed. The dispersion of Anisakidae nematodes in the Baltic sea may be linked to a rise in the abundance of grey seals, which serve as the final host in their life cycle.

The research is funded by a targeted grant from the Polish Ministry of Agriculture and Rural Development.

Keywords: European flounder, Anisakidae nematodes

OS – oral session

Session: S8 Helminths in terrestrial and aquatic environments

Gastrointestinal parasites in sheep kept in confinement

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Abstract

The infection of sheep with gastrointestinal nematodes and coccidia was studied in a flock of 900 animals kept in confinement. From May to November 2024, a total of 509 individual faecal samples were collected every two months from randomly selected sheep of various ages, and analysed using the McMaster method. Additionally, pooled faecal samples were used for coproculture to identify infective third-stage (L_3) nematode larvae, and for sporulation to determine coccidia species.

Overall, 66.4% of the examined sheep were infected with coccidia of the *Eimeria* genus, with a mean oocyst output of 2,238 (range 20–158,400) oocysts per gram of faeces (OPG), and 18.9% of sheep were infected with Trichostrongylidae nematodes, with a mean of 728 (20–12,000) eggs per gram (EPG). In addition to strongyle-type eggs, sporadic occurrence of *Skrjabinema ovis*, *Strongyloides papillosus*, *Trichuris ovis* and *Aonchotheca* sp. eggs were also noted. The highest intensity of trichostrongylid infection was recorded in May, prior to deworming, whereas prevalence gradually increased in the subsequent months. Lambs aged 6–12 monts and ewes showed higher levels of trichostrongylid infection compared to lambs aged 2–5 months. Identification of 150 trichostrongylid L_3 larvae revealed a predominance of *Teladorsagia circumcincta* (61%), followed by *Trichostrongylus* sp. (27%), *Bunostomum trigonocephalum* (9%), and *Haemonchus contortus* (3%). With regard to coccidia, after the administration of a coccidostat to lambs, *Eimeria* infection slightly decreased in the months following the peak observed in May. Sporulation revealed various *Eimeria* species, with the highly pathogenic *E. ovinoidalis* among the dominants, and the pathogenic *E. crandalis* less frequently detected.

In conclusion, despite the use of coccidiostats in lambs, and whole-flock deworming in May, coccidia and nematodes remained significant parasitic threats in confined sheep, although a second pick of nematode infection didn't occur in late summer.

Keywords: sheep, nematodes, coccidia

OS – oral session

Session: S8 Helminths in terrestrial and aquatic environments

Parasite fauna and diet of the garfish (*Belone belone*) from the southern Baltic Sea

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Abstract

Since 2015, the increasing importance of garfish in local fishing, especially in Puck Bay, has been observed. Seasonal garfish fishing also has cultural significance for the local community. The garfish is a pelagic fish found in brackish and marine waters in the eastern North Atlantic Ocean and adjacent seas. In the Polish waters of the southern Baltic Sea, fish occur mainly in Puck Bay. In this area, garfish is a species that is eagerly caught during its occurrence. It is observed in the coastal zone between April and June, during spawning migration. Knowledge related to the parasite fauna and food composition of that fish is scarce. Diet might not only be a source of nutrients but also might be an important source of fish infection.

Our studies aimed to describe the changes in the helminth fauna and diet of the garfish from the southern Baltic Sea.

The research material was collected in spring 2024 and 2025. Standard analyses of fish were conducted, and the viscera of the fish were frozen for further study. The parasitological analysis of the liver (after digestion in artificial digestive juice) was performed. All found parasites were collected and identified based on anatomo-morphological features. The stomach's diet composition analysis was performed, and all found organisms were identified to the lowest possible level, depending on the level of decomposition.

The prevalence of parasitological infection was approximately 40% (2024) and 44% (2025). In the liver, the most abundant nematode parasites were *Anisakis simplex* larvae and *Contracaecum osculatum*. The dominant element of the diet was Ammodytidae and Gasterosteidae fish in both examined years.

Results were compared with studies conducted in that area a decade ago to analyse the temporal changes in the parasite fauna and diet of garfish. Furthermore, it was analysed whether food elements could be the source of infection.

The project is funded by the Polish Ministry of Agriculture and Rural Development.

Keywords: garfish, parasite fauna, diet, Baltic Sea

OS – oral session

Session: S8 Helminths in terrestrial and aquatic environments

Pigeon digestive tract parasites – screening tests in the Lublin province

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Abstract

Parasitic infections are one of the most common health problems in pigeon flocks. Keeping birds in a flock, often at high density, significantly increases the risk of infection with infectious and invasive pathogens. The aim of the study was to investigate the occurrence of parasitic infestations in pigeon flocks in south-eastern Poland. In the years 2023–2025, pigeons from 168 flocks were examined. The material for the tests was collected directly from the birds. The pigeons were delivered for testing in transport cages. They stayed in them for 2 to 6 hours in order to obtain fresh feces. The study included the analysis of faeces using the Fulleborn flotation method and the examination of mucus suspended in warm physiological fluid taken with a baguette directly from the birds' crop. In birds from 138 flocks, various forms of parasites were found (82.14%). The identified parasites included protozoa of the genus *Eimeria* – oocysts of various species were confirmed with varying intensity of occurrence in 91 flocks (54.16%). Eggs of the roundworm *Ascarida columbae* were found in 53 flocks (31.54%), eggs of *Capillaria spp.* in 62 flocks (36.9%), eggs of *Ornithostrongylus quadriradiatus* in 15 flocks (8.92%), eggs of *Syngamus trachea* in 18 flocks (10.71%), eggs of *Strongyloides avium* in 9 flocks (5.35%) and eggs of tapeworms in 12 flocks (7.14%). Trophozoites and pseudocysts of *Trichomonas gallinae* were found in 68 flocks (40.47%). Individual flocks showed single or "multi-taxon" infections (mixed infections involving different families and genera of parasites). Monoinfection occurred in 26.78% of flocks. Double infections were found in 23.21% of flocks. Mixed infections with three types of parasites were found in 24.4% of herds. Infections with four types of parasites were found in 6.55% of herds, while infections with five types of parasites were found in 1.19% of herds.

Keywords: pigeons, flocks, parasites

OS – oral session

[S9]
New trends in parasitology taxonomy

Session: S9 New trends in parasitology taxonomy

Can dogs be infected with different lineages of *Dirofilaria immitis*? Whole genome sequencing has the answer

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Abstract

Dirofilaria immitis are nematodes that are vectored by mosquitoes and infect mainly members of the canine family causing the lethal disease pulmonary dirofilariosis. the question regarding the possibility of a single host being infected with different lineages (haplotypes) of the nematode arises? This question was not answered by population genetics studies on filarial nematodes so in our work we intend to utilize the Whole Genome Sequencing (WGS) to answer this question. Nine blood samples stored in EDTA in −20 Celsius from canine hosts with high microfilaremia were chosen, Microfilaria was filtered out from each blood sample by lysing the blood with Saponin and Sodium Chloride and the microfilaria was suspended in PBS, DNA was extracted from all MF blood samples, DNA was fragmented and DNA library was prepared for each sample and sequenced with WGS using the Ilumina NovaSeq 6000, where we obtained 6G with 150 bp paired-end reads and were mapped them against a reference genome.

Preliminary results show that a single host to be infected with different haplotypes (variants) of *D. immitis* originating from different lineages and not just offspring. In one sample, the reads based on the *COI* gene showed 16 different haplotypes where the obtained sequence differed from the reference genome with either indels or SNPs based on the reference and alternative alleles, these SNPs are backed by Allelic Depth (AD) and Allelic Frequency (AF) which can; according to bioinformatics; distinguish between haplotypes and their origin, further samples are currently being sequenced and analyzed to obtain a comprehensive overview over the genetic diversity within the same host.

This study will answer this important question and can help establish the direction of spread of the parasite by identifying different lineages and comparing them to previously delinated haplotypes.

This project was funded by the National Science Centre, Poland, OPUS-LAP, grant number: 2023/51/I/NZ6/00988.

Keywords: *Dirofilaria immitis*, genetic diversity, WGS, haplotypes

OS – oral session

Session: S9 New trends in parasitology taxonomy

Preliminary insights into the genetic diversity of *Dirofilaria repens* from Poland: A molecular analysis on whole mitochondrial genome

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Abstract

The genus *Dirofilaria* comprises parasitic nematodes responsible for dirofilariasis, a vector-borne zoonotic disease affecting both canines and humans. Comprehensive genetic characterization of these parasites is crucial for understanding their population structure, transmission dynamics, and host specificity. We compared complete mitochondrial genome about (13000 bp) of *D. repens* originating from humans and dogs in Poland.

Whole mitochondrial genomes were analyzed to assess intra- and inter-host genetic variability. Phylogenetic reconstruction revealed a clear separation between *D. repens* and *D. immitis*, with all Polish isolates clustering within the *D. repens* clade. Additionally, the phylogenetic analysis revealed slight genetic diversity among *Dirofilaria* spp. based on the geographical origin of the samples.

Analysis of the complete mitochondrial genome provided greater resolution, uncovering more extensive genetic variability among *Dirofilaria* species.

This project was funded by the National Science Centre, Poland, OPUS-LAP, grant number: 2023/51/I/NZ6/00988.

Keywords: *Dirofilaria repens*, mitochonderial DNA

OS – oral session

Session: S9 New trends in parasitology taxonomy

Whole-genome sequencing in ecological studies of wildlife parasites: Population genomics of the seal louse *Echinophthirius horridus*

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Abstract

Whole-genome sequencing has become much more accessible in recent years, also for ecological studies of non-model parasitic organisms. In the present study, we investigated factors shaping population-genetic structuring and genetic diversity of the seal

louse *Echinophthirius horridus*, a specialist parasite of Northern Hemisphere seals. We found that of the 12 different host populations examined, geographically isolated, endemic seal (sub) species from the Caspian Sea and Lakes Baikal and Saimaa host the genetically most distinct louse populations. In turn, lice associated with geographically co-occurring seals show signatures of occasional gene flow across hosts. Such population connectivity appears to be enhanced by seal aggregation behaviour and sharing of haul-out sites, as in the case of the near-panmictic population of lice associated with grey and harbour seals in the Baltic and North Seas. Measures of genetic diversity (i.e., mean heterozygosity and theta) of louse populations were statistically significantly related to host population size. The most genetically diverse lice were those associated with the harp seal, the most abundant seal in the Northern Hemisphere, and the least genetically diverse were those associated with the endangered Saimaa ringed seal. Taken together, our results point to a non-adaptive model of parasite diversification and a parallel loss in host and parasite genetic diversity in small isolated populations.

Keywords: coevolution, marine mammals, host-associated genetic differentiation, genetic diversity, specialist parasites

OS – oral session

Session: S9 New trends in parasitology taxonomy

Recent advances and current state of knowledge of phylogenetics and systematics of the Dicrocoeliidae

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Abstract

The Dicrocoeliidae is a highly diverse and broadly distributed family of digeneans typically parasitic in the gall bladder and liver of amniotic tetrapods, characterized by terrestrial life cycles. Some of them are associated with diseases in vertebrates. In the previous 100-plus years several researchers attempted to create a system using traditional characters such as general morphology, life cycles or host specificity. However, due to the nearly universal lack of agreement on the relative value of various characters, none of the proposed systems has been broadly accepted and the systematic history of the group has been extremely tumultuous. In 2008 Teresa Pojmańska summarized the existing knowledge and presented a system with 4 subfamilies. Introduction of DNA sequencing as a readily accessible research tool has brought a revival of attention in systematics. Representatives of several genera have been sequenced and incorporated into molecular phylogenies. Analyses of host associations indicated multiple host-switching events throughout evolution of dicrocoeliids. In addition, phylogenetic data provided evidence that the complete or partial loss of intestinal structures has occurred independently more than once in their evolutionary history. Molecular phylogenies have demonstrated that the members of the Anenterotrematae belong to the Dicrocoeliidae which resulted in the synonymization of the two families. Lastly, molecular phylogenetic analyses have demonstrated non-monophyly of dicrocoeliid subfamilies, which led to the abandonment of the subfamily-based structure of the family. Nevertheless, despite the recent increase in taxonomic and geographic coverage of studies devoted to the Dicrocoeliidae, a robust molecular phylogenetic framework of dicrocoeliid systematics is still lacking. We provide a brief overview of history and the current state of knowledge of dicrocoeliid phylogenetics and systematics, and outline some of the questions and future directions.

Keywords: Digenea, Dicrocoeliidae, phylogeny, taxonomy

OS – oral session

Session: S9 New trends in parasitology taxonomy

From confusion to illumination: will genomic data change the digenean taxonomy? – the use of NGS in the taxonomy of *Cotylurus* sp.

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Abstract

Traditional taxonomy of Digenea, based on morphological traits and a limited set of molecular markers (e.g. rDNA or mtDNA), has long faced challenges due to the convergence of morphological features and the presence of cryptic forms. This is particularly evident in the genus *Cotylurus*, whose representatives display high morphological similarity yet substantial genetic differentiation. In this study, we report preliminary results of applying next-generation sequencing (NGS) to address these issues. We developed a DNA isolation protocol that enables whole-genome data acquisition through de novo sequencing by commercial laboratories. Initial quality control of sequencing data (15 samples representing four taxa) confirms that the dataset is of high quality: each paired-end file contains an average of 50 million reads of ~150 bp length, with consistently high base quality scores across the entire read length. The GC content (~39%) is within expected ranges, and the proportion of ambiguous bases is negligible. These results confirm proper library preparation, minimal technical artifacts, and no evidence of contamination. The data provide a reliable foundation for downstream genomic analyses, including mitochondrial genome comparisons. Importantly, preliminary analyses show that the genetic variability observed at the *COI* gene (860 bp) differs significantly from the variability found in other regions of the mitochondrial genome. These findings highlight both the potential of genomic approaches to redefine species boundaries within Digenea and the limitations of relying on standard barcoding markers. This study will address whether genomic data can ultimately illuminate the complex taxonomy of digenean trematodes and set a new standard for parasite systematics.

This study was supported by NCN project (MINIATURA 6, 2022/06/X/NZ8/01644).

Keywords: *Cotylurus*, taxonomy, NGS

OS – oral session

[S10]
Parasite-host interactions

Session: S10 Parasite-host interactions

Apodemus agrarius as a biomarker of environmental plastic pollution

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Abstract

Plastics represent a global environmental problem, and their negative impact on ecosystems and living organisms has become the focus of numerous studies. The aim of this study was to assess the potential use of the striped field mouse (*Apodemus agrarius*) as a biomarker of environmental pollution by microplastics. The study involved 22 individuals (11 males and 11 females), with analysis of microplastic presence in the stomach and intestines based on quantity, shape, color, and size. Additionally, fecal samples were examined for the presence of parasite eggs to evaluate a possible relationship between microplastic contamination and parasitic infections.

Microplastics were found in all individuals examined. Transparent fibers were the most common type, suggesting both their environmental prevalence and ease of ingestion by animals. A greater accumulation of microplastics was observed in the intestines than in the stomach. In the parasitological analysis (coproscopy), the most frequently detected genus was *Eimeria* spp. (in 77.3% of individuals), while intestinal helminths of the genera Syphacia and Cestoda were detected sporadically. No statistically significant correlations were observed between microplastic presence and parasite occurrence. The results suggest that the striped field mouse may serve as a useful bioindicator for monitoring environmental contamination with microplastics.

Keywords: plastics, parasites, *Apodemus agrarius*

OS – oral session

Session: S10 Parasite-host interactions

Neosporosis in dairy cattle in Poland – a recurring problem

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Abstract

Abortion and neonatal mortality are common and significant issues in veterinary practice. One of the primary parasitic causes of abortion in cattle is the protozoan parasite *Neospora caninum*. The presence of this pathogen leads to substantial economic losses in the dairy industry.

This study presents a retrospective analysis of the health status of a dairy herd with a history of abortions confirmed to be associated with *Neospora caninum* infection. Fifteen years ago, the herd was classified as high-risk for abortion due to various infectious agents, including bovine viral diarrhoea virus (BVDV), infectious bovine rhinotracheitis (IBR), chlamydiosis, and neosporosis. Among these, neosporosis was the most prevalent. In response, the herd owner opted to cull the infected heifers. However, after a few years, abortion problems re-emerged in the herd.

The objective of this study was to assess the current status of *Neospora caninum* infection in the herd by measuring the seroprevalence of specific antibodies in selected animals. Blood samples were collected from 60 cows of reproductive age. Serum samples were tested using standard serological methods for diagnosing of neosporosis. Antibodies against *Neospora caninum* were detected in 20 out of the 60 cows (33.33%).

Neosporosis is a complex and persistent disease. Its detection and eradication from affected herds are difficult and may require several years. The overall prevalence of neosporosis among Polish dairy cattle remains insufficiently documented, with available data limited to certain regions. However, serological studies indicate widespread herd-level exposure, resulting in significant financial losses for dairy producers.

In the absence of an effective vaccine or treatment, continued surveillance and control measures are essential. These should include regular health monitoring and biosecurity practices to prevent natural transmission within and between herds.

Keywords: *Neospora caninum*, neosporosis, cattle, seroprevalence

PS – poster session

Session: S10 Parasite-host interactions

From worms to genomes: 50 years of parasitic time travel in primates at Wroclaw Zoo

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Abstract

A retrospective analysis of parasitic invasions in non-human primates at Wroclaw Zoo reveals striking shifts over the past 50 years in parasite prevalence, diagnostic approaches, and animal husbandry practices. In the 1970s, helminths were the dominant parasitic agents, identified mainly through conventional coproscopic techniques. While appropriate for their time, these methods lacked the sensitivity to detect low-intensity or chronic infections, often underestimating true parasitic diversity.

In contrast, recent studies utilizing molecular diagnostics have unveiled a different parasitological profile – protozoan infections now predominate, with prevalence rates reaching 80–100% in some primate groups. This transition reflects both a change in parasite ecology and the enhanced resolution of modern diagnostic tools, capable of detecting subclinical and mixed invasions previously undiagnosed.

Concurrently, substantial improvements in primate welfare have been implemented. Advances in environmental enrichment, group management, and stress reduction strategies have transformed captive conditions, resulting in fewer stereotypic behaviours and improved health. Nevertheless, persistent protozoan infections suggest that enhanced welfare does not eliminate parasitic risks but may alter their manifestation.

By comparing historical data with current findings from Wroclaw Zoo, this work provides insight into the co-evolution of diagnostic capability, host conditions, and parasite dynamics. It underscores the value of long-term monitoring and modern methodologies in understanding and managing parasitic invasions in zoological collections.

