

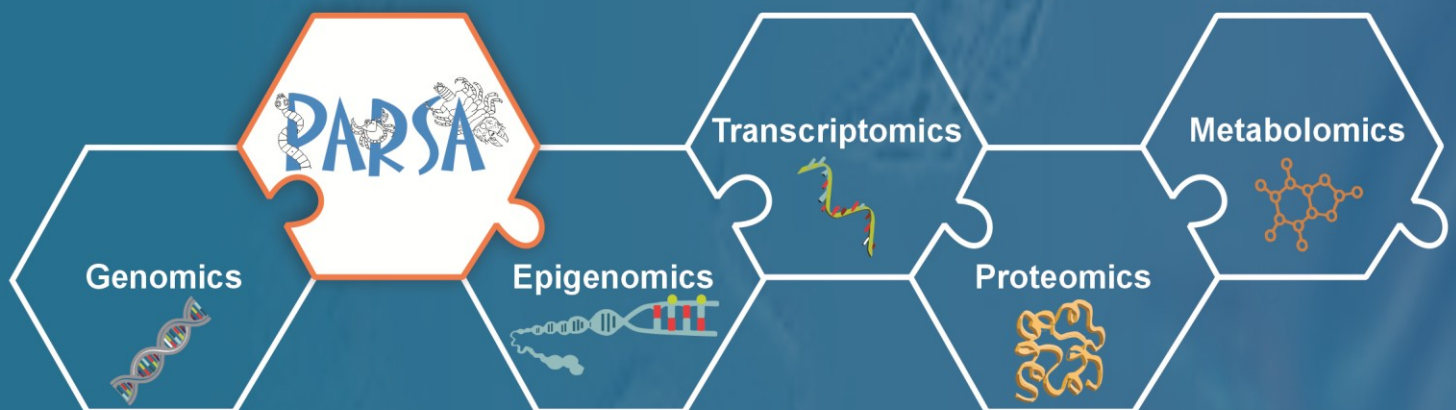
PARSA 2026

54TH ANNUAL CONFERENCE

30 August - 02 September 2026

ATKV Klein-Kariba, Bela-Bela

**Exploring Parasites in the Era of OMICS:
From Data to Discovery**



Programme & Abstracts



Welcome note from the PARSA President

Dear Colleagues, Friends and Fellow Parasitologists,



It is my great pleasure and privilege, on behalf of the Parasitological Society of Southern Africa (PARSA), to warmly welcome you to the 54th Annual PARSA Conference, taking place at ATKV Klein Kariba under the theme ***“Exploring Parasites in the Era of OMICs.”***

This year’s theme reflects the exciting transformation taking place in parasitology. Advances in genomics, transcriptomics, proteomics, metabolomics and other OMICs technologies are providing new opportunities to understand parasites and their interactions with hosts at an unprecedented level. As a community, we have an important role to play in translating these advances into meaningful solutions for parasite surveillance, control and prevention.

The PARSA Conference has always been more than a platform for presenting scientific findings. It is a place where established researchers, emerging scientists, students, practitioners and collaborators come together to exchange ideas, challenge conventional thinking and build lasting partnerships. I am particularly pleased to welcome our students and early-career researchers, whose enthusiasm, innovation and fresh perspectives are vital to the future of our discipline.

I encourage all delegates to make the most of the programme, engage openly with fellow participants, share your knowledge and experiences, and take the opportunity to establish new collaborations. Equally important, I hope you will enjoy the collegial atmosphere that has become such an integral part of the PARSA community.

I would like to express my sincere appreciation to the Scientific and Local Organising Committees, our speakers, reviewers, sponsors, exhibitors and everyone who has contributed to making this conference possible. Your commitment and support are fundamental to the continued success of PARSA.

Thank you for being part of the 54th Annual PARSA Conference. I look forward to an inspiring and productive meeting, filled with scientific discoveries, meaningful discussions, new connections and renewed enthusiasm for parasitology.

Welcome to PARSA 2026 - let us explore, connect and shape the future of parasitology together!

Warm regards,

Prof Kgomotso Sibeko-Matjila
PARSA President

Welcome note from the PARSA Conference Chairperson

Dear PARSA Participants,



It is my great honour to welcome you to the 54th Annual Conference of the Parasitological Society of Southern Africa. This year, we're gathering at the stunning ATKV Klein-Kariba Resort in Bela-Bela in the Limpopo Province, under the theme: '***Exploring parasites in the era of OICS; From data to discovery***'. The theme highlights the critical role that partnership and interdisciplinary cooperation play in driving the field of parasitology forward.

I would like to extend a special thank you to our keynote speakers, presenters, and adjudicators for their invaluable contributions to this conference.

During the next few days, we will enjoy a series of fascinating talks on both terrestrial and aquatic parasites, and I hope that the research shared will inspire numerous discussions during our tea breaks. I encourage all of you to make the most of these networking opportunities - connect with fellow parasitologists, share your insights, and foster collaborations that will drive scientific progress forward.

Lastly, I would like to thank every delegate for taking the time to attend and participate in this event. The annual PARSA conference provides an excellent opportunity for researchers who share a common interest in parasites to come together and exchange ideas. I am optimistic that this year will be no different, and that each participant will leave feeling fulfilled, inspired, and revitalised by this enriching experience.

So, enjoy the buffet of parasite research in this beautiful setting and I wish you a fantastic conference experience!

Best wishes,

Iva

Dr Iva Přikrylova
PARSA LOC Chairperson

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With appreciation to the following people for their assistance during the conference

Conference Local Organising Committee

1. Iva Přikrylová
2. Zamantungwa Mnisi
3. Susan Dippenaar
4. Wilmien Luus-Powell
5. Tshepo Mangena

Session Chairpersons

1. Wilmien Luus-Powell
2. Maxwell Barson
3. Luther van der Mescht
4. Danisile Tembe
5. S. Marcus Makgabo
6. Zamantungwa Mnisi
7. Samson Mukaratirwa
8. Andrea Spickett

Presentation Adjudicators - Oral

1. James Outa
2. Marliese Truter
3. Chris Marufu
4. Karien Labuschagne
5. Nicola Collins
6. Andrea Vetešníková Šimková

Presentation Adjudicators - Posters

7. Collins Mashilwane
8. Boris Krasnov
9. Modibe Raphahlelo
10. Priyanka Agarwal
11. Willem Smit
12. Khethiwe Mtshali

With appreciation to our sponsors



Programme - Oral

Sunday 30 August 2026

15h00	Registration Opens
15h00	Poster applications
17h00	Drinks, light snacks and networking <i>Important: Wear your oldest PARSA T-Shirt or bring your oldest PARSA bag and stand a chance to win a prize!</i>

Monday 31 August 2026

Time	Abstract #	Description	Speaker
Session 1 – Diversity, taxonomy and host-parasite interactions in African Fish Chair: Prof. Wilmien Luus-Powell, University of Limpopo			
08h00	Registration & Industry Networking		
08h30	Welcome and Opening		Dr Iva Přikrylova, University of Limpopo & Prof. Kgomoiso Sibeko-Matjila, University of Pretoria
08h45	Keynote 1 - Fish host immunity, pathogens and microbiota in the OMICS era		Prof. Andrea Vetešniková Šímková, Masaryk University and University of South Bohemia
09h30	49	Revisiting and reviewing fish parasitology in the Okavango Delta, Botswana – a preliminary report	Prof. Maxwell Barson, University of Botswana
09h45	26	Detection and characterisation of GIT associated Apicomplexan parasites in tilapia (<i>Oreochromis mossambicus</i> and <i>O. niloticus</i>) in South Africa	Dr Kevin W. Christison, Department of Forestry, Fisheries and the Environment
10h00	55	Taxonomic resolution reveals cryptic diversity and reframes host–parasite associations in <i>Myxobolus</i> spp. infecting African cichlids	Dr Kevin W. Christison, Department of Forestry, Fisheries and the Environment
10h15	Mid-morning refreshments		
Session 2 - Aquatic Parasite Diversity, Ecology and Disease Dynamics Chair: Prof. Maxwell Barson, University of Botswana			
10h45	07	Scratching the surface: unravelling the diversity of freshwater fish blood flukes in Europe	Dr James Omondi Outa, State Scientific Research Institute Nature Research Center
11h00	36	Invasion dynamics and host range expansion of the alien copepod <i>Neogergasilus japonicus</i> in South African freshwater systems	Dr Willem Smit, University of Limpopo
11h15	62	Diversity of snail-borne trematode infections in the Okavango Delta: Integrating morphological and molecular approaches	Ms Florah G. Gaongalelwe, University of Botswana
11h30	20	Invasive snails and trematode transmission: the case of <i>Pseudosuccinea columella</i> and an African buffalo (<i>Syncerus caffer</i>)	Ms Emilie Goossens, Hasselt University
11h45	46	Integrative morphological and molecular characterisation of <i>Contracaecum</i> spp. and host-linked genetic diversity	Ms Ketumile H. Thobejane, University of Limpopo
12h00	Poster Session 1		
12h30	Lunch		

Time	Abstract #	Description	Speaker
Session 3 – Diverse Parasitology			
Chair: Dr Luther van der Mescht, University of the Free State			
13h30	Presentation by Gold Sponsor		Mr Ernest Mokoena, Inqaba
13h45	08	Hidden in plain sight: first report and descriptions of blood flukes from South African cyprinids	Dr James Omondi Outa, State Scientific Research Institute Nature Research Center
14h00	17	Seasonal prevalence of gastrointestinal nematodes infecting horses in the Potchefstroom area, South Africa	Ms Roney Yssel, North-West University
14h15	53	Epidemiology of gastrointestinal nematodes infection in indigenous and crossbreed goats in St. Kitts, West Indies	Prof. Samson Mukaratirwa, Ross University School of Veterinary Medicine
14h30	29	A can of worms: anthelmintic (in)efficacy in Northern KwaZulu-Natal communal goats	Prof. Chris Marufu, University of Pretoria
14h45	11	Parasites and Practice: Longitudinal Insights into FAMACHA®-Guided Endoparasite Management in Smallholder Goats	Dr Andrea Spickett, ARC-OVR
15h00	48	Livestock, companion animals, and wildlife schistosomiasis in Africa: a scoping review on existing research and knowledge gaps	Ms Bongekile Lungile Khoza, University of Pretoria
15h15	Mid-afternoon refreshments		
Session 4 - Vectors and Vector-Borne Pathogens			
Chair: Dr Danisile Tembe, University of KwaZulu-Natal			
15h45	19	Preliminary results of <i>Simulium</i> species associated with streams in Gauteng, South Africa	Dr Karien Labuschagne, ARC-OVR
16h00	41	Evaluating the efficiency of baited BioFlyTrap P38T, H-trap, Nzi and Vavoua traps towards biting flies of Glossinidae, Tabanidae and Muscidae (Stomoxyni) families in north-eastern KwaZulu-Natal	Dr Moeti Taioe, ARC-Onderstepoort Veterinary Research
16h15	35	Occurrence and molecular detection of tick-borne pathogens in dogs from selected households at Ben Farm, Phalaborwa, Limpopo Province	Ms Pontsho Tshabalala, University of Pretoria, Clinvet International
16h30	56	Unravelling the occurrence of <i>Sarcocystis</i> species in South African meat-producing animals: A multi-provincial molecular approach	Ms Okuhle N. Sekujika, University of Pretoria
16h45	Close of Day 1		
17h00	PARSA AGM - MEMBERS ONLY		
18h30	Optional Dinner at the Restaurant (pre-booking required)		

19h00	Quiz Night for all Students in the Restaurant
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Tuesday 01 September 2026

Time	Abstract #	Description	Speaker
Session 5 – OMICS approaches to Anaplasma			
Chair: Dr S. Marcus Makgabo, Agricultural Research Council			
08h30	Keynote 2 - An <i>Anaplasma</i> adventure in South Africa: Exploring strain diversity, wildlife reservoirs and the quest for a better bovine anaplasmosis vaccine		Dr Nicola E. Collins, University of Pretoria
09h15	42	More than meets the eye: OMICs-driven insights into the hidden epidemiology of <i>Anaplasma</i> in South African cattle	Dr Zamantungwa T.H. Mnisi, University of Limpopo
09h30	63	Diversity of ticks and circulating tick-borne pathogens in selected farm at Namakgale Village, Limpopo Province, South Africa	Mr Fhulufhelo Mulaudzi, University of Pretoria
09h45	18	Genetic diversity of <i>Anaplasma marginale</i> in African buffalo (<i>Syncerus caffer</i>) from the Kruger National Park suggests host-specific divergence from cattle-associated strains	Ms Marche Duarte, University of Pretoria
10h00	Mid-morning refreshments		
Session 6 – Ticks and tick-borne diseases			
Chair: Dr Zamantungwa Mnisi, University of Limpopo			
10h30	43	Patterns of <i>Rhipicephalus</i> tick infestation in commercial cattle herds of the Free State, South Africa	Ms Elizna Molony, University of the Free State
10h45	10	Battle for dominance: Invasion dynamics between the invasive Asiatic (<i>Rhipicephalus microplus</i>) and native African (<i>Rhipicephalus decoloratus</i>) blue tick in the Eastern Cape province, South Africa	Dr Luther van der Mescht, University of the Free State
11h00	15	Modelling the potential suitable habitats for blue ticks in the Free State Province, South Africa	Ms Leah L. Blayi, University of the Free State
11h15	47	Analytical validation of novel xMAP assays for the detection of tick-borne haemoparasites in dogs	Ms Nokuzola Faith Nkosi, University of Pretoria
11h30	Poster Session 2		
12h0	Lunch & Networking		
Session 7 - Host-Parasite Interactions			
Chair: Prof. Samson Mukaratirwa, Ross University School of Veterinary Medicine			
13h00	02	Phylogenetic and functional niche breadth in two taxa of arthropod ectoparasites: correlations with ecomorphological traits are scale-dependent	Prof. Boris Krasnov, Ben-Gurion University of the Negev
13h15	44	Blood parasites in Muridae from the Nama and Succulent Karoo, Fynbos, and Grassland biomes of South Africa	Mr Divan de Koker, University of the Free State
13h30	40	Human and Climate Drivers of Helminth Communities in Wild Canids: Lessons for Zoonotic Surveillance in Southern African Interfaces	Dr Sibusiso Moloi, University of Pretoria
13h45	57	Prevalence and first molecular characterization of <i>Gongylonema ingluvicola</i> in free-range chickens from eight localities in KwaZulu-Natal and Eastern Cape provinces of South Africa	Ms Irene Walter, University of KwaZulu-Natal
14h00	06	Prevalence and distribution of chewing lice in free-range chickens from selected rural localities of KwaZulu-Natal and Eastern Cape provinces, South Africa	Ms Silindokuhle Mlondo, University of KwaZulu-Natal (Westville Campus)
15h15	Mid-afternoon refreshments		