Keywords: non-human primates, captive primate management , parasitic invasions, diagnostic evolution, coproscopy, molecular diagnostics, parasite prevalence

OS – oral session

Session: S10 Parasite-host interactions

Analysis of the species composition of mosquitoes (Diptera: Culicidae) in the urban area of Wroclaw: discovery of a new species for the Polish fauna

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Abstract

Mosquitoes (Diptera: Culicidae), as vectors of numerous pathogens, are of major public health concern, making their monitoring in urbanized areas, especially urban areas a critical aspect of epidemiological surveillance and control strategies. The continuing expansion of urban areas and the associated changes in habitat and microclimate have facilitated not only the proliferation of local mosquito populations but also the introduction and establishment of invasive species. The study aims to estimate the diversity and abundance of mosquito species in the urban environment of Wroclaw and to assess the associated public health risks. Mosquito trapping was carried out as part of regular monitoring from May to October 2024, using CDC traps placed at 14 sites across Wroclaw. A total of 17104 adult mosquitoes were collected during the season, of which 16728 individuals were identified. The distribution of mosquitoes varied significantly between sites and between months. 15 species of mosquitoes belonging to the genera *Anopheles*, *Aedes*, *Culiseta, Coquillettidia* and *Culex* were identified. The dominant species in the total collected material were *Ae. vexans* and *Cq. richiardii*. In addition, a previously unrecorded species for the Polish fauna, *Culiseta longiareolata*, which was found at one site on Żółta Street. The diverse species composition of mosquitoes and the seasonal dynamics of their occurrence indicate the need for continuous monitoring to develop and update strategies to control mosquito populations and prevent diseases transmitted by these insects in urban areas. Moreover, the discovery of a new species for the fauna of Poland, *Cs. longiareolata*, represents a significant contribution to the knowledge regarding the diversity of the country's entomofauna. This outcome underscores the necessity for further research on the distribution, occurrence, and ecology of the species, which will facilitate a more comprehensive understanding of its role within the ecosystem.

Keywords: mosquitoes, new species, Poland

OS – oral session

Session: S10 Parasite-host interactions

Occurrence and significance of infections caused by selected protozoa and intracellular fungi in geese

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Abstract

There is limited information in the available scientific literature on protozoan infections in geese, particularly those caused by *Cryptosporidium spp.*, *Tetratrichomonas spp.*, and intracellular fungi classified within the *Cryptomycota* phylum, namely *Microsporidia spp.*

Cryptosporidium spp. are opportunistic parasites belonging to the phylum Apicomplexa, that infect epithelial cells of the gastrointestinal and respiratory tracts of birds. In geese, infections can be either symptomatic or asymptomatic, the latter contributing to the prolonged shedding of oocysts into the environment. The lack of effective treatment and the high resistance of oocysts to environmental factors significantly hinder control efforts in poultry farming. Documented cases of infections caused by species such as *C. meleagridis* and *C. baileyi* indicate a potential zoonotic risk.

Tetratrichomonas spp. are microaerophilic flagellates that colonize the digestive tract of birds, including geese. They are most commonly found in the ceca, rectum, and cloaca. *Tetratrichomonas gallinarum* is the most frequently detected species, previously considered non-pathogenic but increasingly associated with conditions such as necrotic enteritis and hepatitis, as well as lesions in the brain and conjunctiva. Transmission occurs via the fecal–oral route and through retrograde cloacal movements, known as "cloacal drinking". The presence of morphologically similar forms in the human oral cavity suggests potential zoonotic relevance.

Microsporidia are obligate intracellular fungal parasites belonging to the *Cryptomycota* phylum, which in more severe cases may cause systemic infections involving multiple organs. In birds, the most frequently detected species is *Enterocytozoon bieneusi*, although diagnosis is complicated by the potential presence of latent infections. Documented cases in both humans and other avian species highlight the need for further research on their prevalence and epidemiological significance.

Keywords: *Cryptosporidium* spp., *Tetratrichomonas* spp., *Microsporidium* spp., geese

OS – oral session

Session: S10 Parasite-host interactions

Environmental determinants and microbiome-associated effects of microsporidian infections in mosquitoes

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Abstract

Microsporidians (Microsporidia) are obligate, intracellular parasites that frequently infect mosquitoes, including species of medical and veterinary importance. Their occurrence and ecological role may be more complex than was previously thought. This study aimed to investigate how environmental conditions influence microsporidian prevalence in mosquitoes and how these parasites interact with the mosquito-associated microbiome at both compositional and functional levels, using field specimens analysed by high-throughput sequencing.

We analysed over 3,000 mosquitoes representing nine species across three seasons to assess microsporidian prevalences and their environmental determinants. Using DNA metabarcoding, we identified 12 microsporidian species, with an overall prevalence of 34.6%. Microsporidian occurrence was 1.6 times more frequent during warm periods (>19 °C, RH <65%) than during colder seasons. Additionally, screening revealed that mosquitoes can be positive for the human-infecting *Encephalitozoon hellem* genotype 1A.

Microbiota profiling of larvae and adult mosquitoes showed that microsporidian-positive individuals consistently harbored distinct microbial communities enriched in Aerococcaceae, Lactobacillaceae, Microbacteriaceae, and Polyangiaceae. Indicator species analysis revealed strong associations between infection and the presence of *Weissella* cf. *viridescens*, *Spiroplasma* sp. Notably, the intracellular symbiont *Wolbachia pipientis* was more frequent in infected mosquitoes. Functional predictions of gut microbiota indicated enrichment in biosynthetic pathways for vancomycin and ansamycin antibiotics in infected mosquitoes, as well as the exclusive presence of multidrug-resistance modules (MexJK-OprM). Our results show that microsporidian infection in mosquitoes is influenced by environmental conditions and alters the structure and predicted function of the host-associated microbiome. These interactions may affect mosquito physiology and vector competence.

Keywords: Microsporidia, mosquitoes, microbiota, host microbial interactions, environmental indicators, biosynthetic pathways

OS – oral session

[P1]

Vectors and pathogens

Session: P1 Vectors and pathogens

Further study upon epidemiological importance of *Dermacentor reticulatus* in new endemic locality in Central–Southern Poland

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Abstract

Dermacentor reticulatus is the second tick species of greatest medical and epidemiological importance in Poland after *Ixodes ricinus*. Therefore, the aim of this study was to monitor the occurrence of selected tick-borne pathogens in *D. reticulatus* in a new endemic site of its occurrence in Upper Silesia. Ticks were collected from vegetation during the spring peak of activity using the flagging method from two locations in Sławków. Then, individuals were identified under a stereoscopic microscope using a systematic key. DNA was isolated from ticks using the ammonia method. Real-time PCR and a commercial kit (EURx, Poland) were used to detect *Borrelia burgdorferi* sensu lato. The nested PCR method and two pairs of primers specific for the *16S* rRNA gene were used to detect *Anaplasma phagocytophilum*. The PCR method and primers specific for the *18S* rRNA genes, *rpoB*, and *gltA* were used to detect *Babesia* spp., *Bartonella* spp., and *Rickettsia* spp. 17 females and 14 males of *D. reticulatus* were collected from the ecotone habitat, as well as one female and one male of *I. ricinus*. Three females and one male of *D. reticulatus* were collected from the meadow habitat, while only one female of *I. ricinus* was found in this area. Among the *D. reticulatus* collected from the ecotone habitat, *Rickettsia* spp. were observed in 47% of the females and 86% of the males, while only one female of *D. reticulatus* collected from the meadow habitat tested positive for this pathogen. In the case of *I. ricinus*, *Rickettsia* spp. was detected in one female from the meadow habitat. Co-infection with *B. burgdorferi* s.l. and *Rickettsia* spp. was demonstrated in one female and one male of *I. ricinus* from the ecotone habitat. The study confirms the presence and dominance of *D. reticulatus* in both studied habitats. Furthermore, molecular analysis indicates a potentially high exposure of both animals and humans to tick-borne infection with *Rickettsia* spp. and *B. burgdorferi* s.l. in the studied areas.

Keywords: *Dermacentor reticulatus*, *Rickettsia* spp., tick-borne diseases

PS – poster session

Session: P1 Vectors and pathogens

Urban lizards as hosts of ticks and *Rickettsia*: a study from Wrocław

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Abstract

With advancing urbanization, research on the role of wild animals as potential reservoirs of pathogens in the urban environment is becoming increasingly important. Although lizards, despite being rarely considered in studies of urban zoonoses, may be an important link in the life cycle of ticks and the pathogens they transmit. The aim of this study was to assess the presence of ticks on lizards and to analyze the prevalence of *Rickettsia* spp. in ticks collected both from lizards and from the environment in the Rędziński Forest in Wrocław.

Questing ticks were collected using the flagging method in meadows and forested areas of the Rędziński Forest between March and October 2024. Lizards were captured by hand in the same area from April to August 2024. Each lizard was examined for the presence of ticks. All collected ticks were morphologically identified to species and then tested for the presence of *Rickettsia* spp. A total of 194 ticks were collected using the flagging method, of which 56.2% were identified as *Ixodes ricinus* and 43.8% as *Dermacentor reticulatus*. Additionally, 127 ticks were collected from 20 lizards, including 4 *Lacerta agilis* and 16 *Zootoca vivipara*. Among these, 45 were larvae and 82 were nymphs, all identified as *I. ricinus*. DNA of *Rickettsia* spp. was detected in 46.4% of questing ticks, including 40.4% of I. ricinus and 54.1% of *D. reticulatus*. Among ticks collected from lizards, 22.0% were positive for *Rickettsia*. The infection rate was higher in ticks collected from *Z. vivipara* (24.3%) than from *L. agilis* (19.3%).

The results indicate that lizards, particularly *Z. vivipara*, may serve as hosts for *I. ricinus* and potential reservoirs of pathogens in urban environments. The detection of infected ticks both in the environment and on lizards highlights the need for further research into their epidemiological role in urban green spaces. Conducted under Polish permit WPN.6401.239.2022.MH

Keywords: urban ecology, lizards, ticks, *Rickettsia*

PS – poster session

Session: P1 Vectors and pathogens

First European record of *Rickettsia bellii* in *Amblyomma rotundatum* from *Rhinella marina* imported to Poland

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Abstract

This study presents the first documented case of *Amblyomma rotundatum* ticks, a species native to the Americas, parasitising an imported toad in Poland. A total of 12 ticks were collected from a single *Rhinella marina* toad. Based on morphological characteristics and molecular analysis, all ticks were identified as female *A. rotundatum*. Polymerase chain reaction testing revealed that 75.0% (9/12) of the ticks were positive for *Rickettsia* spp. Sequencing of the positive samples confirmed the presence of *R. bellii*. No DNA evidence of *Borrelia* spp. and *Anaplasma* spp. was detected in the tested ticks. However, due to the limited number of tick specimens collected from a single host, further research is necessary to fully characterize the pathogen profile of this tick species. This report represents the second record of *A. rotundatum* in Europe in association with imported animals, highlighting the importance of monitoring the global wildlife trade for the potential introduction of non-native ticks and tick-borne pathogens.

Keywords: Amphibians, *Anaplasma*, *Borrelia*, cane toad, ticks, wildlife trade

PS – poster session

Session: P1 Vectors and pathogens

Orthoflaviviruses in *Ixodes ricinus* ticks in Pomeranian Voivodeship, Poland

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Abstract

In recent years, there has been a notable rise in tick-borne diseases, largely driven by a combination of climate change, urbanization, and the rapid growth of the human population. These factors, along with their disruptive impact on natural ecosystems, have created favourable conditions for ticks and the pathogens they carry. Global warming, in particular, has facilitated the dispersal of ticks, their animal hosts, and the pathogens they transmit into new regions, causing diseases once confined to tropical areas to appear in temperate zones. In many European countries, this trend is especially concerning, as tick populations have increased significantly. Studies show that ticks are now vectors for a growing number of pathogens, leading to a substantial rise in the incidence and diversity of tick-borne diseases.

In this study, viral pathogens from the *Flaviviridae* family were analyzed. Ticks of the species *Ixodes ricinus* collected from different locations, such as Sobieszewska Island, Otomiński Forest, and Mikoszewo, were examined. RNA was isolated from the collected 712 *I. ricinus* ticks, which were then transcribed into cDNA. A fragment of the flavivirus *NS5* gene was then amplified using nested PCR. No viruses typical of tropical zones (e.g., West Nile virus or Dengue virus) from the *Flaviviridae* family were detected among the studied population of *I. ricinus* ticks.

Keywords: *Ixodes ricinus*, tick-borne pathogens, flaviviruses

PS – poster session

Session: P1 Vectors and pathogens

New data on the occurrence of *Dermacentor reticulatus* (Fabricius, 1794) (Parasitiformes: Ixodidae) in northern Poland

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Abstract

The ornate dog tick, *Dermacentor reticulatus*, is the second most common tick species in Poland after *I. ricinus* and is of significant medical and veterinary importance. In Europe, the tick's distribution is disjunct. In Poland, until the 1980s, reports were limited to the eastern and northeastern regions of the country. Recently, reports of this tick have increased from many regions across Poland, where it had not been previously recorded. An expansion of the species into urban areas is also being observed.

Recent surveys conducted in Pomerania have shown the occurrence of *D. reticulatus* also in the Tri-City metropolitan area. Between 2018 and 2023, one new locality was found in Gdynia, and three in different districts of Gdańsk. The ticks were most abundant on Wyspa Sobieszewska (Gdańsk). The most recent surveys conducted in this area during the 2024/2025 season showed that a spring peak of *D. reticulatus* activity occurs in March–April. About 98% of all collected individuals were recorded during this period. It seems that the presence of ticks was related to the temperature-during the mentioned periods, it ranged between 6 and 15°C, while in the other periods (June–September), it reached more than 20°C. This data aligns with previous information on the annual dynamics of this tick species, although it is difficult to talk about the autumn peak in the current study.

Inspection of other sites in the Tri-City area yielded negative results. The population on Wyspa Sobieszewska appears to be stable and may confirm information on the range expansion of *D. reticulatus* and the westward expansion of the eastern population. Climatic factors (such as global warming) and environmental factors, including land use changes, have been cited as reasons for the spread. Ticks can also be spread by large ungulates (in Sobieszewo there are elk, among others) and pets, such as dogs. This may contribute to the spread of the ornate dog tick to other parts of the Tri-City metropolitan area.

Keywords: *Demacentor reticulatus*, ornate dog tick, ticks, Tri-City, Poland

PS – poster session

Session: P1 Vectors and pathogens

Seasonal activity patterns of the meadow tick *Dermacentor reticulatus* – influence of environmental factors in Poznań on its occurrence and spread

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Abstract

Dermacentor reticulatus is a tick species that mainly attacks dogs and horses but is also found on other forest animals and humans. It is present in open grassy areas, on shrubs, tree trimmings, shorelines, and floodplains. Its range, according to the literature, consists of two European populations meeting in Poland. Evidence of the observed spread of this tick is the more frequent and higher number of recorded infections in recent years. This increases the epidemiological risk of transmission of babesiosis and tick-borne encephalitis (TBE) in its area of distribution.

We confirmed the presence of *D. reticulatus* in several locations in Poznań as early as 2024, at which time we pointed out that its highest abundance was before the start of spring — quite different from the common tick *Ixodes ricinus*. Therefore, the goal of our project is to check the seasonal activity of the meadow tick in the recreational areas of Poznań, with particular attention to its active presence in the winter and early spring months.

Three areas were monitored, where ticks were collected using the flagging method at cyclic intervals — from January until now. In order to avoid disturbance of the surveyed populations, a rotation was introduced in the monitored areas, and the caught ticks, after being identified to species and developmental stage, were released at the trapping site. Weather conditions were also recorded during flagging.

The collected data indicate that *D. reticulatus* has been present in many areas of Poznań since the end of January, with the highest activity in February and March, significantly decreasing since April. During the spring peak of *I. ricinus* activity (in May and June), the meadow tick was no longer recorded in the controlled areas.

The monitoring was funded by the student project Study@Reaserch number from the Decision 155/34/UAM/0084.

Keywords: *Dermacentor reticulatus*, tick, epidemiology, Poznań

PS – poster session

Session: P1 Vectors and pathogens

The impact of the tick microbiome on *Borrelia* occurrence *in Ixodes ricinus* and transmission to humans – a preliminary study

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Abstract

Understanding the microbial ecology of arthropod vectors is crucial for developing innovative strategies to prevent the transmission of vector-borne pathogens. The tick microbiome comprises diverse microbial communities, including both pathogenic and non-pathogenic organisms. However, the role of these microbial assemblages in pathogen transmission remains poorly understood, particularly in *Ixodes ricinus*, the principal vector of *Borrelia* spp. in Europe. Current knowledge is largely derived from studies on North American species such as *I. scapularis* and *I. pacificus*, while European data remain scarce.

This preliminary study aimed to investigate the relationship between the microbiome of *I. ricinus* and the presence of *Borrelia*, as well as its potential impact on tick-to-human transmission. Individual nymphs and adult females were subjected to metagenomic profiling by sequencing the V3–V4 region of the *16S* rRNA gene using the Illumina NovaSeq platform.

Alpha diversity analysis revealed no significant differences in bacterial community structure related to *Borrelia* infection or the development of Lyme borreliosis (LB) in bitten individuals. However, microbial composition appeared to vary with the tick's developmental stage. These findings suggest that while overall bacterial diversity may not directly influence *Borrelia* infection or transmission success, tick life stage may play a modulatory role. Further research is needed to elucidate the functional interactions within the tick microbiome and their influence on pathogen dynamics, potentially paving the way for microbiome-based strategies to control tick-borne diseases.

The study was funded by the National Science Centre (NCN) OPUS grant no. 2020/37/B/NZ6/01587.

Keywords: metagenomics, *Borrelia*, *Ixodes ricinus*, microbiome

PS – poster session

Session: P1 Vectors and pathogens

Serological evidence for exposure to tick-borne rickettsiae among residents of north-eastern Poland

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Abstract

The aim of the study was to evaluate serological evidence of exposure to tick-borne spotted fever group (SFG) *Rickettsia*, as well as to determine the level of co-infection with *Borrelia* spirochaetes among adult residents of north-eastern Poland.

A total of 155 serum samples were collected in 2023–2024 from residents (≥18 years) of north-eastern Poland. The study group had varying degrees of exposure to tick bites. The high-risk group (HR) consisted of 102 forest workers from two forest inspectorates in the Warmia and Mazury region. The low-risk group (LR) included 53 volunteers, residents of the Olsztyn city area.

The presence of IgG antibodies to antigens of SFG rickettsiae and *Borrelia* spirochaetes was examined using the ELISA kit of DRG International Inc., USA and Biomedica Laboratories, Austria, respectively. Serological tests were conducted and interpreted according to the manufacturer's instructions by qualified laboratory diagnosticians.

The presence of IgG antibodies against SFG *Rickettsia* was detected in 38.7% of adult residents of north-eastern Poland. The seroprevalence among forestry workers was nearly five times higher than in the LR group (52.9% vs. 11.3%). The overall IgG seroprevalence for *Borrelia* antigens was 21.3%, nearly two times lower than that for *Rickettsia*. The prevalence of anti-*Borrelia* IgG was significantly higher in the HR group (30.4%) compared to the LR group (3.8%). Co-exposure to both SFG rickettsiae and *Borrelia* spirochaetes was detected in 16.1% (25/155) of the tested participants. The IgG seroprevalence for co-infection was significantly higher among forest workers than among Olsztyn residents (23.5% vs. 1.9%).

These findings provide important evidence filling the gap between environmental detection of SFG *Rickettsia* in vector populations and the limited number of diagnosed clinical cases in humans.

The study was approved by the Bioethics Committee of the University of Warmia and Mazury in Olsztyn (No. 35/2024).