Time	Abstract #	Description	Speaker
Session 8 – Molecular characterization of Pathogens			
<i>Chair: Dr Andrea Spickett, ARC-OVR</i>			
14h45	30	Digenean parasites and their influence on shaping the pullet carpet shell clams <i>Venerupis corrugata</i> aquaculture in Republic of South Africa	Ms Hlengiwe Mbanjwa, University of Free State
15h00	38	Impala (<i>Aepyceros melampus</i>) as a potential reservoir host of a novel <i>Anaplasma</i> species in Mpumalanga Province, South Africa	Dr S. Marcus Makgabo, ARC-Onderstepoort Veterinary Research
15h15	45	The South Africa <i>Theileria parva</i> population is unique	Dr Boitumelo Maboko, ARC-Onderstepoort Veterinary Research
15h30	52	Molecular characterization of <i>Theileria</i> parasites in horses and zebras: Comparative analysis of the 18S rRNA, ema and cox-1 genes for species discrimination	Ms Caelan Sue McKenzie, University of Pretoria
15h45	13	Subtype distribution of <i>Blastocystis</i> among animals in Vhembe District, Limpopo, South Africa	Prof. Samie Amidou, University of Venda
16h00	Close of Conference & Words of Thanks		
19h00	Conference dinner & awards (Theme: Denim & Diamonds)		



Wednesday 02 September 2026

10h00 | Breakfast & Departure

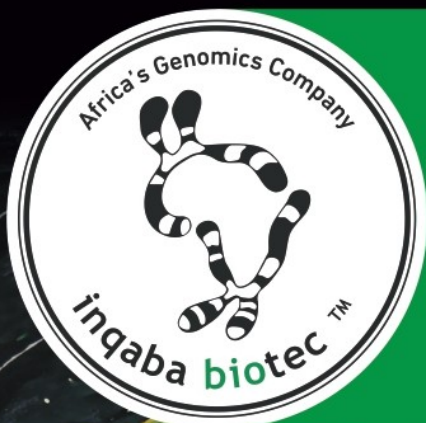
Programme - Posters

Monday 31 August 2026 – Poster Session 1: 12h00-12h30

Abstract #	Description	Speaker
04	Haemoparasite infections in free-range chickens from rural communities of KwaZulu-Natal and Eastern Cape provinces of South Africa	Danisile Tembe, University of KwaZulu-Natal
23	Molecular characterization of <i>Taenia solium</i> and <i>Taenia saginata</i> infecting domestic animals collected from different abattoirs in of Zimbabwe	Dr Vimbai T. Mucheka, University of Pretoria
27	Parasite diversity of <i>Oreochromis mossambicus</i> and <i>Clarias gariepinus</i> in the water bodies within the Mankweng rural area, Limpopo province	Dr Iva Přikrylova, University of Limpopo
32	Prevalence of serum antibodies of tick-borne diseases and the presence of <i>Rhipicephalus microplus</i> in communal grazing cattle in the north-eastern region of the Eastern Cape Province of South Africa	Dr Mandla Yawa, Dohne Agricultural Development Institute
33	Hidden <i>Rickettsia</i> diversity at the human-animal-environment interface in rural Mpumalanga	Ms Magen Brits, University of Pretoria
34	Assessment of parasite diversity in fish species occurring in selected dams around Gauteng and North West Provinces of South Africa	Dr Khethiwe Mtshali, Tshwane University of Technology
37	Gut microbes of <i>Stomoxys</i> flies from different ecological settings northeastern KwaZulu-Natal province, South Africa	Mr Percy Moyaba ARC-OVR
39	Hidden germ of the University of Limpopo: <i>Cichlidogyrus</i> spp. (Monopisthocotyla: Dactylogyridae) from <i>Oreochromis mossambicus</i> (Peters) in the artificial pond on the Turfloop campus	Dr Modibe Raphahlelo, University of Limpopo
50	Molecular characterization of <i>Echinococcus granulosus</i> of cattle from the Matabeleland region, Zimbabwe	Dr Madeline S. Sibula, National University of Science and Technology
51	Communal sheep farmer's knowledge and attitudes on the incidence of gastrointestinal parasites in the Eastern Cape, South Africa	Mr Mlungisi S. Jansen, Department of Agriculture
54	First insights into the parasite diversity of the critically endangered cichlid <i>Chetia brevis</i> from the Mlumati River, Eswatini	Prof. Wilmien Luus-Powell, University of Limpopo

Tuesday 01 September 2026 – Poster Session 2: 12h00-12h30

Abstract #	Description	Speaker
58	An Overview of Foot and Mouth Disease in the Eastern Cape Province: The Invisible Danger to Animal Trade and National Growth Eastern Cape Province, South Africa	Mr Sindile Felix Magoda, Eastern Cape Department of Agriculture
59	Host-associated patterns of ectoparasite infestation in sympatric <i>Rattus rattus</i> and <i>Rattus tanezumi</i> in rural communities, Mpumalanga Province, South Africa	Dr Dina M. Fagir, Durban Natural Science Museum, South Africa
60	Assessing ecosystem health in Loskop Dam using fish health and parasite diversity of <i>Oreochromis mossambicus</i>	Mr Sabelo M. Mdaka, University of Limpopo
61	Exploring the microbial communities of <i>Rhipicephalus</i> tick species parasitizing domestic animals in South Africa	Ms Asiashu Matshotshi, University of South Africa
64	Monopisthocotylian diversity of threatened Anabantidae and Cyprinidae, and an invasive cichlid, from the Cape Fold Ecoregion	Dr Marliese Truter, North-West University
65	Who lives inside the parasite? A first look at the microbiome of the temporary fish parasitic isopod <i>Gnathia pantherina</i> (Isopoda: Gnathiidae)	Dr Linda de Klerk, North-West University
66	Repurposing Drugs as Acetylcholinesterase Inhibitors Against the Malaria Vector <i>Anopheles</i> : An Integrated In Vitro and In Silico Study	Mr Jabu S. Mahlangu, University of the Witwatersrand
67	An Integrated Computational and Experimental Framework for Investigating Atovaquone Resistance and Discovering Novel Antimalarial Leads	Dr Priyanka Agarwal, University of the Witwatersrand
68	Evaluation of Phenylhydrazine Quinoline Hybrids as Selective Inhibitors of <i>Anopheles</i> Acetylcholinesterase	Mr Sahil Lala, University of the Witwatersrand
69	Assessing community knowledge and preventative practices for <i>Plasmodium</i> infections in the Vaal Triangle, Gauteng, South Africa	Prof. Robyn L. van Zyl, University of the Witwatersrand
70	Global phylogeny of <i>Gyrodactylus</i> (Monogenea) revealing origin and diversification of Nearctic species	Prof. Andrea Vetešníková Šimková, Faculty of Science of Masaryk University



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KEYNOTE PRESENTATIONS

Keynote 1 - Fish host immunity, pathogens and microbiota in the OMICS era

Andrea Vetešníková Šimková

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Host immunity in fish represents a complex and dynamic system that determines susceptibility or resistance to a wide range of pathogens, including bacteria, viruses, and parasites. In the OMICS era, advances in high-throughput technologies, such as genomics, transcriptomics, proteomics, and metabolomics, have revolutionized our understanding of fish host-pathogen interactions. These approaches enable comprehensive profiling of gene expression, protein activity, and metabolic pathways during infection, providing unprecedented insight into the molecular mechanisms underlying immune responses. Our research in the last year was conducted to investigate host immunity using transcriptomics (head kidney, spleen) to identify key immune-related pathways associated with specific pathogen infection or to explore potential links between host immunity, microbiota and parasites. Using high-throughput RNA sequencing, transcriptomic profiles of the head kidney were generated in two cyprinid species, *Cyprinus carpio* and *Carassius gibelio*, and their hybrids after spring viremia of carp virus (SVCV) infection. Hybrid heterosis for the F1 generation was associated with downregulation of differentially expressed genes. Hybrid breakdown was found in the paternal backcross generations and in the F2 generation hybrids, suggesting a disrupted cytonuclear coadaptation system in the post-F1 generations. The asexual triploid and sexual diploid system of *Carassius gibelio*, belonging to the *Carassius auratus* complex, known for its high global invasion rates, was investigated. Using high-throughput RNA sequencing, we focused on immunity-associated pathways in the two reproductive forms after challenge with monogenean parasites. Our study revealed many shared, especially upregulated, immunity-associated genes, however, sexual diploids showed an overall higher number of differentially expressed immunity-associated genes and a high number of correlations between immunity genes and parasite load. Our study suggests a limited ability of the gynogenetic form, representing the first waves of invasion, to cope with parasite infection and to mount an effective immune response, potentially associated with genomic reorganization in the triploid gynogenetic form. In a subsequent study, we aimed to investigate the impact of the invasive species *Carassius gibelio* on the native species *Carassius carassius* and to reveal the potential transfer of parasites and microbiota from the invasive species to the native species. An increase in the diversity of monogenean parasites was found with the hybridization rate of the fish. Partial sharing of bacterial communities revealed by DNA metabarcoding at sympatric sites may reflect the influence of a shared environment or is potentially a consequence of the influence of the invasive species on the native species or their direct or indirect interactions with each other.

Individual studies were supported by the Czech Science Foundation, projects no. 19-10088S and 22-27023S and the Technological Agency of the Czech Republic, project no. SQ01010194.



Biography

Andrea Vetešníková Šimková is a professor of zoology at the Faculty of Science of Masaryk University in Brno and at the Faculty of Fisheries and Water Conservation of the University of South Bohemia in České Budějovice (Czech Republic). In 2004, she founded the Host-Parasite Interactions team within the Parasitology research group at the Department of Botany and Zoology of the Faculty of Science of Masaryk University. Together with her research team, she conducts internationally recognized research that significantly and continuously contributes to the deepening of current knowledge about the diversity of freshwater fish parasites, their ecological interactions and host-parasite coevolution, the role of parasites in fish hybrid systems and asexual-sexual complexes of fish, and in the diversification of fish immune system. She is the author or co-author of more than 140 scientific papers, mainly in the fields of parasitology, freshwater fish biology,

evolutionary biology, fisheries, and ecology, indexed in the Web of Science (Clarivate Analytics). She has participated in 18 scientific projects as a project leader and 15 other projects as a team member. Over the past 15 years, she has established international cooperation with more than 20 scientific institutions across Mediterranean Europe, North America, South America, North Africa and Asia in the implementation of various scientific projects. She has served as a member of the scientific or organizational committees of several international parasitological conferences (ISM, ISFP) and as a reviewer in various parasitological, ecological, evolutionary and multidisciplinary journals. She works as a project evaluator for the Czech Science Foundation. In 2023 and 2025, she was ranked among the 2% most cited scientists in the world (Elsevier Data Repository). Since 2004, she has been teaching courses in ecology and parasitology at the Faculty of Science of Masaryk University, served as a member of several committees of bachelor's, master's and doctoral study programs, and supervised 26 undergraduate and 13 doctoral students.

MONDAY, 08h45

Keynote 2 - An *Anaplasma* adventure in South Africa: Exploring strain diversity, wildlife reservoirs and the quest for a better bovine anaplasmosis vaccine

Nicola E. Collins

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Bovine anaplasmosis, caused by the tick-transmitted rickettsial pathogen, *Anaplasma marginale*, is endemic across most cattle-farming regions in South Africa and continues to impose significant economic losses on the livestock industry. The live blood vaccine based on the cross-protective organism *Anaplasma centrale*, developed by Sir Arnold Theiler over a century ago, remains in use but is costly, inconsistently protective, and carries biosafety risks. This presentation summarises the research our group has done to characterise *Anaplasma* in South Africa with emphasis on *A. marginale*, and to evaluate the feasibility of a recombinant vaccine. Duplex qPCR, the most sensitive of three nucleic acid-based detection methods evaluated, revealed *A. marginale* and *A. centrale* prevalences of 57% and 17%, respectively, with a co-infection rate of 15% in South African cattle. *Msp1α* genotyping demonstrated that South African cattle are predominantly infected with multiple co-infecting strains, with 71.7% of the *Msp1α* repeats identified being unique to South Africa, underscoring the importance of considering local strain diversity in vaccine design. Despite this diversity, five outer membrane protein vaccine candidates showed strong antigenic conservation between South African and North American strains, supporting their inclusion in a globally applicable DNA vaccine currently under evaluation. Longitudinal surveillance of calves in the Mnisi community, bordering the Kruger National Park (KNP), revealed contrasting infection dynamics between peri-urban and wildlife-livestock interface habitats, and identified novel *Anaplasma* 16S sequence types in blood microbiome data. Sampling of KNP wildlife, including African buffalo, uncovered nine additional novel sequence types, reflecting greater *Anaplasma* diversity than previously recognised. *Msp1α* genotyping of buffalo-derived *A. marginale* strains suggests host-associated divergence with limited spillover between buffalo and cattle *A. marginale* populations. Molecular characterisation of newly identified *Anaplasma* organisms is hampered by low infection levels in carrier animals. Efforts to obtain whole genome sequences directly from field samples using long-read next generation sequencing technologies are ongoing, with preliminary assemblies achieved for both erythrocyte- and leukocyte-infecting *Anaplasma* species. The work presented here, extending from classical diagnostic approaches to genome sequencing technologies, reflects over a decade of enquiry into the epidemiology and diversity of *Anaplasma* species and the control of *A. marginale* in South Africa.



Biography

Dr Nicola E. Collins is a part-time Senior Researcher in the Department of Veterinary Tropical Diseases, Faculty of Veterinary Science, University of Pretoria. She has published 66 scientific papers, and has been an NRF-rated researcher since 2004. Over 40 PhD and MSc students have graduated under her supervision. Her research career of more than 25 years has focused on the molecular detection and characterisation of haemoparasites of veterinary importance. Early highlights include the completion of the *Ehrlichia ruminantium* genome sequence, the first bacterial genome completed in Africa, and the development of a real-time PCR assay for *Theileria parva*, a modified version of which was adopted by

the Onderstepoort Veterinary Institute as a national diagnostic test. Subsequent work established the genetic diversity of *Theileria equi* and *Babesia caballi* in South African equids and developed real-time assays to detect and distinguish between different lineages. Her current research centres on *Anaplasma* species. Her research group has demonstrated that most South African cattle are infected with multiple genetically diverse *A. marginale* strains as co-infections or super-infections. Five outer membrane protein vaccine candidates are antigenically conserved between South African and North American strains, supporting their potential as components of a global bovine anaplasmosis vaccine. Ongoing work under a USDA-NIFA grant is investigating the ability of a DNA vaccine comprising a cocktail of ten outer membrane protein genes to protect cattle against *A. marginale* challenge in the USA and South Africa. Bacterial microbiome sequences from bovine blood indicated the presence of novel *Anaplasma* 16S genotypes in addition to *A. marginale*, and subsequent sequencing from Kruger National Park wildlife revealed nine novel genotypes, highlighting a greater genetic diversity within the genus than previously recognised and an unexpectedly broad host range. Further characterisation of these obligate intracellular organisms is needed to determine their epidemiological importance, but whole genome sequencing efforts have been hampered by the difficulty of obtaining sufficient host-free DNA. Ongoing research is therefore focusing on genome sequencing of *Anaplasma* species directly from field samples using ONT with adaptive sampling.