Keywords: spotted fever grup rickettsiae, forest workers, city inhabitants, seroprevalence, *Borrelia burgdorferi* s.l., co-exposure

PS – poster session

Session: P1 Vectors and pathogens

Impact of *Babesia ovis* infection on the bacterial communities of *Rhipicephalus bursa* midguts and salivary glands

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Abstract

Ticks harbor complex microbial communities that influence pathogen transmission, vector competence, and tick physiology. This study aimed to characterize and compare the bacterial communities in the midgut and salivary glands of *Rhipicephalus bursa* females under two conditions: uninfected and experimentally infected with *Babesia ovis*. Infection was confirmed by PCR in larvae hatched from artificially infected females. Adult females derived from these larvae, maintained in colonies at CEVDI/INSA, were dissected to isolate midguts and salivary glands, from which genomic DNA was extracted. The V3–V4 regions of the bacterial *16S* rRNA gene were sequenced using the Illumina MiSeq platform. Microbiome analysis was performed using a custom pipeline based on the DADA2 package in R Studio, with taxonomic assignment using the SILVA database. Alpha and beta diversity metrics were calculated to assess within- and between-sample variation. NMDS and PCoA revealed structural differences in microbial communities. No significant differences in alpha diversity (Shannon and Simpson indices) were observed between groups; however, increased inter-individual variability was noted in the salivary glands of infected ticks. Beta diversity analyses (Bray-Curtis, UniFrac) showed clear separation between infected and uninfected groups, indicating tissue-specific shifts in microbiota. Relative abundance and heatmap analyses highlighted changes such as depletion of Coxiellaceae in midguts and expansion of Burkholderiaceae, with individual-specific responses. Despite the small sample size, results suggest *B. ovis* infection alters both composition and structure of the tick microbiome in a tissue-dependent manner. These findings enhance our understanding of tick-pathogen-microbiota interactions and may inform future strategies for controlling ticks and tick-borne diseases.

Keywords: pathogen–microbiota interaction, *16S* rRNA sequencing, tick tissues

PS – poster session

Session: P1 Vectors and pathogens

The expanding threat of *Dermacentor reticulatus*: pathogen and microbiome analysis

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Abstract

Ticks represent significant vectors of pathogens of both medical and veterinary importance, as they transmit a wide range of viruses, bacteria, and parasites. The ornate cow tick, *Dermacentor reticulatus*, is a tick species that is spreading intensively into new areas as a result of climate and socioeconomic changes. This species transmits the causative agents of serious diseases such as canine babesiosis, TIBOLA/DEBONEL, tularemia, and Q fever. The aim of our study was to identify pathogens transmitted by *Dermacentor reticulatus* ticks collected from various localities in eastern Slovakia using molecular-genetic methods. In the samples, we detected the presence of pathogenic bacteria of the genus *Rickettsia* in 39% of the ticks. The most frequently detected species was *Rickettsia conorii* subsp. *raoultii* (26.24%). We also identified *R. monacensis*, *R. slovaca*, and *R. aeschlimannii*. In one sample, we detected *Babesia venatorum* and *Babesia odocoilei*. Further analyses using next-generation sequencing (NGS) revealed a total of 851 different bacterial genera in the ticks. The most frequently represented were bacteria from the phylum *Proteobacteria*, class *Gammaproteobacteria*, order *Pseudomonales*, and genus *Pseudomonas*. This was followed by the genera *Coxiella*, *Candidatus* Midichloria, *Neoehrlichia*, *Anaplasma*, and *Rickettsia*. All studied groups also contained symbiotic or environmentally common genera such as *Rickettsiella*, *Lactobacillus*, *Variovorax*, *Rhodococcus*, *Stenotrophomonas*, *Acinetobacter*, *Brevibacterium*, *Arsenophonus*, *Prevotella*, *Sphingomonas*, *Morganella*, and *Wolbachia*. Differences between sexes were also observed — for example, bacteria of the genus *Coxiella* were more frequently found in male *D. reticulatus*.

This research was supported by the grant APVV-23-0320 and VEGA 1/0762/25.

Keywords: tick, *Dermacentor reticulatus*, pathogens, microbiome analysis

PS – poster session

Session: P1 Vectors and pathogens

Preliminary study upon efficacy of lassoing method in complete tick removal

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Abstract

Anti-tick prophylaxis relies on several key principles: preventing tick contact with the skin by wearing protective clothing, carefully inspecting the body after returning from tick habitats, and using effective, non-toxic repellents. However, a large percentage of people do not employ any preventive measures against ticks and lack sufficient knowledge about the prophylaxis of tick-borne diseases and the recommended methods for tick removal. The harmful effects of tick parasitism can be reduced by complete tick removal performed as soon as possible after its attachment. Therefore, in this study, we assessed the effectiveness of the lassoing method applied to remove ticks feeding on humans. Because ticks were removed from patients reporting to the Non-public Health Care Facility B.D.M. UNI-MED in Lublin, as part of the health services, and no personal data or any sensitive data of patients were collected, approval by the ethics committee was exempted. The only data collected in this scientific analysis were the body integrity of parasites removed from patients. The nursing staff employed lassoing method for routine tick removal due to its high effectiveness, as demonstrated in scientific articles.The removed ticks underwent morphological analysis using a stereoscopic microscope to evaluate the integrity of their bodies and the completeness of their mouthparts.

In total, 73 ticks removed by lassoing method were analysed, including 55 (75.3%) *Ixodes ricinus* and 18 (24.7%) *Dermacentor reticulatus* specimens. In the case of *D. reticulatus,* all feeding ticks were completely removed, 45 specimens of *I. ricinus* were removed in total (41 females and 4 nymphs), and in the case of 3 females and 7 nymphs, part of the hypostome remained in the skin and required removal by another method. The study revealed that lassoing method was highly effective (86.3%) regardless of the tick species and feeding period, reducing the risk of tick damage and complications like tick bite granuloma.

Keywords: lassoing method, tick removal, *Ixodes ricinus*, *Dermacentor reticulatus*

PS – poster session

Session: P1 Vectors and pathogens

First report, genotyping and phylogenetic analysis of *Anaplasma marginale* in European bison (*Bison bonasus*)

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Abstract

European bison, *Bison bonasus* is strictly protected species of large mammal, with 25% of the World's population living in Poland. The most numerous populations of European bison live in Białowieża Primeval Forest, NE Poland and in Bieszczady Mountains, SE Poland. The purpose of this study was to investigate *Anaplasma* spp. occurrence in *B. bonasus* from Poland. Tissue samples were collected from 45 European bisons between 2021 to 2024 in Białowieża and Bieszczady areas. Molecular methods (PCR, nested-PCR, sequencing) were used for the detection, genotyping and phylogenetic analysis of bacteria from *Anaplasma* genus with use *16S* rDNA and *msp4* partial genes. Prevalence of *Anaplasma* spp. was 40% (18/45) in examined samples and eight of them were identified as *Anaplasma marginale*. According to all of information,and our best knowledge this presented research is the first confirmed report of *A. marginale* in Poland, first report of *A. marginale* in *B. bonasus* and first report of this pathogen occurrence further north than Hungary, in Europe.

Keywords: *Anaplasma marginale*, *Bison bonasus*, *16S* rDNA, *msp4*

PS – poster session

Session: P1 Vectors and pathogens

Introduction to monitoring of canine babesiosis cases in Southern Poland and indication of potential outbreaks of this disease in Silesia

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Abstract

The etiological agents of canine babesiosis are protozoans from *Babesia* genus, which are transmitted by ticks during feeding. So far, *Babesia canis* has been the most prevalent species, especially in central and eastern parts of Poland. The purpose of this study was to assess the prevalence of *Babesia* cases in dogs with clinical suspicion of babesiosis, which tested positive for *B. canis* from Southern Poland.

The prevalence of *Babesia* in dogs was assessed using data generated by the Vetlab veterinary laboratory in Katowice (Poland) on blood smears from 3032 dogs analyzed between August 2018 and December 2022. Blood samples were sent for microscopic analysis from veterinary clinics of Southern Poland. Blood smears were prepared from the EDTA-treated blood samples and the Wright–Giemsa staining method. They allowed for the microscopic evaluation of *Babesia* protozoans' size and shape in order to classify them as large or small forms. Chi-square test ($\chi2$) with Yates's correction was used to compare the categorical variables. Overall, 3032 dog blood samples were examined. This study, showed that 9.3% (n=282) of examined samples were *Babesia*-positive. The highest number of positive samples came from Śląskie Voivodeship n=183 (64.9%), then from Podkarpackie n=61 (21.63%) and Małopolskie Voivodeships n=32 (11.35%). Statistical analysis showed significant difference between the number of *Babesia*-positive cases in Silesia and Subcarpathia ($\chi2 = 35.89$; $p \leq 0.00001$). In addition, dog blood samples were more often *Babesia*-positive in Silesia than in Lesser Poland ($\chi2 = 59.61$; $p \leq 0.00001$). Moreover, this study showed the presence of potential outbreaks of canine babesiosis in Częstochowa and its surroundings, where 45.3% of all positive samples from Śląskie Voivodeship came from.

The obtained results showed that infection with large *Babesia* in dogs from Southern Poland should be taken into consideration during the differential diagnosis of tick-borne diseases at veterinary clinics.

Keywords: *Babesia canis*, *Babesia* spp., canine babesiosis, tick-borne pathogens, tick-borne diseases, veterinary parasitology, epidemiology, *Dermacentor reticulatus*

PS – poster session

Session: P1 Vectors and pathogens

Hydrological regime of soils as an ecological factor of the occurrence of the tick *Dermacentor reticulatus* in Slovakia

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Abstract

The *Dermacentor reticulatus* (DR) tick is one of the fastest spreading parasites since the beginning of the new millennium in Europe. The geographical range of DR is highly focal, mainly in lowland areas with an affinity for the vicinity of rivers. Despite the wealth of knowledge on its biology and ecology, it remains an open question what are the limits of its spatial spread. A specific feature of this tick is its mixed ecological type of development. The adult ticks are exophilic, the larvae and nymphs are endophilic, live in burrows of small rodents, and are very sensitive to drought and excessive soil moisture, and do not survive the winter.

Analysis of 90 available published data from DR monitoring in Slovakia up to 2011, transferred to the Map of Ecological Types of Soil Water Regime in Slovakia from 1999, shows its high affinity to slightly wet and slightly dry ecological soil types in areas with an average annual rainfall of 600–800 mm. DR was only sporadically recorded in lowlands on dry soil types with annual rainfall below 600 mm and on fully saturated soil types up to 550 m altitude with 800–1250 mm annual rainfall.

By analyzing the relative density of adult DR in ground vegetation in April 2025 at three stations in eastern Slovakia with long-term monitoring of the soil moisture regime to a depth of 1 meter with three different soil types, medium heavy sandy loam soil to heavy clay-loam soil appears to be the optimal texture for the development of DR larvae and nymphs in the burrows of small rodents. Less suitable to unsuitable soils are light sandy soils, which lose moisture rapidly, and heavy clay soils, which

retain water. We assume that soil moisture in the summer period, influenced by its structure and annual rainfall are potential ecological limits to the occurrence and spread of RD in Slovakia. This hypothesis is being tested over a larger area.

The work was supported by the project APVV-19-0440, APVV-23-0320, VEGA 1/0287/22, VEGA 2/2205/24.

Keywords: tick, *Dermacentor reticulatus*, soil hydrology, ecological factor, distribution, Slovakia.

PS – poster session

Session: P1 Vectors and pathogens

Dermacentor reticulatus in space and time at the beginning of the millennium in Poland

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Abstract

The tick *Dermacentor reticulatus* (DR) is one of the fastest spreading parasites in Europe since the beginning of the new millennium. Its geography consists of two main macro-regions: the Western European, which extends from northern Spain to western Poland and the Eastern European, which extends from eastern Poland through the Baltic States, Belarus and Ukraine. In Poland, these two macro-regions are currently merging.

Despite the wealth of knowledge about its ecology, it remains an open question what are the limits of its occurrence and spatial distribution. A specific feature of this tick is that larvae and nymphs live in burrows of small ground-dwelling rodent hosts, where their development and metamorphosis to higher developmental stages takes place during the summer months, while larvae and nymphs are very sensitive to both drought and excessive soil moisture, in contrast to DR adults.

We analyzed the relationship of DR findings in Poland from 10 publications summarized in Rubel et al. (Tick and Tick-borne Diseases 7 (2016) 224–233), transferred to the "Map of georeferenced *Dermacentor reticulatus* locations" with the soil type of a given DR occurrence site from the Soil Map of Poland. The analysis of 85 documented records shows high affinity of DR to podzolic and alluvial types of zonal soils (20% each) and muddy and wetland types of azonal soils (37% and 12% of sites, respectively), sporadically to zonal brown soils (9%) and to azonal chernozems (1%). After transferring the DR sites to the map of mean annual rainfall from 1891–1990, the optimum area appears to be that with annual rainfall of 500–600 mm (89 % of sites), partly 600–700 mm (9 %), and sporadically up to 800 mm (2 %).

We hypothesize that soil type and soil moisture are one of the limiting factors for the spread of DR to new areas and propose a comprehensive investigation of this phenomenon.

This work was supported by the APVV projects SK-PL-0074 and APVV-23-0320, NAWA BPN/BSK/2021/1/00078/U/00001.

Keywords: tick, *Dermacentor reticulatus*, soil hydrology, ecological factor, distribution

PS – poster session

Session: P1 Vectors and pathogens

The occurrence of ticks on the Casimir Pulaski border tourist trail in the Outer Western Carpathians in southern Poland (Lesser Poland and Subcarpathia voivodeships)

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Abstract

Climate warming is expanding the range of ticks and the diseases they carry. For this reason, it is important to constantly monitor border areas for tick diversity.

The study was conducted to determine the species of ticks occurring on the Casimir Pulaski border trail in southern Poland, along the Polish-Slovak border. The aim was also to determine the number of ticks on the route covered by the study, assess the risk of contact between people visiting the tourist trail and ticks, and indicate preventive measures to minimize the likelihood of tick attacks.

The research was conducted on 31 May 2025 and covered a section of the Casimir Pulaski trail, which runs through the area of the Magura National Park and its buffer zone. The 24.5-km-long section of the trail begins within the non-existent village of Radocyna and ends at border post no. 1/165. Ticks were collected along the trail using the flagging method. The specimens collected with tweezers were marked, placed in empty tubes and frozen at −20 ℃ for later molecular testing.

A total of 221 ticks representing the species *Ixodes ricinus* were collected in the field. Among the individuals collected, 42 females, 22 males and 157 nymphs were identified.

The first stage of the study, involving the collection of ticks from vegetation, showed the occurrence of *I. ricinus* ticks on the Casimir Pulaski border tourist trail. The obtained results therefore confirm the existence of a risk of contact with ticks and the research will be continued. Based on the data obtained, it is reasonable to implement appropriate preventive measures by trail users to reduce the risk of tick attacks.

Keywords: ticks, Casimir Pulaski trail, Magura National Park, Carpathians, Poland

PS – poster session

[P2]
Experimental parasitology and modern research methods

Session: P2 Experimental parasitology and modern research methods

Determination of parasite eggs viability by incubation – necessary incubation time for eggs from different sources

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Abstract

The study aimed to determine the optimal incubation time required for accurately and efficiently assessing the viability of parasitic nematode eggs as part of optimising reliable parasitological diagnostics.

For the experiment *Ascaris suum* eggs were obtained from three sources: the uteruses of mature female nematodes (group U), pig faeces (group F), and dewatered sewage sludge obtained from a wastewater treatment plant (group S). The eggs were incubated at a temperature ranging from 26 to 28 °C and observed weekly for 12 weeks. Then the eggs were categorised as dead (those with clear deformations – DE), live – those with developing motile larvae (LE), or those of uncertain viability – retaining structural integrity but lacking embryonic development (QE).

The results revealed differences in egg viability among the U, F, and S groups. Eggs isolated from nematodes uteri exhibited high viability and rapid larval development, contrasting with eggs from faeces and sewage sludge that displayed delayed larval development. The time taken to confirm the viability status of all the eggs (i.e. the time taken for the eggs with uncertain viability to either develop into larvae or show signs of internal structural decay) varied significantly, ranging from three weeks for group U to eight to twelve weeks for groups F and S. Furthermore, 96% of the eggs in group U developed into larvae, compared to 52% in group F and 3% in group S, suggesting the need for longer incubation periods in diagnostic methods, particularly for sewage sludge samples.

In conclusion, this study provides insights into the optimal incubation times required for the accurate assessment of *A. suum* egg viability and highlights the challenges and requirements for reliable diagnostic techniques in parasitology. It also highlights the unreliability of methods based solely on a single assessment of internal egg structures without incubation.

Keywords: *Ascaris*, eggs, viability determination

PS – poster session

Session: P2 Experimental parasitology and modern research methods

Assessment of the biocidal efficacy of ACCMK against *Eimeria* sp. oocysts – preliminary studies

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Abstract

The aim of the study was to evaluate the coccidiocidal effect of the ACCMK preparation (manufacturer: DDD-1), which contains phenols (27%), propan-2-ol (20%), and alkylbenzenesulfonic acid (16%). This study was conducted using coccidian oocysts isolated from the feces of poultry and rabbits, with the objective of evaluating the effects of the tested substance on oocysts morphology and their sporulation capacity.

The preparation was used in 0.5%, 1%, and 3% solutions and tested against Coccidia (*Eimeria* spp.) isolated from the feces of naturally infected chickens and rabbits. Both unsporulated and sporulated oocysts were exposed to the product for 16 hours and evaluated in five replicates for each concentration, host species, and control groups. Oocysts showing morphological changes in their wall or in the structure of the zygote/sporocyst were classified as dead/damaged.

In all test groups, the efficacy criterion – defined as ≥95% damaged oocysts – was met after exposure to 1% and 3% solutions for chicken oocysts, and to 3% for rabbit oocysts. According to Abbott's formula (≥90% efficacy), the criterion was met at 0.5% solution for rabbit oocysts and at 1% and 3% for both chicken and rabbit oocysts. Statistically significant differences were found in all experimental groups when comparing exposure to 0.5% and 3% concentrations in both chickens and rabbits oocysts ($p<0.05$). Significant differences were also observed at the 0.5% concentration between coccidia from chickens and rabbits ($p=0.0001$). The results indicate that the ACCMK product, when used at concentrations of 1% and 3%, can be effectively used for the inactivation of *Eimeria* spp. oocysts in livestock environments, thereby reducing the risk of coccidiosis outbreaks.

Keywords: coccidiosis, prevention, phenols

PS – poster session

Session: P2 Experimental parasitology and modern research methods

Towards protection against toxoplasmosis: An experimental DNA vaccine approach

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Abstract

Toxoplasmosis is a parasitic disease caused by the intracellular protozoan parasite *Toxoplasma gondii*, which is capable of infecting all warm-blooded animals, including humans. It is estimated that approximately 30% of the human population is infected with this parasite. While *T. gondii* infection is mostly asymptomatic in immunocompetent individuals, immunocompromised individuals are susceptible to severe toxoplasmosis. Toxoplasmosis constitutes a further problem in the context of livestock farming, given its association with financial losses. The only vaccine available against *T. gondii* is based on the attenuated strain S48. Its utilisation is restricted to veterinary use and it does not prevent horizontal transmission. Consequently, novel solutions for the immunoprophylaxis of toxoplasmosis are currently being sought. The objective of the present studies was to develop and evaluate the efficacy of a DNA vaccine encoding *T. gondii* chimeric antigens SGR (SAG2-GRA1-ROP1) and SMMG (SAG1-MIC1-MAG1-GRA2), using a mouse immunisation procedure. The experiment involved vaccination with pDNA alone or pDNA complexed with developed cationic liposomes and subsequent infection of mice with *T. gondii* to determine the degree of post-vaccination protection. A further immunological *in vitro* assessments, incorporating both humoral and cellular response measurements, were conducted post-vaccination. The administration of plasmid DNA encoding chimeric *T. gondii* antigens elicited a faint cellular response, which consequently engendered a relatively modest level of post-vaccination protection. The employment of liposomes allowed a reduction in the dose of DNA administered, whilst simultaneously resulted in enhanced protection for the SGR antigen-based vaccine, thus further studies are required to improve the immunoprotective capacity of developed experimental DNA vaccines against toxoplasmosis.

The work was funded by the National Science Centre, Poland (UMO-2018/31/D/NZ6/02839).

Keywords: toxoplasmosis, immunoprophylaxis, immune response, immunoprotection

PS – poster session

Session: P2 Experimental parasitology and modern research methods

Analysis of drug susceptibility to fungi isolated from the oral cavity of pediatric patients with acute lymphoblastic leukemia

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Abstract

Children with acute lymphoblastic leukemia (ALL), undergoing high-dose methotrexate (HDMTX) treatment (protocol M of the AIEOP-BFM ALL 2017 Poland regimen), receive no routine antifungal prophylaxis, which raises concern about the risk of invasive fungal infections. Invasive candidiasis affects up to 12% of pediatric ALL patients. Yet, there is no data on fungal colonization dynamics during methotrexate therapy. Given that fungal colonization may precede invasive infection and that antifungal resistance complicates treatment, this study aimed to evaluate the level of oral mucosal fungal colonization and antifungal susceptibility in children undergoing HDMTX treatment.

Oral swabs were collected from 22 children at four time points during protocol M: before 1st, 2nd, 3rd and 4th infusions of HDMTX. The swabs were cultured on Sabouraud's agar with chloramphenicol. The obtained yeast isolates were passaged on fresh agar and then identified on the basis of the biochemical profile. Susceptibility of yeast to selected antifungal drugs was analyzed according to the EUCAST Definitive Document E.Def 7.4 procedure.

Fungi were detected in 9 (40.9%) children with ALL, with the incidence of fungal colonization varying across treatment time points. In 3 patients, fungi were detected at 4 time points. *Candida albicans* was isolated most frequently (19 isolates), followed less frequently by *Candida dublinienisis* and *Candida tropicalis* (2 isolates each). The highest mean minimum inhibitory concentration (MIC) value was recorded for fluconazole (28.4mg/L), followed by voriconazole (7.1mg/L), whereas the lowest MIC value was observed for amphotericin (0.3mg/L).

These findings highlight a need for routine monitoring of fungal colonization and antifungal susceptibility in children undergoing high-dose methotrexate treatment.

Keywords: *Candida*, drug susceptibility, minimal inhibitory concentration, leukemia

PS – poster session

Session: P2 Experimental parasitology and modern research methods

A potential plant-based oral vaccine against *Fasciola hepatica* for protection of domestic ruminants

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Abstract

Oral vaccination is a promising strategy for fasciolosis control in livestock. Our approach involves the use of freeze-dried transgenic lettuce expressing *Fasciola hepatica* cysteine protease (CP). When administered orally as a soluble protein, CP is weakly immunogenic and therefore needs to be conjugated to a carrier. Here, hepatitis B core antigen (HBcAg) which assembles into stable and highly immunogenic virus-like particles (VLPs) was used. The plant-based vaccine can be administered orally to animals, providing a stress-free, scalable, and cost-effective alternative to injection-based immunization. Preliminary studies using HBcAg with inserted CP as a vaccine have shown that this strategy has immunoprotective potential.

Here, a genetic construct consisted of an HBcAg coding sequence with an inserted CP domain, joined to a regular HBcAg sequence was prepared. The heterodimer (hHBcCP) sequence was used for *Agrobacterium*-mediated transformation of lettuce. The resulting transgenic plants produced up to several µg of hHBcCP per g of fresh weight.

Plant tissue was processed by lyophilization using lyoprotectants, followed by pulverization. Four ELISA assays were developed: (1) for total HBcAg (2) for VLPs formed by HBcAg (3) for hHBcCP using an anti-CP antibody for capture and an anti-HBc antibody for detection, and (4) for hHBcCP using an anti-HBc antibody for capture and serum from *F. hepatica* infected sheep for detection. The ELISA assays proved to be effective and consistent, confirming the preservation of specific components of VLP-assembled hHBcCP during long-term storage. These results indicate the successful development of a semi-finished product for an oral anti-parasitic vaccine, offering a concentrated and at least partially standardized antigen dose. This product is planned to be tested in animal immunization experiments.

The study was funded by the National Science Center (2019/35/B/NZ6/04002).

Keywords: *Fasciola hepatica*, oral vaccines, virus-like particles, cysteine protease

PS – poster session

Session: P2 Experimental parasitology and modern research methods

New active substances in *Dermanyssus gallinae* control

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Abstract

Dermanyssus gallinae, commonly known as the poultry red mite, is one of the most significant ectoparasites affecting hens worldwide. Its presence in poultry farms is associated with substantial economic and welfare consequences, including reduced egg production, anemia, increased mortality, behavioral disturbances, and heightened susceptibility to secondary infections. Moreover, *D. gallinae* has zoonotic potential, posing health risks to farm workers and veterinarians through dermatological and allergic reactions. One of the key challenges in the effective control of *D. gallinae* is the increasing resistance of mite populations to commonly used acaricidal agents. As a result of prolonged and often improper use of chemical compounds, such as pyrethroids, organophosphates, and carbamates, a gradual decline in the efficacy of these treatments has been observed, significantly complicating infestation management. There is a continuous demand on the market for new, effective control agents against the poultry red mite that are also safe for consumer health.

The aim of the study was the use of quinoline-6-carboxylic acid methyl ester to control mites of the species *D. gallinae* (Patent No. PL 440066). The killing efficacy of this substance was assessed using the Zdybel et al.2011 method in its modification. For each plate containing a veneer disc soaked in the substances, the mortality of mites was calculated with a correction taking into account the mortality in the control group (Abbott's correction). The average was the final count from four repetitions. The tested compound demonstrated 100% effectiveness against *D. gallinae*. This high level of efficacy supports its potential as a promising agent for the control of poultry red mites

Keywords: *Dermanyssus gallinae*, red mite, mite control

PS – poster session

Session: P2 Experimental parasitology and modern research methods

From malaria to babesiosis: repurposing antimalarial drugs to tackle an emergent disease

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Abstract

Babesiosis is an emerging tick-borne disease caused by protozoan parasites of the genus *Babesia*, with significant economic, veterinary and public health implications worldwide. Among the more than 100 species described of this genus, *Babesia ovis* is the most pathogenic species in small ruminants, leading to high mortality rates and substantial economic losses. The limitations and challenges associated with existent therapies underline the urgent need for the development of new, effective and safer therapeutics options. Given the evolutionary proximity between *Babesia* and *Plasmodium* species, several antimalarial compounds have been explored as potential alternatives for babesiosis treatment.

In this study, a selection of fifteen antimalarial compounds, including quinoline derivatives, antifolates, artemisinin-based compounds, and novel compounds, were evaluated for their *in vitro* activity against *Babesia ovis* using an optimized SYBR Green I fluorescence assay. Cultures of *B. ovis* (1% parasitemia) were exposed to 5 µM of each compound, maintained in 10% (vol/vol) defibrinated lamb erythrocytes in a HEPES-buffered Medium 199 (1x) containing 20% lamb serum, in a microaerophilic, stationary-phase culture system, during 96 h. The activity of the compounds was monitored every 24 h. Most compounds tested exhibited variable levels of growth inhibition, with several demonstrating promising antiparasitic activity. The compounds showing the highest inhibitory effects (>90% inhibition), namely Cipargamin, Halofantrine, Methylene Blue, and LDT-146, were subsequently selected for half-maximal inhibitory concentration (IC_{50}) determination using the same fluorescence-based method. These preliminary results suggest that repurposing antimalarials may be a promising strategy for the treatment of babesiosis and underline the value of fluorescence-based screening as a powerful tool for identifying candidate compounds in antiparasitic drug discovery.

Keywords: babesiosis, *Babesia ovis*, antimalarial compounds, fluorescence-based assay

PS – poster session

Session: P2 Experimental parasitology and modern research methods

Development of a recombinant chimeric multiepitope protein for diagnosis of Lyme disease

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Abstract

Lyme disease is a multisystem infectious disease caused by *Borrelia burgdorferi*, transmitted mainly by *Ixodes* ticks. Although erythema migrans is a hallmark of early infection, it is often absent, making diagnosis difficult. Early symptoms like fatigue, fever, and joint pain are nonspecific and can mimic common viral infections.

Standard diagnosis uses a two-step serological approach: an ELISA followed by confirmatory Western blot. This is due to the antigenic complexity of *B. burgdorferi* sensu lato, which includes multiple genospecies with high genetic and protein variability. ELISAs based on whole-cell lysates can suffer from cross-reactivity and batch variability due to inconsistent antigen expression and plasmid loss during culture. While Western blot improves specificity, it adds cost, time, and interpretive difficulty.

Recombinant chimeric antigens offer a promising alternative. These engineered proteins fuse conserved, immunodominant epitopes from multiple diagnostically relevant *B. burgdorferi* antigens into a single polypeptide, improving diagnostic accuracy. In this study, we report the design and production of a recombinant chimeric protein that combines B/32-G and B/32-M — two previously reported recombinant chimeric proteins containing IgG- and IgM-specific linear epitopes of BmpA and BBK32 antigens, constructed based on epitope mapping data. Gene fragments encoding B/32-G and B/32-M were amplified, fused, and cloned into the pUET1 expression vector. The recombinant construct was expressed in *Escherichia coli* BL21(DE3)pLacI, and the protein was purified via one-step metal affinity chromatography, facilitated by the presence of His-tags. This yielded 10.5 mg of protein per liter of bacterial culture. The immunoreactivity of the obtained recombinant protein was preliminarily evaluated by Western blot.

This research was funded by The National Science Centre, Poland (project no. 2023/49/B/NZ6/02881).

Keywords: Lyme Disease, *Borrelia burgdorferi*, serodiagnosis, recombinant antigens, chimeric antigens

PS – poster session

Session: P2 Experimental parasitology and modern research methods

Determination of immunoreactive fragments of a novel *Toxoplasma gondii* antigen with potential diagnostic utility

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Abstract

Toxoplasma gondii is the causative agent of toxoplasmosis—a parasitic disease typically asymptomatic in healthy individuals but potentially severe in immunocompromised patients and pregnant women. Congenital transmission can cause miscarriage, intrauterine death, or irreversible neurological and developmental defects. Due to its often subclinical presentation, toxoplasmosis is mainly diagnosed by serological tests detecting *T. gondii*-specific antibodies. Most commercial assays use *Toxoplasma* Lysate Antigen (TLA), derived from whole-parasite extracts. However, TLA production is time-consuming, costly, and poses a biohazard risk due to the need to propagate live parasites. Recombinant antigens offer a safer, more standardized alternative, with benefits such as lower cost and improved reproducibility, making them promising candidates for the development of next-generation serodiagnostic assays.

In this study, gene fragments encoding the full-length GRA29 protein, as well as its N-terminal and C-terminal regions, were amplified from *T. gondii* cDNA and cloned into the pET30/Ek-LIC and pUET1 expression vectors. The resulting recombinant constructs were expressed in *Escherichia coli*, and the proteins were purified using one-step metal affinity chromatography, facilitated by His-tags. Expression conditions were optimized to maximize protein yield, resulting in production levels of 75 mg/L for full-length GRA29, 30 mg/L for the N-terminal fragment, and 63 mg/L for the C-terminal fragment. The immunoreactivity of each recombinant protein was evaluated by ELISA using a small panel of sera from individuals infected with *T. gondii*. The tested protein fragments showed varying immunoreactivity.

These findings underscore the importance of not only optimizing recombinant protein expression systems but also carefully selecting the most immunoreactive protein regions to enhance the sensitivity and specificity of serological assays.

Keywords: *Toxoplasma gondii*, toxoplasmosis, serodiagnosis, recombinant antigen

PS – poster session

Session: P2 Experimental parasitology and modern research methods

Regulation of anti-amoebic activity of green tea extract by silver nanoparticles

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Abstract

Given the relatively small repertoire of antiparasitic drugs, there is a need for research into the development of new drugs. Among the investigated substances are nanoparticles, whose antiparasitic properties may be enhanced when combined with plant extracts rich in bioactive compounds, that are toxic to parasites and safe to the host. This study evaluated the antiparasitic effect of silver nanoparticles coated with green tea GT(AgNPs) compared to silver nanoparticles (AgNPs) or green tea extract alone. The research was carried out *in vitro*, using a water-derived free-living strain of *Acanthamoeba castellanii* genotype T4. Expression of ATPase, GTPase and cysteine proteinase II genes, related to the process of phagocytosis, was evaluated using RT-qPCR.Changes in cell morphology and ultrastructure were assessed by transmission electron microscopy. All three kinds of treatment, AgNPs, GTs and GT(AgNPs), showed concentration-dependent antiparasitic activity. A transmission electron microscopy visualised phagocytosis of silver nanoparticles that accumulated in vacuoles. In contrast, amoebae treated with GT(AgNPs) showed vacuolisation of the cytoplasm, as well as disintegration of cytoplasmic organelles. Treatment with green tea alone also showed toxicity towards *A. castellani*. It also induced high expression of cysteine proteinase II gene, with active autophagy, but without vacuolisation of the cytoplasm. The toxicity mechanisms of silver nanoparticles and green tea extract appear to differ, with implications for processes such as vacuole formation in trophozoites of *A. castellani*.

Keywords: *Acanthamoeba castellanii*, silver nanoparticles, green tea, antiparasitic activity

PS – poster session

Session: P2 Experimental parasitology and modern research methods

A new, standardized environmental model for studying repellents and tick behavior

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Abstract

Hard ticks are vectors of many pathogens, especially *Borrelia burgdorferi* sensu lato, and tick-borne encephalitis virus. To avoid infection, it is best to prevent parasitic infestation by using repellents. The problem is the choice of a reliable and standardized method for testing repellents. Previously used repellent tests have not taken into account the influence of many biotic and abiotic factors. Air temperature, humidity and skin temperature of the host are factors that have a significant impact on the mechanism of tick infestation. Moreover, there is no *in vitro* model that can replace human skin tests for testing tick repellents.

The prototype, presented in this study is an alternative to both field and human skin tests. The use of thermal and chemical attractants on the leg phantom should provide an alternative to the experimental model requiring human participation in the research. Environmental conditions were recreated by using strictly controlled abiotic factors, such as humidity and temperature. In addition, this model includes the tick behavior of climbing on the host. The environmental chamber with human leg phantom was made of a transparent polycarbonate cylinder with a lid on the top. Optimum environmental conditions were generated by an ultrasonic air humidifier, a heating system, and a fan ensuring air circulation. The vertical element of the phantom had three thermal zones. The heating elements of the chamber and the leg phantom was equipped with thermostats ensuring precise temperature control. Humidity levels were measured with

a built-in hygrometer and stabilized by a humidifier controller. This environmental chamber with human leg phantom creates a new possibility of conducting tests in repeatable conditions of air temperature and humidity. The effectiveness of tick repellents and substances will be tested in the constructed chamber with controlled conditions similar to those in the natural environment where people are exposed to ticks.

Keywords: tick repellent test, ticks, repellents

PS – poster session

Session: P2 Experimental parasitology and modern research methods

Phytosanitation of sewage sludge and digestates from agricultural biogas plants – a way to remove parasite eggs before using these substances as fertilizers

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Abstract

The aim of processing municipal sewage sludge and digestates from agricultural biogas plants using phytosanitation was to remove indicator pathogens, including live eggs of intestinal nematodes of the genera *Ascaris*, *Toxocar*a and *Trichuris* and oocysts of protozoa of the genus *Cryptosporidium*. The proposed phytosanitation consisted in sowing plants onto a substrate containing sewage sludge or digestate, which, on the one hand, can later be used as a so-called green manure, and at the same time, during growth, exhibit a cidal effect on soil nematodes in their root zone. After preliminary studies, among many plants showing the assumed properties, the oilseed radish *Raphanus sativus,* white mustard *Sinapis alba*, French marigold *Tagetes patula* and common buckwheat *Fagopyrum esculentum* were indicated as the best adapted to growth on substrates composed mainly of sludge and digestates. These plants were sown in experimental plots established on the basis of sewage sludge and post-fermentation. Substrate samples were taken at monthly intervals to assess the pathogen content. After the first year of vegetation, the plots were ploughed and at the beginning of the second season, selected plants were sown again, repeating the sampling and testing scheme. Among the plants tested, oil radish demonstrated effective action against all indicator pathogens both present in the post-fermentation and sewage sludge. Its action ensures the elimination of all pathogens after just one vegetation season. The effectiveness of other plant species depends on the type of substrate and the type of pathogen detected, and the required phytosanitation time is 2 vegetation seasons (subject to the incomplete effectiveness of post-fermentation sanitation using French marigold and white mustard against Cryptosporidium sp. oocysts).

The research was financed by the National Center for Research and Development (NCBiR); Project No: GOSPOSTRATEG-III/0061/2020-00

Keywords: phytosanitation, sewage sludge, digestates, parasite, eggs

PS – poster session

[P3]

Human parasitosis, environmental and zoonotic threats

Session: P3 Human parasitosis, environmental and zoonotic threats

Blastocystis sp. in urban wild boars: epidemiological and genetic insights from North-Eastern Pomeranian Province

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Abstract

Blastocystis is a unicellular anaerobic protozoan frequently found in the gastrointestinal tract of humans and animals. Its pathogenicity remains unclear, but is thought to depend on over 30 known subtypes (STs), showing variability in the SSU-rRNA gene. In wild boars, *Blastocystis* prevalence varies across Europe, with highest rates in Portugal (34.3%), followed by Spain (10.0%) and Eastern Slovakia (5.95%). ST5 is most commonly reported in this host. This study aimed to assess the prevalence and subtype distribution of *Blastocystis* in an urban wild boar population in north-eastern Pomerania, as well as evaluate the potential for zoonotic transmission.

Faecal samples from 118 wild boars from four districts (Gdańsk, Gdynia, Wejherowo, Puck) were collected. DNA was isolated using the Genomic Mini AX Stool kit (A&A Biotech.). Nested PCR targeting SSU-rRNA was performed (primers RD5/RD3 and RD5StenF/BhRDr) following COST *Blastocystis* guidelines. Positive products were sequenced using the Sanger method and analyzed by Geneious programme and the BLAST tool.