TUESDAY, 08h30

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Oral Presentations

in order of appearance as on the programme

49 - Revisiting and reviving fish parasitology in the Okavango Delta, Botswana – a preliminary report

Maxwell Barson¹, Gorata Father¹, Peggy K. Radipati¹, Florah G. Gaongalelwe¹, Nashaat M. Mazrui² & Sununguko W. Mpoloka¹

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The Okavango Delta, located in north-western Botswana, is a hotspot for aquatic biodiversity and a UNESCO World Heritage Site that has seen a surge in fish parasitological research in the past two decades. In a study aiming to develop aquatic parasitological capacity in Botswana, BSc and MPhil students have been recruited at the University of Botswana to systematically study parasites of fish and other aquatic organisms in the Okavango Delta. Between September 2025 and March 2026, twenty species of fish (n = 104) were sampled from Mohembo, Guma Lagoon and the Thamalakane River, and screened microscopically for ecto- and endoparasites, 13 of which were found to harbour at least one parasite. More than 15 parasite species have been identified so far representing seven taxa: Ciliophora, Myxozoa, Monogenea, Trematoda, Cestoda, Nematoda and Acanthocephala. Some of these parasites show new host records in Botswana while most of them show new locality records in the Okavango Delta. There was no apparent effect of parasite infection and infestation on host condition factors, although ectoparasitic copepods (*Lamproglana monodi* and *Ergasilus mirabilis*) showed pronounced gill lamella damage. Heterophyid metacercariae and *Cichlidogyrus* sp. (Monogenea) were the most abundant ectoparasites on cichlid gills while *Contracaecum* sp. and *Eustrongylides* sp. dominated the endoparasite communities in catfishes. Notably, these nematodes survived freezing at 0°C for 48 hours in fish muscle tissue, presenting a serious zoonotic potential. Most of the larval trematodes, cestodes and nematodes are still undergoing molecular confirmatory diagnosis, but this preliminary study shows potential transmission to birds, reptiles and mammals, including humans. Comparison of trematode metacercarial DNA sequences with cercariae shed by gastropods in a related study will substantiate some unresolved life histories of these parasites, as well as the role of invasive species, climate change and increasing human activities in shaping host-parasite dynamics in the Okavango Delta.

MONDAY, 09h30

26 - Detection and characterisation of GIT associated Apicomplexan parasites in tilapia (*Oreochromis mossambicus* and *O. niloticus*) in South Africa

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The finfish aquaculture sector supports socio-economic growth in Africa by promoting food security, poverty alleviation and improving the livelihood of marginalised communities. Tilapia is the second most important finfish species in aquaculture globally and two species are currently being farmed in South Africa: Nile tilapia (*Oreochromis niloticus*) and Mozambique tilapia (*Oreochromis mossambicus*). Parasitic infection poses a major threat to aquaculture. Apicomplexan parasites of the gastro-intestinal tract (GIT) such as *Eimeria* spp. and *Cryptosporidium* spp., are obligate intracellular parasites. Despite their potential impact, little is known about Apicomplexan infection in wild and farmed freshwater fish in

South Africa. Therefore, this study characterised *Eimeria* and *Cryptosporidium* through morphometric and genetic analysis. The research also developed an assay using PCR to detect *Eimeria* and *Cryptosporidium* infection in tilapia tissue. Aquatic animal health and biosecurity are important for the sustainability of the aquaculture industry and biodiversity which is threatened by infectious diseases. This study contributes to the knowledge and understanding of parasitic infections in tilapia, which is currently understudied in South Africa.

MONDAY, 09h45

55 - Taxonomic Resolution Reveals Cryptic Diversity and Reframes Host-Parasite Associations in *Myxobolus* spp. Infecting African Cichlids

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The purpose of taxonomic resolution in parasitology is to provide accurate identification of pathogens in order to support interpretation of host–parasite relationships, disease risk, and epidemiological patterns. In myxosporean parasites, particularly species within the genus *Myxobolus*, this objective is often constrained by reliance on morphological characters that may be conserved across multiple taxa. A structured synthesis of published records indicates that *Myxobolus* spp. are widely reported from African cichlids, most frequently from *Oreochromis niloticus* and related tilapiine hosts. These parasites are recorded across multiple geographic regions and organ systems, with gill and kidney infections most commonly reported. However, morphology-based identifications have resulted in the same nominal species being reported from multiple hosts, tissues, and localities, which limits interpretation of host specificity and distribution. Phylogenetic analysis of 18S rDNA identified a distinct lineage closely related to *Myxobolus bejeranoi*, supporting the presence of previously unrecognised diversity within morphologically defined taxa. This finding demonstrates that morphologically similar parasites may represent genetically distinct entities, and that current records may overestimate host range and geographic distribution. Observations from farmed tilapia indicate that myxosporean infections may involve multiple organ systems; however, in the absence of species-level resolution, it remains unclear whether these patterns reflect true systemic infection or the presence of multiple co-infecting taxa. The integration of systematic review, molecular identification, and histopathological observation provides a more robust framework for interpreting host–parasite associations. Improved taxonomic resolution is therefore required to support disease diagnosis, risk assessment, and management in tilapia aquaculture systems.

MONDAY, 10h00

07 - Scratching the surface: unravelling the diversity of freshwater fish blood flukes in Europe

James Omondi Outa¹ & Olena Kudlai¹

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Fish blood flukes infect the circulatory system of their hosts and are detrimental to fish health. However, knowledge of the diversity and host range of freshwater fish blood flukes remains fragmentary because they are extremely difficult to detect and isolate. In Europe, only seven species of a single genus, *Sanguinicola* (Digenea: Sanguinicolidae), have been recorded. What is more, genetic data is available for only two species: *Sanguinicola volgensis* and *Sanguinicola plehnae*. In the current study, 1083 fish specimens, representing 47 species were obtained from 24 water bodies in Lithuania. Blood flukes were recorded from 10 fish species belonging to Cyprinidae, Leuciscidae and Tincidae. The flukes were found in the heart, bulbus arteriosus, gills, cranial vessels and eyes of their hosts. Characterisation of the

specimens was done using morphological data, and analyses of nuclear 28S rDNA and mitochondrial *cox1* DNA. Phylogenetic reconstruction revealed 11 sanguinicolid lineages in Europe (10 from Lithuania). Previously, only three species (*Sanguinicola armatus*, *Sanguinicola inermis* and *Sanguinicola intermedius*) were known in Lithuania. The current study provides the first genetic data for *S. armatus* (type species) and *S. inermis*. *Sanguinicola armatus* was recovered in an all-European clade comprising of *S. plehnae*, *S. volgensis* and a new *Sanguinicola* sp. This clade was sister to a large clade consisting of *S. inermis*, six lineages from Czechia, Lithuania and Poland, and five from South Africa. Herein, we describe new sanguinicolid species from Lithuania and assess the taxonomic positions of the species within the Europe-South Africa clade. Overall, the diversity of freshwater fish blood flukes has been greatly underestimated in Lithuania and in Europe at large. We suggest that new research in other parts of Europe, that integrate genetic and morphological analyses, will unearth new taxa of fish blood flukes. This research received funding from the Research Council of Lithuania (LMTLT) (S-PD-24-132).