PCR confirmed the presence of *Blastocystis* DNA in 50 samples (42.7%), with sequencing confirmation in 37 cases (31.35%). Subtyping showed ST3 dominance (91.89% of positive samples), while ST5 accounted for 8.11%. In the total population, ST3 and ST5 were found in 29.06% and 2.56% of individuals, respectively. No statistically significant correlation was found between ST3 infection and age (p=0.956) or sex (p=0.508). The highest number of positives was recorded in Gdańsk (44.3%), followed by Gdynia (29.4%) and Wejherowo (5.6%); no positives were found in Puck.

Areas inhabited by humans are also becoming natural areas for wild boars. The presence of ST3—commonly found in humans—suggests possible anthroponotic transmission. These findings support the hypothesis that close contact between urban wild boars and humans may facilitate cross-species transmission of *Blastocystis*, similarly to domestic pigs.

Keywords: *Blastocystis*, wild boar, zoonosis, anthroponosis, one health

PS – poster session

Session: P3 Human parasitosis, environmental and zoonotic threats

Cordylobia anthropophaga in travellers returning from Gambia and Senegal – case reports

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Abstract

Blowflies of the genus *Cordylobia* Grünberg, 1903 (Diptera: Calliphoridae) cause obligatory myiasis in mammals. Endemic to the Afrotropical realm, *C. anthropophaga* (Blanchard & Bérenger-Féraud, 1872), *C. rodhaini* Gedoelst, 1910, and *C. ruandae* Fain, 1953 are known to cause cutaneous myiasis in humans, with *C. anthropophaga* being the most frequently reported due to its wide distribution across Africa.

We present two cases of myiasis in travellers returning from The Gambia and Senegal. Larvae were submitted directly by the patients to the Division of Tropical Parasitology for examination. A third instar larva was identified based on morphological features including spines, peritreme slits, and labial sclerites. Identification of a first instar larva required amplification and sequencing of the barcoding fragment of the cytochrome c oxidase subunit I gene.

Case 1: An 11-year-old girl returned to Poland from a Gambian region bordering Senegal, where she spent the 2022/23 festive season. She noticed a lesion on the lateral side of her left calf. At a hospital in southern Poland, an aperture in the skin (maintained by the larva as a breathing hole) was widened and cleaned, and she was discharged. Five days after return, she removed a third instar larva of *C. anthropophaga* herself.

Case 2: A 49-year-old man returned to Poland after a 6-day trip to The Gambia, including one day in Senegal. During his stay, he noticed a small abscess and later removed a first instar larva of *C. anthropophaga* himself.

With growing numbers of tourists visiting tropical destinations, exotic parasitic infections are increasingly relevant for travellers from temperate regions. While not life-threatening, myiasis causes discomfort and carries a risk of secondary infection. Preventive measures include wearing clothing that has been dried in direct sunlight and well-ironed.

Keywords: *Cordylobia*, myiasis, tumbu fly, travel medicine

PS – poster session

Session: P3 Human parasitosis, environmental and zoonotic threats

Assessment of zoonotic parasites in marine fish imported to Poland from third countries

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Abstract

Nematodes of the genus *Anisakis* are commonly present in marine fish. Consumption of fish containing parasites may lead to anisakiosis manifested by gastrointestinal symptoms and also allergic response even after consumtion of cooked fish.

The aim of this study was to evaluate the safety of fish imported to Poland originated from outside of European Union.

In this study 100 of fish samples from 7 major fishing areas were collected by Border Veterinary Inspectorates. These were samples of the following fish species: tuna (4 samples), wild sockeye salmon (37), blue grenadier (5), patagonian grenadier (16), walleye pollock (11), cape hake (4), yellowfin sole (8), and atlantic cod (15). The samples were tested by the digestion method according to EN ISO 23036-2. PCR-RFLP and sequencing was used to identify the species of found parasites.

Parasites were found in 28 out of 100 (28%) tested samples. These were: wild sockeye salmon (24), walleye pollock (2), yellowfin sole (1) and atlantic cod (1). The percentage of fish containing parasites was 64.9% (24/37), 18.2% (2/11), 12.5% (1/8) and 6.7 (1/15), respectively. The number of larvae detected in wild sockeye salmon ranged from 1 to 11/100g, with a total of 67 larvae, in case of two walleye pollock and one atlantic cod 1 larvae/100g was detected, while in yellowfin sole 1 larvae/200g was detected. The ITS gene was amplified for preliminary identification of larvae species. Sixty-nine larvae were preliminarly classified as *A. pegreffi*, *A. simplex* s.s., while 1 larvae was not identified.

The sequencing of ITS gene allowed to confirm that 69 larvae were *Anisakis simplex*. The unidentified larva from yellowfin sole belonged to the species *Contracecum* spp.

These results indicate that parasites may be present in fish originated from outside of EU posing a potential risk for consumers.

Keywords: *Anisakis* spp., *Contraceum* spp., marine fish

PS – poster session

Session: P3 Human parasitosis, environmental and zoonotic threats

Distribution of *Trichobilharzia* species in recreational waters in North-Eastern Poland

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Abstract

In Europe, human cercarial dermatitis (swimmer's itch) is most commonly caused by avian schistosomes of the genus *Trichobilharzia*. The disease is characterized by a pruritic cutaneous eruptions resulting from an immunoallergic response to the penetration of cercariae into the skin.

The study aimed to conduct a molecular and phylogenetic analysis of *Trichobilharzia* species occurring in recreational waters in North-Eastern Poland.

The study area covered three water bodies (Lake Skanda, Lake Ukiel, and Lake Tyrsko) over the summer of 2021. In total, 747 pulmonate freshwater snails (*Radix* spp*., Lymnaea stagnalis*) were collected. The phylogenetic analyses of furcocercariae were based on the partial sequence of the ITS region (ITS1, 5.8S rDNA, ITS2 and 28S rDNA). For *Radix* spp. phylogenetic analyses were based on the ITS-2 region.

The prevalence of the *Trichobilharzia* species infection in snails was 0.5%. Two out of 478 (0.4%) *L. stagnalis* were found to be infected with *Trichobilharzia szidati*. Moreover, 2 out of 269 (0.7%) snails of the genus *Radix* were positive for schistosome cercariae. Both of these snails were identified as *Radix auricularia*. One of them was infected with *Trichobilharzia franki*, and the other with *Trichobilharzia* sp.

Molecular identification of avian schistosome species, both at the intermediate and definitive hosts level, constitutes an important source of information on a potential threat and prognosis of local swimmer's itch occurrence, and helps to determine species diversity in a particular area.

Keywords: cercarial dermatitis, *Trichobilharzia*, avian schistosomes

PS – poster session

Session: P3 Human parasitosis, environmental and zoonotic threats

Is the problem of intestinal parasites in children still relevant?

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Abstract

Intestinal parasitic infections are widespread throughout the world and have a high prevalence in many regions, making them a serious public health problem.

Children under five years old are the most vulnerable to infections, due to their immature immunity, developing exploratory behaviors, lack of hygiene practices, and frequent contact with peers.

This study aimed to assess the prevalence of intestinal parasites and influence of demographic, environmental and behavioral factors on the risk of infection in pre-school children from selected regions of the north-eastern Poland.

The material consisting of stool samples and perianal swabs was collected three times at 2–3-day intervals. In addition, the children's parents were asked to complete a questionnaire on demographics and potential risk factors. Detection of enteric parasites was conducted by coproscopy and Real Time PCR methods by qualified laboratory diagnosticians.

From February 2019 to April 2025, a total of 7,396 samples from 1,633 children aged 1–6 years were examined. Among them, 49.2% were girls and 50.8% were boys. 70.5% children lived in urban areas, while 29.5% lived in rural areas. Intestinal parasites were detected in 644 children (40.2%). The most frequent were: *Dientamoeba fragilis* (33.6%), *Enterobius vermicularis* (11.6%) and *Blastocystis* spp. (3.7%). The statistical analysis showed association between gender, place of residence and prevalence rate of intestinal parasites. There were no statistically significant differences between sibling number, household sanitation, feeding habits, pet ownership, hand washing, playing in the sand, frequency of travel and prevalence rate of intestinal parasites.

We found that potentially pathogenic parasites such as *D. fragilis* and *Blastocystis* spp., are common in healthy preschool children in the investigated regions.

These results emphasize the importance of asymptomatic carriers in the spread and preservation of pathogens that can cause gastrointestinal symptoms.

Keywords: intestinal parasite, prevalence, children, Poland, coproscopy, Real-Time PCR

PS – poster session

Session: P3 Human parasitosis, environmental and zoonotic threats

Contamination of water sources with *Echinococcus multilocularis* and possible implications for human health – 10 years of studies in Poland and China

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Abstract

Echinococcus multilocularis is a parasite causing a dangerous zoonosis, alveolar echinococcosis (AE), with 90% of cases recorded in China, especially in the Qinghai Tibet Plateau (QTP) area; in Poland, Warmia-Masuria is considered the most endemic province. Although water has been indicated as possible source of infection with *E. multilocularis*, data on the distribution of the tapeworm in water reservoirs is very limited. The aim of the study was to determine the occurrence of *E. multilocularis* in different types of water supplies in the area of QTP, China and Pomerania and Warmia-Masuria provinces, Poland.

In China, 510 samples were collected, including 186 wastewater samples and 326 samples collected from streams and shallow waterholes that serve as sources of drinking water consumed unprocessed by humans and animals. In Poland, 105 samples were collected from rivers, lakes and surface wells. 40 L water samples were either filtered on site with capsule filters (Poland) or first collected in sterile vessels and transported to the laboratory for further filtration with membrane filters (China). Final pellet was subsequently analysed with molecular detection methods including real-time PCR, nested PCR and DNA sequencing.

Of the samples examined, *E. multilocularis* DNA was confirmed in 11 (5.9%) wastewater samples and 3 (0.9%) stream water samples from Qinghai province, China and in 2 (1.9%) lake water samples from Warmia-Masuria province, Poland.

Results indicate the potential role of surface water in dissemination of *E. multilocularis* in endemic areas of the QTP, China and Warmia-Masuria, Poland and contamination of drinking water sources. This raise a question about the risk for humans and animals echinococcosis living in at-risk regions.

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Keywords: *Echinococcus multilocularis*, contamination, water, Poland, China

OS – oral session

Session: P3 Human parasitosis, environmental and zoonotic threats

Subtype distribution of *Blastocystis* sp. in wild roe deer (*Capreolus capreolus*) in Central Poland as an underestimated source of human infection

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Abstract

Blastocystis sp. is one of the most common protists colonizing the gastrointestinal tract of humans and animals worldwide. The transmission is via the fecal-oral route, and zoonotic potential is crucial according to the lack of host specificity of *Blastocystis* sp. subtypes (STs). The roe deer (*Capreolus capreolus*) has evolved to be an inhabitant of diverse habitat types, and its overabundant population in Poland is expanding, living near or in suburban areas where they frequently encounter humans, companion animals, and livestock. This may result in interspecies infections. Therefore, it is important to clarify the pathogen species carried by roe deer to understand its potential role as reservoirs for human infection. There is no data on the occurrence of *Blastocystis* sp. in wild roe deer in Poland, and data from Europe are sparse. The aim of the present work is to provide the first examination of the occurrence and subtype distribution of *Blastocystis* sp. in wild roe deer living in Central Poland.

A total of 151 fecal samples were collected from roe deer living in three areas of Central Poland—Iłża, Rawa Mazowiecka, and Węgrów—according to standard dissection techniques. Among these, 49 (32.5%) were *Blastocystis*-positive in molecular identification by PCR using RD5 and BhRDr primers. Sequencing on PCR-positive samples was performed, and three subtypes (ST10, ST13, and ST14) were identified. Of the 49 samples, 25 were identified as ST14 (51%), 16 were ST13 (32.7%), and five were ST10 (10.2%). Three samples (6.1%) were identified as *Blastocystis* sp. ST10 and ST14 may have zoonotic potential without showing host specificity, and ST13 in humans has not been reported.

This study explored the prevalence of *Blastocystis* sp. subtypes in forest roe deer for the first time, emphasizing the potential threat of zoonotic transmission. Thus, continuous attention should be provided to the potential for transmission between wildlife and domestic animals and humans.

Keywords: *Blastocystis*, zoonosis, wild roe deer

PS – poster session

Session: P3 Human parasitosis, environmental and zoonotic threats

Public health and prevention on the example of toxoplasmosis circulation in Poland

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Abstract

Public health is an action to protect and improve health, and prevention is a key element in improving quality of life and avoiding disease. If we don't understand it properly, we neglect public health, the result is endemics, for example. Here, what people know about the subject was examined, taking into account where they live, the number of pregnancies they have had, and their non-medical and medical professions.

250 people took part in the survey. Questions included, for example, knowledge of sources of infection, effects of infection, diagnostic tests, the role of animals in the circulation of toxoplasmosis and daily hygiene practices. For 81% of the women surveyed, toxoplasmosis was not new. The most common indicated sources of infection were contact with a cat (77%-not empirically confirmed), consumption of raw meat (40%-an underestimated route of infection) and unwashed ground vegetables and fruits (36%). Testing for toxoplasmosis was done by 39% of the women surveyed, most often during pregnancy 32%. Bourgeois women knew more about the subject without paying attention to preventive measures, while rural women instinctively avoided potential toxoplasmosis infections, e.g. they were more likely to test their pets (48%) than urban residents (17%).

The general knowledge of gynecological staff about toxoplasmosis was high, with 60% of them having proper knowledge about the routes of infection. Thus, it seems that preventive measures in 40% of the respondents were poorly managed. Surprisingly, there was a problem with diagnosis and interpretation of results.

The survey showed: superficial knowledge of the subject, gaps in practical knowledge of circulation and toxoplasmosis infection, differences in women's awareness depending on where they live, gaps in the professional preparation of medical personnel, ineffectiveness of preventive measures.

In view of this, toxoplasmosis prevention should be analyzed, for example, in the context of miscarriages in pregnant women.

Keywords: *Toxoplasma gondii*, toxoplasmosis, transmission routes, public awareness, infection prevention, pregnant women, zoonosis, medical personnel, health education and awareness, public health, epidemiology of toxoplasmosis, risk factors for infection

PS – poster session

Session: P3 Human parasitosis, environmental and zoonotic threats

Isolation and genotyping of free-living amoebae in a water reservoir in Wrocław

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Abstract

Free-living amoebae (FLA) are protists that occur in a variety of environments and are distributed worldwide. They occur in natural and hydric environments such as water, soil, and air. Pathogenic FLA including *Balamuthia mandrillaris, Acanthamoeba spp., Naegleria fowleri* and *Vermamoeba vermiformis* are the etiological factors of several human diseases. FLA play an important role in the transmission and dispersal of pathogenic microorganisms, called endocytobionts. The occurrence of FLA in the freshwater aquatic ecosystems of temperate climates is poorly known.

Aim of the study: Study of the presence of free-living amoebae in water reservoirs in Wrocław.

Surface water samples were collected in July 2022, 2023 and 2024 from 25 water bodies in Wrocław (8 fountains, 14 ponds in city parks and 3 bathing places/ swimming pools). The water temperature in the tested reservoirs ranged from 18.1 °C to 26.4 °C. NNA solid medium (1.5 % non-nutrient agar, Difco) in petri dishes pre-coated with *Escherichia coli* was used for the isolation and culture of amoebae. Positive samples were subcultured and incubated at 42oC which allowed it to be assessed for its ability to thermotolerance. Species classification was performed using partial *18S*-rDNA PCR-sequencing analysis.

In 12 (48 %) water collection points the presence of FLA was detected, 9 natural, 3 artificial reservoirs. Based on PCR detection *Acanthamoeba hatchetti*, *Vermamoeba vermiformis*, *Naegleria australiensis* , *Naegleria clarki*, *Naegleria* spp. and *Vannella* spp. were identified in examined water bodies.

The studies confirmed the presence of medically important FLA species in both natural and artificial water bodies in Wrocław and indicate the potential threat to human infection. The research also indicates the need to conduct more extensive environmental studies of water bodies, especially considering climate change and rising water temperatures during the summer months.

Keywords: free-living amoebae (FLA), *Naegleria* spp., *Acanthamoeba* spp., *Vermamoeba vermiformis*

PS – poster session

Session: P3 Human parasitosis, environmental and zoonotic threats

Assessment of parasitological threats to human and animal health associated with the use of waste and by-products of livestock farming as fertilizers. Results of the Multiannual Program implemented in 2019–2023

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Abstract

The aim of the study was to determine the level of parasitological contamination of organic fertilizers containing by-products of animal origin or produced on the basis of municipal sewage sludge. In 2019–23, 220 samples were obtained for testing. Veterinary Inspection submitted 113 samples for testing, including 85 samples of digestate from biogas plants, 16 from composting plants and 12 from plants processing animal-by products for fertilizer purposes. State Plant Health and Seed Inspection Service submitted 17 samples of fertilizers from market inspections. 90 samples of fertilizers were purchased by National Veterinary Institute from fertilizers allowed for trade. The samples were tested using the method according to PN-Z-19005:2018-10 and the PN-Z-19006:2023-4.

Eggs of the genera *Ascaris*, *Trichuris* and *Toxocara* were found in a total of 72 samples (32.7%). Eggs of the genus *Ascaris* were found in 54 samples (24.5%), *Trichuris* in 38 samples (17.3%), *Toxocara* in 15 samples (7.7%). Live parasite eggs were found in a total of 12 samples (7%), including 5 samples provided for testing by Agricultural and Food Quality Inspection and 7 samples of organic fertilizers purchased from the market. The highest percentage of parasite eggs was found in samples of organic fertilizers tested in 2019 and amounted to 55%. Also, this year the highest percentage of samples contaminated with live parasite eggs was observed. This percentage amounted to 35%. In other years, the level of samples contaminated with parasite eggs, as well as samples containing live parasite eggs, had a downward trend and in 2021 dropped to 0.

The trend line based on results from 2014–2018 continues through 2019–2023 and shows a decreasing pattern. The findings confirm the need for continuous parasitological monitoring of organic fertilizers—both before market approval and for products already in circulation—to reduce the risks to human and animal health, and to protect the environment.

Keywords: organic fertilizers, parasitological contamination

PS – poster session

[P4]
Parasites of terrestrial and aquatic environments in the context of parasite-host interactions

Session: P4 Parasites of terrestrial and aquatic environments in the context of parasite-host interactions

Seroprevalence of *Toxoplasma gondii* and *Neospora caninum* in grey wolves (*Canis lupus*) from northern Poland. Preliminary study

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Abstract

The prevalence of *Toxoplasma gondii* and *Neospora caninum* antibodies in grey wolves varies by region. Seropositivity to *T. gondii* ranges from 0% in Alaska to 26.6% in Italy, while *N. caninum* antibodies were found in 3.7–21.4% of wolves in Europe and North America. Chronic apicomplexan infections are causing reproductive and neurological disorders and may alter host behaviour due to the ability of inducing the production of dopamine precursor in host brains. Infected wolves may take more risks, such as dispersal and/or securing a breeding position in wolf packs. As there is no data on apicomplexan infections in grey wolves in Poland, the aim of this study was to determine the extent of seropositivity to *T. gondii* and *N. caninum*.

Blood samples were obtained from 23 grey wolves, 22 of them post mortem. Nineteen animals died in road collisions; other causes included drowning, spleen trauma and illegal poaching. One sample was collected from a live-trapped, collared individual. Sera were analysed using indirect ELISA – IDvet Screen® kits microplates coated with non-infectious *T. gondii* P30 antigen and purified *N. caninum* strain extract (IDvet, Grabels, France). OD values were measured at 450 nm and seropositivity was determined per manufacturer's instructions.

Antibodies to *T. gondii* were detected in 6 out of 23 individuals (26.1%), and antibodies to *N. caninum* in 3 animals (13.0%). No dual infections were found. Positive results occurred in both juvenile and adult wolves. No clear pattern of seropositivity by sex or age category was observed. This study confirms exposure of grey wolves in northern Poland to *T. gondii* and *N. caninum*. The detected seroprevalence suggests these parasites are present in the local environment. These findings highlight the importance of monitoring protozoan infections in large carnivores as part of ecosystem health assessments, given their potential behavioural and ecological impacts.

Keywords: *Toxoplasma*, *Neospora*, grey wolf

PS – poster session

Session: P4 Parasites of terrestrial and aquatic environments in the context of parasite-host interactions

Distribution and molecular characterization of *Alaria alata* (Goeze, 1782) mesocercariae in wild boars (*Sus scrofa*), raccoon dogs (*Nyctereutes procyonoides*), and badgers (*Meles meles*) in Poland

Aneta Bełcik[1], Ewa Bilska-Zając[1], Weronika Korpysa-Dzirba[1], Aneta Gontarczyk[1], Ewelina Antolak[1], Martyna Chojecka[1], Małgorzata Samorek-Pieróg[1], Jacek Karamon[1], Tomasz Cencek[1]

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Abstract

Between 2018 and 2024, an extensive study was conducted to evaluate the occurrence of *Alaria alata* in selected wild mammals in Poland and to investigate the genetic diversity of this trematode species. Muscle and adipose tissue samples were collected from 2299 wild boars (in 2018 and 2023), as well as from 101 raccoon dogs and 58 badgers (in 2024). The animals came from 11 provinces in different regions of the country.

Detection of mesocercariae was performed using the *Alaria* mesocercariae migration technique (AMT) described by Riehn et al. (2013). Identification of parasites at the species level was based on the amplification and analysis of fragments of the *18S* rRNA and mitochondrial cytochrome c oxidase subunit I (*COI*) gene fragments. *Alaria alata* mesocercariae were detected in 6.8% of wild boars, 43.6% of raccoon dogs, and 36.2% of badgers. All isolates exhibited morphological features consistent with *A. alata*, and molecular analysis confirmed the species identity.

Sequencing of the *COI* gene revealed from 1 to 5 single nucleotide polymorphisms (SNPs), indicating significant genetic variability between the isolates.

These findings highlight the role of wild boars, raccoon dogs, and badgers as paratenic hosts of *A. alata*, and underscore their potential to act as a source of human infection through the consumption of raw or undercooked game meat. The molecular data generated in this study may support the development of national and EU-level guidelines regarding the handling and trade of carcasses infected with *Alaria* spp. mesocercariae.

Keywords: *Alaria alata*, mesocercariae, hosts, wild boars, raccoon dogs, badgers

PS – poster session

Session: P4 Parasites of terrestrial and aquatic environments in the context of parasite-host interactions

Trichinella infections in key predator species in Poland (2024–2025)

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Abstract

Wild carnivorous animals play a pivotal role in the life cycle of *Trichinella* spp. The objective of this study was to determine the prevalence of *Trichinella* spp. in populations of wild carnivores in Poland, based on laboratory examinations conducted between 2024 and 2025. The analysis encompassed key predator species, including the red fox (*Vulpes vulpes*, n=214), European badger (*Meles meles*, n=69), raccoon dog (*Nyctereutes procyonoides*, n=145), and raccoon (*Procyon lotor*, n=30). Muscle samples were collected from the tongue, diaphragm, and forelimb muscles. A 50 g portion of muscle tissue from each animal was tested using the artificial digestion method in accordance with PN-EN ISO 18743. Species identification of detected *Trichinella* larvae was performed using the multiplex PCR method (Zarlenga et al., 1999). The results revealed species- and region-dependent variation in prevalence, with the highest infection rates observed in red foxes (27.5%) and raccoon dogs (13%), underscoring their significant role in maintaining the sylvatic cycle of the parasite. *Trichinella britovi* was the predominant species identified, followed by *T. spiralis*. These findings confirm the importance of wild carnivores as a major reservoir of trichinellosis and highlight the necessity for ongoing epidemiological surveillance. Furthermore, the results emphasize the importance of removing carcasses of hunted carnivores from the environment to limit the spread of the disease and reduce the risk of transmission to domestic animals and humans.

Keywords: *Trichinella* spp., red fox, raccoon dogs, badger

PS – poster session

Session: P4 Parasites of terrestrial and aquatic environments in the context of parasite-host interactions

Molecular identification of nematodes in native carnivores based on faecal samples

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Abstract

In recent years, there has been an increased interest in the study of parasites of wild mammalian carnivores, particularly in the context of their potential zoonotic importance. The objective of the present study was to molecularly identify nematode species found in the European badger (*Meles meles*), the pine marten (*Martes martes*) and the stone marten (*Martes foina*). Faecal samples (n=126) were obtained as part of predator monitoring in the Ruszów Forest District (Puszcza Zgorzelecka, Bory Dolnośląskie), where conservation activities for endangered bird species are carried out. DNA was isolated from faecal samples and then amplified by PCR using a fragment of the *COI* mtDNA sequence. The reaction products were then subjected to electrophoresis and sequencing in order to identify the parasite species present. The analysis revealed the presence of nematode DNA in 62 out of the 126 samples that were tested (49.21%), with 58.14% of badgers and 44.58% of martens samples being positive. In badgers, *Strongyloides* sp. was predominant, as well as *Perostrongylus* sp. and *Molineus* sp. In martens, *Crenosoma* sp., *Skrjabingylus petrowi* and *Strongyloides* sp. were identified. The utilisation of the *COI* mtDNA marker facilitated precise species identification in the majority of the samples analysed, a particularly salient fact in the context of the diagnostic difficulties associated with the morphological identification of nematode eggs. The data obtained provide valuable information on the diversity of parasitic nematodes in native carnivores.

Keywords: carnivores, nematodes

PS – poster session

Session: P4 Parasites of terrestrial and aquatic environments in the context of parasite-host interactions

Parasitofauna of the red fox (*Vulpes vulpes*) from the Lublin province

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Abstract

The red fox (*Vulpes vulpes*), a common predator in Poland is widely distributed across the country. The species shows significant adaptability across various environments, including forests and fields but also urban areas. This migration toward human settlements raises the risk of numerous endoparasitosis, including zoonotic species. This study aims to assess the prevalence of endoparasites in red foxes within the Lublin province.

In 2024–2025, necropsies of 20 red foxes (9 females and 11 males) were performed. During the examination, the inspections of the lungs, liver, gallbladder and urinary bladder were conducted. The intestine was cut lengthwise and checked for the presence of adult parasites. The content of the intestine was collected and mucosa was removed. The obtained suspension of intestinal material was analyzed using flotation and sedimentation techniques.

Results indicated that all examined foxes (100%) were infected with parasites. The nematodes of the respiratory system *Crenosoma vulpis* and *Capillaria aerophila* were found in 18 (90%) individuals mostly as mixed invasions. The same prevalence was observed in case of tapeworms (*Echinococcus multilocularis , Taenia spp., Mesocestoides spp., Dipylidium caninum*). Among flukes the species *Alaria alata* and *Metorchis bilis* were recorded with a prevalence of 55%. The obtained intestinal nematode fauna included *Toxocara canis, Uncinaria stenocephala* and *Trichuris vulpis* presented prevalence of 65%. *Capillaria plica* was observed in 60% of animals. The most common parasite found in foxes was *Capillaria aerophila* (80%) and the least frequent was *Trichuris vulpis* (5%). This study highlights the diverse range of endoparasites present in foxes within the Lublin province, with a particular emphasis on the detection of parasites possessing a significant zoonotic risk.

Keywords: red fox (*Vulpes vulpes*), endoparasites

PS – poster session

Session: P4 Parasites of terrestrial and aquatic environments in the context of parasite-host interactions

Helminths and urbanization: analysis of helminth communities in the marsh frog (*Pelophylax ridibundus*) from three localities in Kyiv, Ukraine

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Abstract

The global decline in biodiversity affects the populations and communities of various living organisms. Amphibians are currently considered the most vulnerable class of vertebrates; nevertheless, they still inhabit diverse ecosystems, both natural and transformed. The latter fact allows the use of amphibians and their parasites as indicators of environmental stress. The present study aimed to investigate the helminth infection of marsh frogs in three urbanized localities with different levels of ecosystem disruption. In total, 77 marsh frogs were collected in Kyiv city (Ukraine): 24 from Lake Telbin (high level of urbanization), 33 from Lake Tyahle, and 20 from Olzhyn Island (moderate level of urbanization). Amphibians were humanely euthanized, helminths were collected manually, fixed with hot 70% ethanol, and identified by morphology.

Twenty helminth species were identified in collected frogs: 14 in Telbin, 15 in Tyahle, and 14 in Olzhyn Island. Six species were common in all three localities: nematode *Icosiella neglecta*, trematodes *Diplodiscus subclavatus*, *Opisthioglyphe ranae*, *Pleurogenoides medians*, *Pleurogenes claviger*, and *Prosotocus confusus*.

In helminth infracommunities, average abundance was the lowest in Telbin (57.5), higher in Tyahle (80.2), and the highest in Olhin Island (260.4). In component communities, the Shannon diversity was the highest in Telbin (1.59) compared to Tyahle (1.45) and Olzhyn Island (1.09). We conclude, therefore, that high-level disruption of ecosystems may result in increasing evenness in helminth communities due to the low abundance of all helminth populations. In moderately urbanized habitats, the evenness was lower due to quantitative predomination of some species (*O. ranae* and *Codonocephalus urniger* in Tyahle and Olzhyn Island).

The study was supported by the National Research Foundation of Ukraine (project 2023.03/0068).

Keywords: helminths, infracommunities, amphibians, marsh frog, ecosystem disruption, Ukraine

PS – poster session

Session: P4 Parasites of terrestrial and aquatic environments in the context of parasite-host interactions

Helminth diversity in the marsh frog (*Pelophylax ridibundus*) in Ukraine

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Abstract

In 2017–2024, we investigated the helminth infection of 345 marsh frogs, *Pelophylax ridibundus*, from 20 localities on the territory of Ukraine. The study aimed to update information on helminth infection of this Western-Palaearctic amphibian host in the central part of its distribution area. Based on morphological and molecular investigation of the collected material, 39 helminth species were identified, including 2 species of cestodes, 2 species of acanthocephalans, 10 species of nematodes, and 25 species of trematodes. *Acanthocephalus ranae*, *Codonocephalus urniger*, *Cosmocerca ornata*, *Diplodiscus subclavatus*, *Haematoloechus asper*, *H. variegatus*, *Icosiella neglecta*, *Opisthioglyphe ranae*, *Pleurogenes claviger*, *Pleurogenoides medians*, and *Prosotocus confusus* were the most widespread species occurring in 10 or more examined localities. Three species were first recorded in Ukraine: the cestode *Ophiotaenia saphena*, and the nematodes *Rhabdias esculentarum* and *Strongyloides spiralis*. The monogenean *Polystoma integerrimum*, the cestode *Nematotaenia dispar*, and mesocercariae of the trematode *Alaria alata* were absent in the studied material, although they were reported from frogs in Ukraine in some previous surveys.

Eight of the collected helminth species (most nematodes, excepting *I. neglecta*) are known as monoxenous parasites, while the other 31 have complex life cycles. Most found heteroxenous helminths (20 species) use amphibians as their definitive hosts, while 11 species were represented in frogs by larval stages. Their definitive hosts are mammals (*Spirometra erinaceieuropaei*), reptiles (*Encyclometra colubrimurorum*, *Paralepoderma cloacicola*, *Plesioastiotrema monticellii*, *Spiroxys contortus*), or birds (*Sphaerirostris picae*, *C. urniger*, *Neodiplostomum* sp., *Tylodelphys excavata*, *Strigea* sp., Echinostomatidae gen. sp.).

The study was partially supported by the National Research Foundation of Ukraine (project 2023.03/0068).

Keywords: helminths, amphibians, marsh frog, Ukraine

PS – poster session

Session: P4 Parasites of terrestrial and aquatic environments in the context of parasite-host interactions

European badgers from the Lubuskie region as reservoirs hosts of cryptosporidia

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Abstract

Cryptosporidium is a parasitic protozoan that infects the epithelial cells of the gastrointestinal tract in both humans and animals. The primary symptom of the disease it causes – cryptosporidiosis – is profuse, watery diarrhea, often accompanied by abdominal pain, vomiting, and weight loss. To date, 44 *Cryptosporidium* species have been described (with as many as 29 reported in mammals) and over 120 genotypes identified. However, most research conducted worldwide has focused on infections in humans and domestic animals, with far less attention given to wildlife.

The Lubusz Voivodeship, being the most forested region in Poland, has seen limited parasitological research concerning wild animals. To date, specific carnivorous species such as the European badger (*Meles meles*) have not been widely studied in this context. This study examined 70 fecal samples collected from European badgers in międzyrzecki district and tested them for the presence of *Cryptosporidium* spp. using nested PCR with primers targeting the actin gene. The parasite was detected in 6 individuals, representing an infection rate of 8.6%. Sequence analysis revealed the presence of the *Cryptosporidium* skunk genotype.

These findings suggest that carnivores may serve as reservoirs for protozoa with zoonotic potential. Notably, the skunk genotype has been implicated in human infections, and European badgers – especially in winter – are known to venture boldly into human settlements in search of food.

Keywords: *Cryptosporidium*, badger, reservoir, zoonotic

PS – poster session

Session: P4 Parasites of terrestrial and aquatic environments in the context of parasite-host interactions

Occurrence of lung nematodes from the genus *Dictyocaulus* in moose (*Alces alces*) in Poland: first record of *Dictyocaulus skrjabini* in this host species

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Abstract

Lung nematodes of the genus *Dictyocaulus* are parasitic helminths infecting various species of wild and domestic ungulates, affecting host health and population dynamics. Despite the growing interest in the parasitofauna of European moose (*Alces alces*), data on lungworm infections in this species remain scarce. The aim of the present study was to identify *Dictyocaulus* nematodes isolated from moose in Poland.

Lungs were collected during field dissections of 38 moose killed in road accidents or found dead in the years 2017 – 2025 in Poland. Samples of the lungs were preserved in 10% formalin for histopathological analysis. The trachea, bronchi, and bronchioles were cut open during parasitological examination. Nematodes were isolated from the lumen of the respiratory tract, preserved in 70% ethanol, and identified by amplification of partial SSU, *cox1* and *cytB*.

Nematodes of the genus *Dictyocaulus* were detected in five moose (13.2%). Molecular identification revealed the presence of species *D. cervi* in four animals from West Polesie and Biebrza valley, and *D. skrjabini* in one individual, living in captivity in the Rehabilitation Center in northeastern Poland. While *D. cervi* has previously been reported in cervids, including moose in Poland, this study provides the first confirmed identification of newly described *D. skrjabini* in this wild ruminant species worldwide. Histopathological examination of the lungs revealed the presence of numerous nematode larvae in the lumen of the alveoli surrounded by massive inflammatory infiltrates (from mononuclear to mixed, depending on the case) containing numerous multinucleated giant cells.

Our study contributes to the available knowledge about parasitic infections in moose in Poland. Detection of the newly described species *D. skrjabini* in moose highlights the need for further research on the cross-species transmission of lungworms, their epidemiology and pathogenicity as well as potential health risk to wild ruminants populations.

Keywords: lung nematodes, *Alces alces*, histopathology

PS – poster session

Session: P4 Parasites of terrestrial and aquatic environments in the context of parasite-host interactions

Ixodid ticks on migratory birds: evidence from Hel, Każa, and Bukowo near Sławno

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Abstract

Migratory birds play an important role in long-distance dispersal of ticks and tick-borne pathogens. Due to climate change and shifting endemic areas, this role is growing. Ticks were collected during bird ringing in April–May 2025 at 3 coastal stations: Hel (54°36′42″N 18°48′29″E), Każa (54°44′55″N 18°31′12″E) at Hel Peninsula; and Bukowo near Sławno (54°20′33″N 16°15′12″E). Ticks were preserved in 75% ethanol and identified microscopically (Siuda 1993, Filippova 1977).

Of 78 birds examined, 61 (78.2%) were infested. *Ixodes ricinus* was dominant; *I. frontalis* was also found.

Infestation by host species

Curruca communis (Hel): 50% (n=2), *I. ricinus*,
Turdus iliacus (Hel): 100% (n=6), *I. ricinus* (larvae, nymphs); (Bukowo): 50% (n=2), *I. frontalis* (female)
Sylvia borin (Bukowo): 50% (n=2), *I. ricinus* (nymphs)
Sylvia atricapilla (Bukowo): 50% (n=2), *I. ricinus* (nymphs)
Turdus merula (Bukowo): 50% (n=6), *I. ricinus* (nymphs), (Hel): 100% (n=8), *I. ricinus* (nymphs, females); (Każa): 1 bird, *I. ricinus* (nymphs)
Sitta europaea (Bukowo): 50% (n=2), *I. frontalis* (nymphs)
Erithacus rubecula (Hel): 100% (n=16), *I. ricinus* (larvae, nymphs); (Bukowo): 66.6% (n=6), *I. ricinus* (nymphs); (Każa): not infested
Turdus philomelos (Hel): 80% (n=5), *I. ricinus* (nymphs); (Każa): 100% (n=2), *I. ricinus* (nymphs)
Acrocephalus palustris (Bukowo): 33.3% (n=3), *I. ricinus* (nymphs)
Acrocephalus scirpaceus (Bukowo): 50% (n=2), *I. ricinus* (nymphs)
Phylloscopus trochilus (Bukowo): 1 infested, *I. ricinus* (nymph); (Każa): 1 not infested
Prunella modularis (Hel): 1 infested, *I. ricinus* (nymph)
Luscinia luscinia (Każa): 1 infested, *I. ricinus* (nymphs)
Troglodytes troglodytes (Hel): 100% (n=3), *I. ricinus* (nymphs)
Anthus trivialis (Hel): 1 infested, *I. ricinus* (nymph)
Fringilla coelebs (Hel): 1 infested, *I. ricinus* (nymph)
Asio otus (Hel): 1 bird not infested

These results confirm *I. ricinus* dominance on migratory birds and presence of *I. frontalis* in Sławno County.