MONDAY, 10h45

36 - Invasion dynamics and host range expansion of the alien copepod *Neoergasilus japonicus* in South African freshwater systems

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The invasive ergasilid copepod *Neoergasilus japonicus* (Harada, 1930), native to eastern Asia, has emerged as a widespread parasite of freshwater fishes globally. In South Africa, its distribution and invasion dynamics remain poorly resolved. This study presents a 19-year longitudinal dataset (2005–2024) spanning 43 fish species, 14 families, and 56 localities (Olifants and Limpopo river systems) to assess temporal, host-specific, and spatial patterns of invasion. No infections were recorded between 2005 and 2011 despite extensive sampling, with the first detections occurring in 2012. Thereafter, prevalence increased significantly over time, rising from 12.85% in 2012 to over 50% in 2021–2022 and peaking at 73.33% in 2024. This parasite was typically attached to the fins, and occasionally the gills. A binomial generalised linear model confirmed a highly significant temporal increase in infection probability ($p < 0.001$), with infection odds increasing by approximately 40% annually. The parasite exhibited low host specificity, infecting 17 host species across six families, with particularly high infection levels in Cichlidae and Cyprinidae. Spatially, infections were restricted to 13 of 56 localities but characterised by extreme local intensities, including a maximum of 1227 (mean intensity = 34) parasites recorded at a single locality (Doorndraai Dam, Limpopo Province) during a survey. These findings demonstrate a clear pattern of rapid emergence, establishment, and expansion consistent with an ongoing biological invasion. The success of *N. japonicus* appears to be driven by host generalism, high transmission efficiency, and the ability to reach high infection intensities despite limited observed pathology. This study highlights the importance of long-term monitoring in detecting parasite invasions and stresses the potential ecological risks posed by invasive ectoparasites in freshwater systems.

MONDAY, 11h00

62 - Diversity of snail-borne trematode infections in the Okavango Delta: Integrating morphological and molecular approaches

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The Okavango Delta, a RAMSAR site, is home to diverse wildlife, livestock, and human populations that interact continuously, creating an ideal environment for transmission of snail-borne parasitic trematodes, which remain poorly understood in the region. This study utilized morphological alongside ongoing molecular techniques to identify trematodes and their host snails along a transect of the Okavango Delta, representing the first molecular based investigation of its kind in Botswana. A total of 1091 freshwater snails belonging to ten species were collected across 15 sites in permanent and seasonal floodplains, lagoons and main river channels of the Okavango Delta between September 2025 and March 2026. Samples were examined for trematode infection through cercarial shedding and crushing. For molecular identification, the study is currently targeting the mitochondrial gene (COI), the nuclear 18S rRNA gene, and ITS2 regions. The most abundant species was *Radix natalensis* (27.9 %) followed by *Cleopatra elata* (13.3 %), with the other eight species accounting for the remaining 58.8 %. The overall infection prevalence through shedding was low (6.8 %) with seven cercarial types reported: furcocercous cercariae, megalurous cercariae, brevifurcate apharyngeate, parapleurolophocercous cercaria, pleurolophocercous, and xiphidiocercaria, and cerarjaeum cercaria. Parapleurolophocercous cercariae were the most abundant type in all sites (26.7%). Infection prevalence was highest in *Radix natalensis* with 45% of the individuals infected. These primary results are complemented by an ongoing molecular analysis where DNA from the cercariae will be sequenced, precisely identified to species level, and grouped into different clades. The distribution and abundance of the trematodes was strongly influenced by the type of habitat, animal, and human activities in each site. The cercariae identified to date are associated with trematode infections of fish, amphibians, birds and mammals, including humans. As such, these findings highlight advances in understanding and applying the One Health concept in the Okavango Delta.

MONDAY, 11h15

20 - Invasive snails and trematode transmission: the case of *Pseudosuccinea columella* and an African buffalo (*Syncerus caffer*)

Emilie Goossens^{1,2,8,*}, Ruben Schols^{2,3,*}, Aspire Mudavanhu^{2,4,5}, Tawanda Manyangadze^{6,7}, Joachim Mariën^{8,9}, Maarten P.M. Vanhove^{1,10} & Tine Huyse^{2,4}

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Parasite transmission and disease outcomes in African wildlife are increasingly shaped by anthropogenic environmental change, yet empirical data linking parasites, intermediate hosts, and wildlife health remain scarce. Following an unexplained increase in mortality among wild ruminants at a Zimbabwean conservancy, we investigated the diversity, transmission, and potential health relevance of snail-borne trematodes within this human-modified landscape. We combined a post-mortem examination of an African buffalo (*Syncerus caffer*), standardized freshwater snail surveys, cercarial shedding experiments, DNA-based screening in snails, and morphological and molecular analyses of snails and parasites. The buffalo was infected with the liver fluke *Fasciola gigantica* and an amphistome identified as *Calicophoron* aff. *microbothrium*. These parasite species are known to impair nutrient absorption, leading to reduced body condition and, in severe cases, mortality. Snail surveys revealed four gastropod taxa: invasive *Pseudosuccinea columella* and *Physa acuta*, and native *Radix natalensis* and a *Lentorbis*-like planorbid. All snail species, except *P. acuta*, hosted trematode infections. Molecular screening linked *C. aff. microbothrium* infections in the buffalo to a shedding *P. columella*, providing the first evidence that this invasive snail is a competent intermediate host for this amphistome. No snails were infected with *F. gigantica*, although *P. columella* is known to transmit *Fasciola* species. Additional trematodes detected in snails included *Plagiorchis maculosus*, *Plagiorchis* sp., *Echinostoma* sp., and another species of *Plagiorchiida*. While trematode infections could not be directly implicated as the sole cause of the observed mortality, their association with the invasive snail *P. columella* highlights their potential as an additional pressure on African wildlife health. Our findings underscore the value of integrated approaches and emphasize persistent taxonomic and ecological knowledge gaps that limit understanding of trematode-driven disease dynamics in African wildlife.

MONDAY, 11h30

46 - Integrative morphological and molecular characterisation of *Contracaecum* spp. and host-linked genetic diversity

Ketumile H. Thobejane¹, Willem J. Smit¹, Zamantungwa T. Mnisi¹, Piet H. King², Nehemiah M. Rindoria^{1,3}, Francois Roux⁴, Wilmien J. Luus-Powell¹

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Contracaecum spp. are heteroxenous nematodes, with larvae infecting aquatic invertebrates and fish, and adults maturing in piscivorous birds and some mammals. Larval stages of *Contracaecum* are commonly reported in farmed fish and fishery products globally, reflecting transmission from infected definitive hosts. To date, research has predominantly focused on larval stages, with comparatively limited attention given to adult forms. In southern Africa, only a few *Contracaecum* spp. have been morphologically identified from cormorant hosts (known definitive hosts), and these descriptions have not been supported by molecular data. Given that *Contracaecum* represents a complex of cryptic species, reliance on morphology alone is often insufficient for accurate species resolution. In response to these limitations, the present study integrates molecular marker-based approaches to investigate the diversity, host associations, and potential cryptic diversity of *Contracaecum* species within aquatic ecosystems. A total of 14 white-breasted cormorants collected from Loskop Dam, Mpumalanga Province, South Africa were subjected to parasitological examination during July 2024 and March 2025. Adult *Contracaecum* specimens were collected from the oesophagus and stomach and prepared for both light and scanning electron microscopy. Specimens previously characterised morphologically as putative *Contracaecum* species were subsequently used for DNA extraction and molecular analysis targeting the 28S rDNA and *cox1* gene regions. Sequences generated from adult parasites in cormorant hosts were compared with larval *Contracaecum* sequences from fish hosts available in public databases to assess host-linked genetic relationships and transmission patterns across life stages, and to evaluate potential cryptic diversity. All examined cormorants were infected (100% prevalence), with a mean

intensity of 115, indicating a high infection burden within the host population. Preliminary results suggest the presence of multiple *Contracaecum* species, with molecular analyses ongoing to further resolve species boundaries and assess cryptic diversity. These findings suggest a complex parasite assemblage within cormorant hosts and highlight the potential for previously unlinked larval and adult stages of *Contracaecum* spp. across aquatic ecosystems. This study highlights the importance of integrating molecular approaches with ecological context to improve species resolution and enhance understanding of parasite transmission dynamics.