Keywords: migratory birds, ticks, *Ixodes ricinus*, *Ixodes frontalis*

PS – poster session

Session: P4 Parasites of terrestrial and aquatic environments in the context of parasite-host interactions

Ectoparasite infestation of wild birds in Central Poland

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Abstract

A total of 22 bird species were examined for ectoparasites. The most common were ticks (*Ixodes*) and chewing lice (Phthiraptera: Amblycera, Ischnocera; formerly *Mallophaga*).

Ticks:

Ixodes ricinus (F, N, L stages) was found in: *Parus major*, *Actitis hypoleucos*, *Curruca communis*, *Turdus philomelos*, *Sylvia atricapilla*, *Turdus merula*, *Sitta europaea*, *Acrocephalus palustris*, *Certhia brachydactyla*, *Phylloscopus trochilus*, *P. collybita*, *Prunella modularis*, and *Erithacus rubecula* (20%). *Ixodes lividus* was found in *Riparia riparia* (75%).

Chewing lice:

Actornitophilus trilobatus was found in *Calidris minuta* and *Chlidonias niger* (100%), *A. flumineus* in *Actitis hypoleucos* (33.3%), *Myrsidea latifrons* and *Hirundiniella domestica* in *Riparia riparia* (25% each), *Seamundssonia sternae sternae* in *Sterna hirundo* (100%), *S. s. albifrons* (66.6%), and *Koeniginirmus punctatus* (33.3%) in *Sternula albifrons*.

Other ectoparasites:

Delichon urbicum hosted the bedbug *Oeciacus hirundinis*. An unidentified chewing louse (100%) was found in *Chroccocephalus ridibundus*.

Birds without lice infestation:

No lice were found in: *Parus major*, *Curruca communis*, *Turdus philomelos*, *Sylvia atricapilla*, *Turdus merula*, *Sitta europaea*, *Acrocephalus palustris*, *Certhia brachydactyla*, *Phylloscopus trochilus*, *P. collybita*, *Prunella modularis*, and *Erithacus rubecula*.

Conclusion:

The most common parasite was *I. ricinus*, especially in passerines. Chewing lice, particularly *Actornitophilus* and *Seamundssonia*, dominated in aquatic and shoreline species. In many cases, infestation prevalence reached 100%.

Keywords: birds, ticks, chewing lice

PS – poster session

Session: P4 Parasites of terrestrial and aquatic environments in the context of parasite-host interactions

Assessment of *Pulex irritans* occurrence in European badger burrows and its potential epidemiological implications

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Abstract
Fleas (Insecta: Siphonaptera) are important hematophagous ectoparasites of mammals and birds with worldwide distribution. The European badger (*Meles meles*) is a widespread mammal in most European countries with an increasingly recognized epidemiological significance due to its preferred habitats. The epidemiological role of badgers is supported by their susceptibility to infections with viruses, bacteria, and internal and external parasites of great veterinary and medical importance. *Meles meles* is susceptible to infection with, e.g., rabies virus, *Mycobacterium bovis*, which causes bovine tuberculosis and can also serve as a host for arthropod vectors including *Pulex irritans* (human flea). The study aimed to assess the occurrence of *P. irritans* in badger burrows and its potential role in the circulation of selected vector-borne pathogens. The material was collected from ten *M. meles* burrows. DNA from individual specimens was extracted using a silica-based spin column according to the manufacturer's protocol. PCR and nested PCR methods were used to detect selected genes of the studied pathogens. *Borrelia burgdorferi* sensu lato, and *Anaplasma phagocytophilum* were detected in the tested material using two pairs of primers specific for the *flaB* and *16S* rRNA genes, respectively. In turn, for the detection of *Bartonella* spp., *Rickettsia* spp., and *Babesia* spp., specific primers for the *rpoB* and *gltA* and *18S* rRNA genes were used, respectively. In total, the tested material showed the presence of four *P. irritans* males in 3/10 (30%) of the tested burrows. Molecular tests confirmed the presence of *Rickettsia* spp. DNA in all collected fleas (4/4) 100%. No *B. burgdorferi* s.l., *A. phagocytophilum*, *Bartonella* spp., and *Babesia* spp. were detected in the tested material. The demonstration of *Rickettsia* spp. in the tested specimens of human flea confirms that they may be vectors of these pathogens in the study area and participate in their circulation in natural foci.

Keywords: European badger, *Pulex irritans*, *Rickettsia* spp.

PS – poster session

Session: P4 Parasites of terrestrial and aquatic environments in the context of parasite-host interactions

Prevalence of intestinal parasites in urban dog parks: a comparative study of fecal and soil contamination in Wrocław and Kraków, Poland

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Abstract
Urban dog parks are increasingly popular spaces that promote socialization and physical activity for companion animals in city environments. However, these areas may also serve as reservoirs for zoonotic infections.

This study aimed to evaluate the diversity and prevalence of intestinal parasites in dog feces and assess the level of soil contamination with geohelminth eggs in selected urban dog parks. A total of 330 samples, 165 fecal and 165 soil samples, were collected during spring and autumn of 2019 from seven dog parks in two Polish cities: Wrocław (4 parks) and Kraków (3 parks). Parasite eggs were detected using a modified flotation method with Fülleborn's solution enriched with sucrose.

In total, eight parasite taxa were identified, including eight in Wrocław and two in Kraków. The overall prevalence in fecal samples was 23%, with a total of 384 helminth eggs and 108 coccidian oocysts detected. The most common taxa were Ancylostomatidae (12.7%), followed by *Trichuris vulpis* (4.2%), *Toxascaris leonina* (2.4%), *Toxocara* spp. (1.8%), Taeniidae (1.8%), and coccidia (1.2%). Statistical analysis showed no significant differences between Wrocław and Kraków in either the prevalence of parasite infections (24% vs. 20%) or the average number of eggs and oocysts per sample (14 vs. 11). In soil samples, overall prevalence was 17%. The most common taxa were Ancylostomatidae (9.7%), followed by *T. vulpis* (3.6%), *Toxocara* spp. (1.8%), *Capillaria* spp. (1.2%), *Ascaridia galli*, and *T. leonina* (0.6%). All positive soil samples originated from Wrocław, with a total of 39 helminth eggs identified.

These findings suggest that urban dog parks can facilitate environmental transmission of intestinal parasites. To reduce infection risks for both animals and humans, it is recommended to implement improved hygiene practices, including regular deworming programs for dogs, as well as systematic disinfection or replacement of the substrate in dog parks.

Keywords: geohelminths, roundworm, urban dog parks, public health

PS – poster session

Session: P4 Parasites of terrestrial and aquatic environments in the context of parasite-host interactions

Hoplopleura malabarica (Phthiraptera, Anoplura) – first comprehensive description of nymphal stages

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Abstract
Many species within the Anoplura remain without detailed descriptions of their nymphal stages, which significantly making it extremely difficult to analyze infestation levels, parasite topography on the host, or host specificity. To thoroughly understand lice parasitism and reliably characterize host–parasite relationships, it is essential to identify and describe the immature stages. *Hoplopleura malabarica*, an oligoxenous parasite restricted to rodents of the genus *Bandicota*, such as *B. bengalensis*, *B. savilei*, and *B. indica*, represents an intriguing subject for research of this kind. The lice material included 29 specimens of *H. malabarica* collected from five of the 12 examined specimens of *B. indica* (Southeast Asia, Lao PDR).

The first-instar nymphs of *Hoplopleura malabarica* can be morphologically differentiated from other species reported in the Indomalayan realm. *H. malabarica* lacks major abdominal setae (MAS) whereas on *H. captiosa*, *H. diaphora*, *H. dissicula*, *H. kitti*, *H. pacifica*, *H. pectinata*, and *H. sicata* it is present. The third-instar nymphs of *H. malabarica* do not have tergal plaques, which are present on *H. pacifica*, *H. pectinata*, *H. sicata*, and *H. rajah*. The same applies to second-instar nymphs of *H. dissicula* and *H. sicata*. Moreover, MAS are present on all nymphs of *H. diaphora* but are absent in *H. malabarica*. Second-instar and third-instar nymphs of *H. malabarica* lack of anal setae (AnS) and some dorso-central abdominal setae (DCAS), which are present in *H. kitti*. Second-instar *H. pacifica* also have AnS. No descriptions of *H. malaysiana* nymphs are available.

Based on our findings and a review of the literature, *Hoplopleura malabarica* emerges as a highly host-specific parasite, recorded exclusively in rodents of the genus *Bandicota*. It is likely monoxenous, restricted to this genus, which comprises only three recognized species globally.

Keywords: nymphal stages, *Hoplopleura*, Indomalayan realm

PS – poster session

Session: P4 Parasites of terrestrial and aquatic environments in the context of parasite-host interactions

Insights into microbiota-parasite dynamics in wild populations of *Myodes glareolus* (bank voles)

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Abstract

Despite increasing interest in microbiome research, investigations in natural wildlife settings remain limited compared to extensive studies in laboratory animals. Controlled experiments provide valuable insights into host–microbiota interactions, but they often fail to replicate the dynamic and multifactorial nature of wild ecosystems. In natural environments, gut helminths and microbial communities coexist and influence one another due to shared ecological niches. Helminth infections can significantly modulate gut environments by affecting mucus production, immune responses, and epithelial integrity, thereby potentially shaping microbial communities. In this study, we focused on wild bank voles to explore how host-related traits (e.g., sex, age, reproductive condition) and environmental variables (e.g., sampling year, geographic site) affect gut microbiota composition and its relationship with parasitic infections. Bank voles were sampled in years 2018 and 2022 in northeastern Poland. Following dissection, the intestinal tract was examined for helminths, and fecal material was collected for microbiome analysis. Using Oxford Nanopore sequencing of full-length *16S* rRNA genes, we profiled the gut bacterial communities of a total of 329 rodents and analyzed their associations with host-intrinsic and environmental factors, as well as the presence of intestinal parasites.

Keywords: microbiome, intestines, wildlife, wild rodents, helminths

PS – poster session

Session: P4 Parasites of terrestrial and aquatic environments in the context of parasite-host interactions

Gastrointestinal parasites and factors affecting *Strongylidae* and *Parascaris* spp. egg shedding in domestic horses: experience from Eastern Slovakia

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Abstract

Strongylids and parascarids are the most widespread horse parasites worldwide. In Slovakia, despite the importance of these parasites, up-to-date information on their prevalence and infection levels remains limited. Our study aimed to examine the prevalence and horse infection levels with the main gastrointestinal parasites in Eastern Slovakia. Simultaneously, information on horse management and parasite control methods practiced on farms was analyzed to assess the main factors impacting the horse infection.

A total of 392 horses from 3 months to 33 years old kept under various management conditions in 24 horse farms in Eastern Slovakia were examined. The coprological McMaster technique (sensitivity of 50 eggs per gram of feces, EPG) and the double centrifugation/combined sedimentation-flotation technique were used. Several risk factors (age, breed, horse use, management, deworming frequency, etc.) were estimated using the Kruskal-Wallis H test.

Strongylids were found in 257 horses (65.6%) in all 24 (100%) farms examined. The level of horse infection varied from 50 to 2800 EPG. In total, 55.6% of the horses had zero or low (<200 EPG) levels of strongylid infection; 44.4% of horses had medium/high levels of infection that required deworming. The fecal egg counts for strongylids were overdispersed, with 29.8% of horses shedding 80% of the total egg output. *Parascaris* spp. and *Anoplocephala* eggs were detected in 4.5% and 0.3% of horses, respectively. For Strongylids, five factors: age, horse use, stocking density, pasture management, and horse deworming frequency, were significantly associated with EPG value. For *Parascaris* spp., only horse age and sex were significantly associated with EPG value. No significant differences in the prevalence or EPG value were observed for other factors.

The study was supported by the EU NextGenerationEU through the Recovery and Resilience Plan for Slovakia, projects 09I03-03-V01-00015, 09I03-03-V01-00046, and VEGA grant 2/0090/22.

Keywords: parasites, horses, *Strongylidae*, *Parascaris*, risk factor analysis, Slovakia

PS – poster session

Session: P4 Parasites of terrestrial and aquatic environments in the context of parasite-host interactions

Occurrence and diversity of Filarioidea nematodes in mosquitoes from central-eastern Ukraine

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Abstract

Over 70 mosquito species (Culicidae) transmit pathogenic Filarioidea nematodes (filariae), including *Dirofilaria immitis*, *D. repens*, and *Setaria tundra*. In Europe, 18 haplotypes of *D. repens* and 9 of *D. immitis* have been identified. Despite increasing dirofilariasis and setariosis cases and vector migration, data from Ukraine remain limited. This study aimed to assess the prevalence and genetic diversity of filariae in mosquitoes from central-eastern Ukraine.

In 2023–2024, 686 female mosquitoes were collected from six locations in Kharkiv, Sumy, and Poltava regions (urban, rural, reserves, landscape parks). The *12S* rRNA mtDNA marker was used for nematode identification. *Dirofilaria* haplotypes were determined based on *COI* and *ND1* gene sequences. Mosquito species were identified using *COI* sequences.

Nematodes were detected in 29 mosquitoes (4.22%): *D. immitis* (1.45%; 10/686), *D. repens* (0.3%; 2/686), and *S. tundra* (2.47%; 17/686). *D. immitis* isolates belonged to haplotype Di1, *D. repens* to haplotype DR1. Nine *D. immitis* and one *D. repens* were found in *Aedes vexans*, and one *D. immitis* and one *D. repens* in *Ochlerotatus cantans*. *S. tundra* was detected in *Ae. vexans* (4), *Anopheles hyrcanus* (4), *Coquillettidia richiardii* (1), *O. cantans* (4), *O. annulipes* (1), *O. cataphylla* (1), *O. leucomelas* (1), *O. punctor* (1). *Dirofilaria* spp. were found only in rural areas, *S. tundra* also in reserves and parks. Frequent detection of *Dirofilaria* in *Ae. vexans* suggests its role as the main vector. *Ochlerotatus*, *Anopheles*, and *Coquillettidia* species may also act as filaria vectors of veterinary and epidemiological importance. Dominance of Di1 and DR1 haplotypes suggests established transmission, consistent with dominant European haplotypes. The absence of nematodes in cities may result from

environmental conditions and veterinary care. Further monitoring and prevention targeting mosquitoes and hosts are necessary.

Keywords: Culicidae, *Dirofilaria immitis*, *Dirofilaria repens*, *Setaria tundra*, genotyping

PS – poster session

Session: P4 Parasites of terrestrial and aquatic environments in the context of parasite-host interactions

Molecular identification of Eimeriidae protozoans occurring in wild carnivores

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Abstract

Protozoans of the family Eimeriidae are widespread gastrointestinal parasites of vertebrates with significant medical, veterinary, and economic importance. Within carnivorous mammals the red fox is one of the most widespread predators, adapting to diverse habitats, including anthropogenic environments. The racoon dog and the racoon are invasive species with rapidly expanding and ecologically plastic populations in Poland. Among mustelids, the European badger and the European pine marten typically avoid human settlements, in contrast to the beech marten, which frequently utilizes human-impacted areas. The knowledge regarding their occurrence in wild carnivores remains fragmentary. Molecular techniques have further revealed that host specificity may be lower than previously assumed.

The aim of this research is the molecular identification of coccidia of the family Eimeriidae occurring in wild carnivores and the assessment of their taxonomic diversity. A total of 519 fecal samples from six carnivore species inhabiting Poland, the Czech Republic and Germany were examined using nested-PCR based on molecular markers *18S* rRNA and *COI*. Selected positive samples were subjected to sequencing. The overall prevalence of Eimeriidae in wild carnivores was 64%. Infection intensity was the highest in raccoons and European badgers (80.1% and 79.7%, respectively), followed by raccoon dogs (59.6%) and red foxes (48%), with the lowest prevalence observed in beech marten (27.6%) and pine marten (25.9%). Sequencing of selected positive samples confirmed the presence of a broad spectrum of Eimeriidae species, showing homology ranging from 92.68% to 100%. These findings suggest the possibility of interspecies and environmental transmission, as well as the reservoir potential of wild carnivores as hosts of Eimeriidae coccidia. Nevertheless, further studies are needed to expand this knowledge.

Keywords: Eimeriidae, coccidia, wild carnivores, prevalence, molecular identification

PS – poster session

Session: P4 Parasites of terrestrial and aquatic environments in the context of parasite-host interactions

The role of red foxes (*Vulpes vulpes*) from the Lublin Voivodeship as transport hosts of ticks

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Abstract

Ticks are commonly occurring blood-sucking ectoparasites of many species of mammals, birds, and reptiles. By transmitting numerous pathogens, they pose a threat to the health of both animals and humans. Tick infestations go beyond vector-borne transmission of pathogens. The disruption of skin integrity caused by the tick's mouthparts, along with the inflammation induced by various compounds found in tick saliva, leads to tissue damage. In some animal species, such as red foxes , raccoon dogs , and domestic dogs, ticks have been found in the subcutaneous tissue. Due to the increasing population of foxes in Europe and their adaptation to urban environments, there is a growing need for a more detailed investigation of the role of these animals as sources of pathogens and parasites relevant to both veterinary and human medicine.

The aim of our study was to assess the frequency and species diversity of ticks located on the host's skin and in the subcutaneous tissue of red foxes originating from the Lublin Voivodeship. During the period 2024–2025, 20 adult red foxes were examined for the presence of ticks on the skin and in the subcutaneous tissue. Preliminary identification of tick species was conducted based on morphological features. Ticks were identified on the skin of 16 out of the 20 examined foxes (80%), with a mean intensity of 17 ticks per individual. Ticks located within the subcutaneous tissue were found in 10 out of 20 individuals (50%). Most affected foxes presented with 1 to 8 nodules, although up to 48 nodules were observed in a single case. Based on morphological characteristics, the following tick species were identified among the external specimens: *Ixodes ricinus*, *I. hexagonus*, *I.crenulatus*, and *Dermacentor reticulatus*. Within the subcutaneous tissue, *I. ricinus*, *I. hexagonus*, and *D. reticulatus* were identified. All subcutaneously located ticks were partially engorged adults. No evidence of cutaneous penetration was observed.

Keywords: tick, red fox

PS – poster session

Session: P4 Parasites of terrestrial and aquatic environments in the context of parasite-host interactions

Eubothrium crassum (Cestoda: Triaenophoridae) – a typical and dominant parasite of the sea trout *Salmo trutta*

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Abstract

Sea trout, the migratory form of brown trout *Salmo trutta* (Teleostei: Salmonidae), are of considerable economic importance to both recreational and commercial coastal fisheries in the southern Baltic Sea and its tributaries. Consequently, parasitological monitoring is necessary to assess the health status of these fish and to determine their role in the transmission and maintenance of parasites in the aquatic environment. *Eubothrium crassum* (Cestoda: Triaenophoridae) is widely distributed across Europe and North America, and its typical life cycle usually involves two intermediate hosts – a copepod and a fish, typically European perch *Perca fluviatilis* – and a definitive host, typically a salmonid such as trout. However, there are indications that, in marine conditions, this cycle may occur with only one intermediate host (a copepod). This study examined 95 specimens collected between January 2003 and January 2020. Of these, 65 and 30 were collected from brackish and freshwater environments – the Gulf of Gdańsk and the River Reda, respectively. The most prevalent parasite species in all the fish, regardless of location or time of capture, was *E. crassum*. In total, 92.6% of the fish were carriers of *E. crassum* (a total of 3,345), with a mean intensity of 38.0 and a range of 1–125 tapeworms per fish. This species is characterised by its location in the definitive host, being associated with the intestine and pyloric caeca. In the present study, the vast majority (98%) of tapeworms

were found attached to the walls of the pyloric caeca the number of which determine the occurrence of tapeworms. Additionally, longer and heavier hosts tended to carry greater numbers of tapeworms. Despite the high infection rate, Fulton's condition factor analysis showed no significant effect of parasitism on the condition of the examined fish.