MONDAY, 11h45

08 - Hidden in plain sight: first report and descriptions of blood flukes from South African cyprinids

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Blood flukes of freshwater fish have 2-host life cycles involving gastropods as intermediate hosts. Adult blood flukes inhabit the cardiovascular system of their hosts and are associated with mortalities of infected fish. Despite their ecological and economic importance, these flukes are underreported due to difficulties that are associated with detecting, isolating and studying them. In Africa, only three species (infecting catfishes) are known: *Sanguinicola chalmersi* from Sudan, *Nomasanguinicola clarias* from Egypt and *Nomasanguinicola dentata* from Namibia. Herein, 61 fish specimens of four common cyprinid species (*Enteromius paludinosus*, *Enteromius trimaculatus*, *Labeobarbus aeneus* and *Labeo capensis*) in South Africa were sampled from the Vaal River system and examined for blood flukes. Infections were detected in *L. capensis* and *L. aeneus*: prevalence = 19.4% and 90.5%, respectively. The flukes were found in the heart, bulbus arteriosus, gills and fluids recovered from washing internal body surfaces of the fish. The specimens were characterized using morphological data and partial sequences of the mitochondrial *cox1* DNA, and nuclear 28S and ITS rDNA. Blood flukes from the current study represent four previously unknown species of the family Sanguinicolidae. Their life cycles were established by linking genetic data of adults to cercariae from limpets belonging to the genus *Burnupia*. Phylogenetic reconstruction using 28S rDNA sequences recovered the current species in a clade comprising of sanguinicolids infecting cyprinids and leuciscids from Europe. This clade appears to represent a new genus that is sister to *Sanguinicola*. The discovery of four blood fluke species in cyprinids whose parasites have been reported for many decades and from a well-studied river in South Africa, underscores the difficulty of detecting fish blood flukes. We opine that many taxa of fish blood flukes are still undiscovered in Africa. This research received funding from the Research Council of Lithuania (LMTLT) (S-PD-24-132).

MONDAY, 13h45

17 - Seasonal prevalence of gastrointestinal nematodes infecting horses in the Potchefstroom area, South Africa

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Gastrointestinal nematodes (GIN) are among the most common parasites affecting equine health and can negatively influence animal welfare, performance, and productivity. The life cycle of GIN depends on climatic conditions that vary seasonally. This study aimed to determine the seasonal prevalence of

GIN infections in horses at Potchefstroom town of North West Province, South Africa. A purposive sample of horses (n=62) was taken from four horse stables in the study area. Faecal samples were collected once from sampled horses during autumn, winter, spring and summer. GIN Eggs were identified, counted and expressed as eggs per gram (EPG) units using the modified McMaster technique. Means Procedure of SAS (SAS, 2025) was used to calculate raw EPG means for both seasons and stable. Strongyle-type eggs were observed in all the stables. The highest mean EPG recorded was in winter (~424 EPG), followed by autumn (~ 255 EPG) and summer (~245 EPG), while spring had the lowest mean (~176 EPG). In Stable B, GIN prevalence peaked in winter (~ 757 EPG) and autumn (~ 473 EPG), then declined sharply in spring (~ 0 EPG) and increased moderately in summer (~ 113 EPG). Stable C showed consistently high prevalence across all seasons, ranging from (~ 339 EPG) in autumn to (~ 711 EPG) in summer. Stable D and E exhibited fluctuating but generally lower prevalence (Stable D ~16 to 335 EPG & Stable E ~0 to 77 EPG) than stables A and B. There are quantitative differences in the prevalence of GIN in horses in season and different stables. These findings highlight the importance of incorporating seasonal dynamics into sustainable parasite control strategies for horses.

MONDAY, 14h00

53 - Epidemiology of gastrointestinal nematodes infection in indigenous and crossbreed goats in St. Kitts, West Indies

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Gastrointestinal parasitic infections represent a major global constraint to small ruminant production, particularly among commercial and subsistence livestock farmers in developing regions. The burden is especially pronounced in sub-Saharan Africa and the Caribbean, where environmental and agro-ecological conditions favor parasite survival and transmission. This study compared the epidemiology of gastrointestinal nematodes (GIN) in indigenous goats and Boer crossbred goats in St. Kitts and Nevis. Adult female goats from each breed were randomly selected from a single farm (indigenous: n = 10; Boer crossbred: n = 10) and monitored over one year. Monthly fecal egg counts (FECs) were determined using the McMaster technique, while fecal cultures and recovery of third-stage larvae (L₃) were performed using a modified Baermann method. Packed cell volume (PCV) was measured from blood samples, and molecular as well as bioinformatic analyses were conducted on fecal material using standard protocols. Strongyle FECs in both indigenous and Boer crossbred goats demonstrated minor seasonal fluctuations, with no statistically significant differences observed either between seasons or breeds (P > 0.05). Six nematode genera were identified from fecal cultures: *Haemonchus*, *Trichostrongylus*, *Cooperia*, *Oesophagostomum*, *Ostertagia*, and *Bunostomum*. *Haemonchus* L₃s predominated in both breeds across wet and dry seasons. All six genera were detected in indigenous goats during the wet season, whereas Boer crossbred goats harbored five genera, with *Ostertagia* absent. Molecular analyses confirmed the presence of *Cooperia cuticei*, *Haemonchus* spp. *Strongyloides papillosus*, *Trichostrongylus axei*, and *T. colubriformis*. No statistically significant associations were observed between FEC, PCV, FAMACHA scores, or body weight between breeds, although subtle differences were noted. The comparable seasonal infection patterns observed between indigenous and Boer crossbred goats highlight the influence of local adaptation and support the strategic use of indigenous and locally adapted crossbred goats as a sustainable approach to mitigating endemic gastrointestinal parasitism in tropical small ruminant production systems.