Keywords: *Eubothrium crassum*, sea trout, host-parasite relationships, Baltic Sea

PS – poster session

Session: P4 Parasites of terrestrial and aquatic environments in the context of parasite-host interactions

Molecular and phylogenetic identification of cestodes from rodents in the Mazury Lake District region of Poland

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Abstract

Rodents serve as important hosts for many species of parasites, including cestodes, but the taxonomy of rodent-infecting tapeworms, especially in Europe, is still understudied. The current study aimed to identify larval and adult cestodes in free-living rodents from Northeastern Poland, focusing on the *Paranoplocephala* complex in bank voles and the catenotaeniid genera *Catenotaenia* and *Skrjabinotaenia*.

The fieldwork was conducted between 2014 and 2023 in three forest sites. Cestodes were collected from four rodent species, identified through morphology and by several genetic markers (*12S* rDNA, *cox1*, *nad1*, *28S* rDNA, *12S-16S* rDNA). Phylogenetic analyses were carried out to identify the species involved.

A total of 58 cestode specimens were analyzed. Species identified included *Catenotaenia henttoneni, Skrjabinotaenia cf. lobata C, Mesocestoides litteratus, Mesocestoides melesi*, and others. Three *Paranoplocephala* specimens were identified as *P. kalelai* based on *nad1* sequences. The prevalence of parasites among the analysed specimens was greater in bank voles, with morphological and genetic analyses indicating the dominant adult stage was *C. henttoneni* and *Mesocestoide*s spp. the dominant larval stage.

This study combined genetic and morphological methods to identify the cestodes infecting rodents in Poland. It confirmed the existence of *P. kalela*i in Poland, suggesting that previously reported *Paranoplocephala* spp., identified by morphological characters, may have corresponded to this molecularly identified species. Our study also highlighted gaps in genetic databases that currently still do not allow precise species identification.

Keywords: *Paranoplocephala*, *Catenotaenia*, *Skrjabinotaenia*, *Mesocestoides*, morphological identification, phylogenetic analysis

PS – poster session

Session: P4 Parasites of terrestrial and aquatic environments in the context of parasite-host interactions

A comparative study of PCR methods targeting *Eucoleus aerophilus* – preliminary findings

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Abstract

Respiratory capillariosis, caused by *E. aerophilus*, poses a significant health risk to wild and domestic animals and, potentially, humans. The parasite exhibits a broad host range among wild animals, but the red fox is recognized as the main reservoir and transmitter (average prevalence of 43% in faecal samples). Most data regarding the occurrence of *E. aerophilus* come from studies on foxes. Despite the global availability of research on this parasite, knowledge of its epidemiology and genetic diversity remains fragmented and incomplete. The prevalence of this parasite differs according to host species, region, size of host population and what is more use of different detection methods, such as microscopic or polymerase chain reaction (PCR) methods, which differ in sensitivity and specificity. This study aimed to compare the effectiveness of two PCR-based diagnostic methods for detecting *E. aerophilus* in fecal samples from naturally infected red foxes. Specifically, we evaluated the performance of a newly designed real-time PCR assay against the conventional PCR. The investigation was conducted using 49 fecal samples collected from red foxes in the Podkarpackie Province, Poland. The samples underwent analysis using three diagnostic methods: microscopic examination (flotation), conventional PCR, and the newly developed real-time PCR. The results highlighted the advantages of the newly designed real-time PCR, which demonstrated greater sensitivity and specificity compared to the conventional PCR. The detection rate of *E. aerophilus* was 59% with conventional PCR and 78% with real-time PCR. The difference was even more pronounced when diluted DNA samples (1/10) were tested, further underscoring the efficacy of the real-time PCR method. Our preliminary research gave promising results. Newly designed qPCR showed better effectiveness in detection of *E. aerophilus* in comparison to conventional one. Nevertheless, it still requires further studies to optimize the procedure.

Keywords: *Eucoleus aerophilus*, capillariosis, PCR, real-time PCR

PS – poster session

Session: P4 Parasites of terrestrial and aquatic environments in the context of parasite-host interactions

The occurrence of *Toxoplasma gondii* in free-living birds and carnivores in selected regions of Poland

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Abstract

Free-living birds and carnivores are commonly considered important vectors of the *Toxoplasma gondii* parasite in the sylvatic

environment, however in Poland there is insufficient data. The aim of the study was to assess the occurrence of *T. gondii* infection in free-living carnivores and birds based on the detection of parasite DNA in their tissues.

Tissues samples from 50 free-living carnivores (36 raccoon dogs, 6 Eurasian lynxes, 8 European wildcats) and 50 wild birds (5 buzzards, 6 swans, 4 terns, 5 pigeons, 2 hawks, 28 storks) from selected locations in Poland (Zachodniopomorskie, Wielkopolskie, Podlaskie, Mazowieckie, Podkarpackie and Warmińsko-Mazurskie regions) were tested for the presence of *T. gondii* DNA using nested and Real-time PCR (B1 gene).

Overall, positive PCR results for the presence of *T. gondii* DNA were found in 20 animals (20%), including: 14 carnivores (28%) and 6 wild birds (12%). Among carnivores, positive results were found in 19.4% of raccoon dogs, 62.5% of wildcats, 33.3% of lynxes. Among birds, positive results were found in 40% of buzzards, 25% of terns, 1 of 2 hawks tested and 3.6% of storks. No positive results were found among the swans and pigeons. No statistically significant differences in prevalence were found depending on the geographical region.

The percentages of positive results obtained in the present study in wild carnivores (28%) and birds (12%) indicate a significant rate of *T. gondii* infection and the need for further monitoring in other region of Poland.

Keywords: *Toxoplasma gondii*, free-living birds, carnivores, PCR

PS – poster session

Session: P4 Parasites of terrestrial and aquatic environments in the context of parasite-host interactions

Dynamics of *Strongylus* spp. nematode infections in horses in the spring season

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Abstract

Monitoring parasitic infections is an important aspect of equine health management. *In vivo* identification of parasitic infections, particularly strongyles at the genus or species level, remains a significant diagnostic challenge. This is primarily due to the morphological similarity of nematodes eggs belonging to the family Strongylidae. Accurate species identification requires either larval culture or post-mortem examination.

Previous studies indicate that small strongyles of the subfamily Cyathostominae dominate among equine intestinal nematodes. In contrast, large strongyles (Strongylinae), particularly *Strongylus* spp., exhibit low prevalence. A prior study conducted in 2002, based on parasitology necropsy, reported a *Strongylus* spp. prevalence of 60%. Follow-up research on a larger population showed a reduced prevalence of 26.5%.

The objective of the present study was to determine the current prevalence and infection intensity of *Strongylus* spp. in horses during the spring season (March–May 2025), with particular attention to age and sex-related variation.

Large intestines were collected from 251 slaughtered horses. The examinations were conducted monthly from March to May 2025. The nematodes isolated from the intestine were differentiated on the basis of detailed anatomical structure. The number of strongyles belonging to the genus Strongylus was evaluated.

The Strongylidae were found in 2.39% of the examined horses. Prevalence rates ranged from 1.56% in April to 4.44% in early March. Among the *Strongylus* species, only *Strongylus vulgaris* was detected. *S. edentatus* and *S. equinus* were not identified in the examined population. Infection intensity was low, with worm burdens ranging from 3 to 9 individuals. Infections were confined to female horses (mares), predominantly those aged 11 to 18 years. These findings indicate a low prevalence of large strongyles, limited to *S. vulgaris.*

Keywords: horses, parasites, *Strongylus* spp., prevalence

PS – poster session

Session: P4 Parasites of terrestrial and aquatic environments in the context of parasite-host interactions

Genetic structuring in the equine ascarids from Poland, Slovakia, Ukraine and Hungary, with *Parascaris univalens* being the only recorded species in the region

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Abstract

Equine ascarids *Parascaris* spp. are of major veterinary importance, and considered the most pathogenic parasites for foals and yearlings worldwide. Traditionally, equine roundworms were referred to as *Parascaris equorum* (with two pairs of chromosomes) due to the prevailing concept of different variants of *P. equorum* during the last century (Lin, 1954). *P. univalens* (with one pair of chromosomes) has received only limited attention, although since the 1990s it has been the only species in Europe and North America confirmed by karyotyping.

The study was designed to analyze the genetic structuring in *Parascaris* in a sample set of 67 specimens collected from horses in 15 geographical locations of central/eastern Europe by sequence analysis of cytochrome c oxidase subunit 1 *(cox1)*, small subunit rRNA (*12S* rRNA) and the internal transcribed spacer 1 (ITS1).

Sequence patterns detected in three genes in roundworms from Poland, Ukraine, Slovakia and Hungary matched the profiles of isolates previously karyotyped as *P. univalens* in the U.S.A. and Poland (Nielsen et al., 2014; von Samson-Himmelstjerna et al., 2021). Among the populations defined by country, genetic distance (d) was highest in Ukrainian samples (0.0450), followed by Hungary (0.0034), Slovakia (0.0017) and Poland (0.0014). The nucleotide diversity index (π) was highest in Hungarian ascarids (0.0034), followed by Slovakia (0.0017), Poland (0.0015) and Ukraine (0.0013). The lowest genetic distance between countries was between Poland and Slovakia (0.0015), the highest between Ukraine and Slovakia (0.0234). The low genetic differentiation between *P. univalens* from Slovakia, Poland and Hungary compared to Ukraine was due to higher gene flow between populations, resulting from extensive horse trade and geographical proximity.

The study was supported by the EU NextGenerationEU through the Recovery and Resilience Plan for Slovakia, project No. 09I03–03-V01–00015 and partially by the VEGA 2/0157/22.

Keywords: *Parascaris*, horses, genotype, central-eastern Europe

PS – poster session

Discussion panel

Session: Discussion panel

Where to publish a parasitological paper? A critical analysis of the ministerial ranking list

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Abstract

The implementation of "*ustawa 2.0*" introduced new publication priorities that have led to inconsistent and often counterproductive publication strategies. Rather than encouraging scientists to publish their best work in top journals within their field, the manually curated Ministerial Journal Ranking System (MJRS) has imposed arbitrary criteria that disregard scientific merit and expert recommendations. As a result, many respected journals have been marginalized, while some local or obscure periodicals have been awarded disproportionately high point values. The system also favors opportunistic mega-publishers with broad, unfocused scopes, further undermining field-specific periodicals. The steep stratification of point values and intense institutional competition have rendered many subject-specific journals practically obsolete. Moreover, the restrictive "slot system" discourages basic research, risking a future in which foundational knowledge is lacking—jeopardizing progress in applied, interdisciplinary, and theoretical domains. We argue that "*ustawa 2.0"* is fundamentally flawed and in need of replacement or substantial reform. While a parametric system is necessary for equitable fund distribution, the current point-chasing frenzy ("punktoza") is deeply damaging. The latest *Journal Citation Reports* (JCR), listed 47 journals within the category *Parasitology*. Our comparative analysis of these JCR-listed journals with the MJRS revealed significant discrepancies. Among the 11 highest-ranked Q1 journals, only one received the top 200-point score from MJRS. Most Q2 journals were undervalued at 70 points, and many Q3 journals scored only 20–40 points. Paradoxically, a number of journals from other disciplines and with no impact factor received 100 or even 140 points. We will critically analyze these inconsistencies and offer recommendations. Following feedback from the Polish Parasitological Society, we will submit a formal proposal to the Ministry.

Cofinanced by the Minister of Science (Poland) under the "Regional Excellence Initiative" Program for 2024-2027 (RID/SP/0045/2024/01).

Keywords: bibliometry, journal, point-chasing frenzy, JCR, publishing ethics

OS – oral session

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Bio-Rad Polska

New developments in fluorescent protein imaging and digital PCR in clinical diagnostics

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Abstract

The term “*digital PCR*” was first used in a paper by Kinzler and Vogelstein in 1999 and was an expansion upon the earlier described “limiting dilution PCR”, published in 1988 by Saiki et al. [1]. Being overshadowed by RT-qPCR for well over a decade, it has recently re-entered mainstream use, with the advent of more affordable and easier techniques. The advantages of digital PCR include but are not limited to absolute quantification without the need for calibration curve, ability to multiplex up to 21 targets per well (utilizing multi-color detection and amplitude multiplexing), relative (as compared to RT-qPCR) resistance to PCR inhibitors (especially useful in wastewater, food and environmental samples) and more. To date, almost all the dPCR research carried out in the field of eukaryotic parasites have used Bio-Rad’s ddPCR platform [2], with an extensive portfolio of assays and instruments to suit a wide range of needs, including high-throughput options as well as essential, more affordable instruments for academic needs. The new continuous flow technology, which eliminates the need for specialized cartridges and simplifies the workflow will be discussed as well.

The new developments in fluorescent imaging encompass a wide range of techniques based on fluorescent protein detection, including in-cell Western Blotting and tissue imaging, allowing for higher sensitivity, less risk of signal saturation and limited background as compared to standard HRP-based chemiluminescent detection. This allows for higher throughput, lower costs and generation of data that is more readily quantifiable.

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BIO-MAR Diagnostyka Sp. z o.o.

The future of parasite screening using AI in Medical and Microbiological Laboratories in Poland

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Accurate diagnosis is the first and most crucial element in monitoring, prevention, and treatment

Our company was founded in 2001 and headquartered in Gliwice, specializes in providing high-quality diagnostic reagent kits and a wide range of laboratory equipment for analytical laboratories. Our mission is to ensure that our products meet the highest quality standards so we provide our customers with a sense of security in their diagnostic processes. We are driven by a vision to meet the evolving needs of analytical laboratories by offering cutting-edge products and technological solutions. The dedication of our team is the driving force behind the company's success. Some employees have been with us since the very beginning, and each one plays a vital role in advancing our mission. We carefully select the companies we represent in the market to ensure that our offerings align with our commitment to quality and reliability.

Founding years and our development

In 2001 we entered the Disposable Equipment, Clinical Chemistry. We introduced Rapid Tests

Clinical Chemistry, Automatic Analyzers in 2006. From 2010 we are the main and only distributor of Aesku Group products for Autoimmunology and Infection Diseases. In 2010 we entered the urine diagnostics market. From 2013 we developed allergy and on 2019 microbiology.

What is the next step?

In last years parasitological diagnostics meets the technological challenges such us: automation of sample analysis, development of imaging methods, use of artificial intelligence (AI) in parasite identification. In this context in 2025 BIO-MAR company entered the parasitological market. The company started cooperation with the KEYU Biological Engineering Co. and launched a new parasitological analyzer KEYU-F600. This is automated stool sample analyzer that addresses all of these challenges. And on top of that it speeds up workflow, increases comfort and ensures highly accurate results. F600 can meet various needs and create a safe, user-friendly, and efficient working experience. Main advantages are: intelligent dilution of sample based on AI algorithm to achieve the standard test concentration, each field of both high and low power objective can take 1-8 layers of pictures, elements are shown more stereoscopic and recognized clearly. Complying with clinical practice and review requirements, different focal lengths pictures can be reviewed by scrolling mouse imitating microscope fine–tuning. Low-power magnification pictures mainly concentrate on fecal eggs with a wide field of vision. While the high-power aims for shooting both lighter substances at the upper layer (fat balls) and elements at the bottom layer (RBC, WBC, etc.). Moreover analyzer has got Iodine Staining Mode. The analyzer provide us higher accuracy recognition achieved with high magnification (accuracy ≥96%) and the report format can be modified according to the user’s needs.

We are very excited about the further development of parasitological diagnostics and we want to be an important part of it.

Sponsor information – Gold Sponsor

A&A Biotechnology

A&A Biotechnology is a Polish biotech company that develops and produces innovative tools for the life science industry. It was founded in 1993 by its current CEO Adam Burkiewicz, PhD. The company has its own research laboratories and production facilities.

A&A Biotechnology offer includes DNA and RNA isolation kits, PCR and reverse transcription reagents, cloning and transformation reagents, molecular biology reagents and services. The company also has facilities able to produce high volumes of molecular biology - grade enzymes.

A&A Biotechnology products and services are mainly used by scientific and diagnostic laboratories at universities, research institutes, veterinary laboratories, health services, laboratories for environmental analyzes, forensic laboratories, and other life science companies.

In addition, as a specialist life science company with its own R&D and production department, we are able to tailor our products and solutions to meet client's individual needs.

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Professor Wacław Szybalski Foundation

In memoriam: prof. Wacław Szybalski

Wacław Szybalski, born in 1921 in Lviv to a noble family, had a remarkable journey. He completed his early education, graduat-ing in 1933 from the St. Joseph Elementary School and in 1939 from Casimir III the Great 8th Gymnasium in Lviv. His passion for chemistry led him to study at the Lviv Polytechnic, where he worked under the guidance of Prof. Adolf Joszt, an expert in fermentation processes. During his studies, he developed a method for separating chemical compounds using paper chromatography and worked at the Institute for Research on Typhus and Viruses, led by the renowned Polish microbiologist Prof. Rudolf Weigl.

After World War II, he had his chemical engineering diploma recognized at the Silesian University of Technology in Gliwice. In the same year, he moved to Sopot and joined the Gdańsk University of Technology, where he became the head of the Department of Fermentation Industry and Biotechnology. It was during this time that he began delving into biotechnology and genetics and successfully defended his doctorate in 1949. In 1950, he emigrated to Denmark and then to the United States, where he made significant scientific contributions. In Denmark, he worked at the Carlsberg Laboratory and also conducted research at the Academy of Technical Sciences and the Niels Bohr Institute for Theoretical Physics. His move to the USA in 1951 marked the beginning of his groundbreaking work at Cold Spring Harbor, where he was part of a team that laid the foundations for molecular biology and genetic engineering. He had the opportunity to work alongside Prof. James Watson, the Nobel Prize-winning co-discoverer of the DNA structure. Subsequently, he continued his research at the Institute of Microbiology at the University of New Brunswick (working with the Nobel Prize winner, prof. Selman Waksman) and later became a professor at the McArdle Laboratory for Cancer Research at the University of Wisconsin-Madison. His pioneering work included developing methods for studying DNA and identifying chemical compounds that induce mutations in bacterial cells. Together with his wife Elisabeth Szybalski, he also played a key role in developing technology for gene therapy. His influential work extended to the coining of the concept and foundations of synthetic biology. His notable scientific achievements were published in prestigious journals such as “Science,” “Nature,” “Proceedings of the National Academy of Sciences of the United States of America (PNAS),” and “Virology.” He also founded and served as the editor-in-chief of the international journal “GENE” and held positions on the editorial boards of numerous scientific journals.

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