MONDAY, 14h15

29 - A can of worms: Anthelmintic (in)efficacy in Northern KwaZulu-Natal communal goats

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Effective gastrointestinal nematode (GIN) control in communal small ruminant systems is increasingly compromised by declining anthelmintic efficacy, driven by unsupervised drug use, underdosing and single-class reliance. Despite KwaZulu-Natal (KZN) supporting the third largest goat population in South Africa, field efficacy data from communal flocks in the province remain scarce. This study evaluated the efficacy of four anthelmintic classes against naturally acquired GIN infections in communal goats across uMkhanyakude District, northern KZN, to inform evidence-based parasite management. Between May and August 2024, faecal egg count reduction tests (FECRT) were conducted across four municipalities: Hluhluwe, Jozini, Mtubatuba and uMhlabuyalingana. In each municipality, 50 naturally infected goats (pre-treatment EPG >150) were allocated to five groups (n=10): untreated controls, or treated with albendazole (BZ), levamisole (IMD), doramectin (ML) or monepantel (AAD). Efficacy and 90% confidence intervals were calculated using Delta, WAAVP and Beta Negative Binomial (BNB-B) methods, following current WAAVP guidelines. GIN genera were identified morphologically from cultured third-stage larvae and confirmed by ITS-2 rDNA PCR and phylogenetic analysis. *Haemonchus contortus* and *Trichostrongylus* spp. were dominant, with *T. axei* confirmed phylogenetically. Widespread ML resistance was detected in all four municipalities (pooled FECR 74.9%, 90% CI 59.4-84.4%). BZ resistance was confirmed in Hluhluwe (FECR 81.1%, 90% CI 67.8-89.3%) and pooled analysis (FECR 88.5%, 90% CI 77.9-94.1%). IMD showed full efficacy overall (pooled FECR 96.6%, 90% CI 93.5-98.3%), though inconclusive in Mtubatuba. AAD was fully efficacious across four municipalities (FECR 97.4%; 90% CI: 95.5-98.8%). Widespread ML and BZ resistance reflect prolonged overuse of these affordable drug classes, compounded by underdosing and lack of rotation. Goats' rapid drug metabolism exacerbates selection pressure, yet IMD and AAD retain full efficacy and should be prioritised in rotational control programmes. Phylogenetic clustering of *T. axei* with isolates from wildlife suggests cross-transmission, potentially introducing resistant alleles into wild ungulate populations. Multidrug AR (ML and BZ) is established in uMkhanyakude communal goats. AAD and IMD remain largely efficacious and should anchor rotational control programmes. Prudent efficacious anthelmintic use, weight-based dosing, drug rotation and quarantine of introduced animals are recommended.

MONDAY, 14h30

11 - Parasites and Practice: Longitudinal insights into FAMACHA®-guided endoparasite management in smallholder goats

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In the era of OMICS-driven parasite research, molecular characterization of helminth communities has reached unprecedented resolution. However, in smallholder goat systems - particularly in resource-

limited rural settings - endoparasite dynamics remain strongly shaped by management practices, animal handling, and farmer decision-making. Without grounding molecular advances in field realities, their practical application remains limited. This study examined endoparasite control practices among nine rural smallholder goat farmers in Winterveld, South Africa, managing herds ranging from 7 to 28 goats. Using structured interviews, repeated faecal sampling, and on-farm clinical assessments, we evaluated how parasite control strategies are implemented in practice, with particular emphasis on the use of the FAMACHA® system to guide targeted selective treatment (TST). Strongyle egg counts showed significant associations with multiple host health indicators, including packed cell volume (PCV), body condition score (BCS), and FAMACHA® score, demonstrating that infection intensity was closely linked to measurable indicators of animal health. Multivariate analysis using principal coordinates analysis (PCoA) revealed clear structuring of parasitological and clinical variables, with the primary axes explaining 82% of the observed variation. Mixed-effects modelling further confirmed significant relationships between strongyle infection intensity and host condition across herds. Despite the demonstrated value of these indicators for identifying animals requiring treatment, farmer-reported drenching practices frequently exceeded that of FAMACHA®-guided targeted selective treatment, with several farmers relying on routine interval drenching. These findings highlight the importance of integrating farmer training and field-based decision tools with emerging molecular surveillance approaches to achieve sustainable endoparasite control in smallholder goat production systems.

MONDAY, 14h45

48 - Livestock, companion animal, and wildlife schistosomiasis in Africa: a scoping review on existing research and knowledge gaps

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Schistosomiasis, also referred to as Bilharziasis, is a snail-borne Neglected Tropical Disease (NTD) caused by trematodes of the genus *Schistosoma*, posing a significant threat to both human and animal health in endemic regions of Africa. Control programmes prioritise human infections, but there is growing evidence of the importance of animal schistosomiasis in sustaining the transmission cycles. Species such as *Schistosoma bovis* and *Schistosoma mattheei* infect livestock, resulting in reduced productivity and economic losses, and can hybridise with other *Schistosoma* species to infect humans. Additionally, wildlife, rodents, and companion animals may serve as reservoir hosts, contributing to environmental contamination and transmission. This scoping review aimed to explore existing literature on animal schistosomiasis in Africa, identify gaps and recommend future research on the continent. Three databases (Pubmed, Web of Science and Scopus) were searched in April 2026 for studies published in English from database inception up to April 2026. A total of 138 studies conducted in Nigeria, Kenya, South Africa, Sudan, Egypt, Zimbabwe, Tanzania and Malawi were retrieved, with a primary focus on sheep (n=12), cattle (n=52), and goats (n= 10), and a few highlighting wildlife (n= 5) and rodents (n= 8). Most studies (9.4%) focused on *Schistosoma* prevalence, while others focused on evaluation of diagnostics (14.5%; parasitological and molecular), and others focused on transmission and distribution (13%). The key gaps include limited data on wildlife and rodents; inadequate data on disease transmission dynamics and maintenance of infection between animals and humans; the significance of hybridisation in the expansion of host-range transmission; inadequate data on the effectiveness of mass drug administration in animals; validation of diagnostic tools for low infection levels in animals; lack of prevalence data from most African countries; and poor integration of animal data into control interventions. Addressing these gaps is pivotal to guiding future research and strengthening One Health interventions in Africa.

MONDAY, 15h00

19 - Preliminary results of *Simulium* species associated with streams in Gauteng, South Africa

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In South Africa, *Simulium* (blackflies) species are not associated with disease transmission; however, they are of considerable economic importance as major nuisance insects. The aggressive blood-feeding behaviour of the adults negatively impacts agriculture, tourism, and recreational activities. It is estimated that 39 *Simulium* species occur in South Africa, although research has predominantly focused on two key species associated with major river systems, such as the Orange and Vaal Rivers. A project was initiated to investigate which *Simulium* species are associated with smaller river systems and streams in Gauteng. Larval and pupal specimens were collected and morphologically identified to species level. To date, four species have been identified. DNA was extracted from representative larval and pupal specimens, and a partial fragment of the cytochrome oxidase I (COI) gene was amplified and sequenced using Sanger sequencing. The sequence data confirmed the presence of four distinct species and verified that the larval and pupal stages corresponded to the same species in each case.

MONDAY, 15h45

41 - Evaluating the efficiency of baited BioFlyTrap P38T, H-trap, Nzi and Vavoua traps towards biting flies of Glossinidae, Tabanidae and Muscidae (Stomoxyni) families in north-eastern KwaZulu-Natal

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In efforts to survey biting flies, urgent need exists for a multi-species trap that can capture diverse hematophagous insect families, thus functioning as a more robust and representative trapping method. The current study evaluated the efficiency of the baited P38T BioFlyTrap against the standard H-trap used in South Africa, the Vavoua (West/Central Africa) and the Nzi (East Africa) to assist in decision-making to undertake enhanced surveillance and control interventions against biting flies in South Africa. A comparative study was done using a 4x4 Latin Square Design (LSD) approach over a period of 16 days in northeastern KwaZulu-Natal. The H-trap was significantly more efficient for Glossinidae, while the Nzi trap was significantly more efficient for Tabanidae. The P38T BioFlyTrap showed moderate performance across all categories (Glossinidae, Tabanidae, Muscidae (Stomoxyni) but lacks a standout specialty. The Vavoua trap was least effective trap for Glossinidae and Tabanidae but relatively effective for Stomoxyni. In this environment, baited P38 BioFlyTrap would be useful for diverse biting flies' investigations, while baited H-trap and Nzi remain specifically more performant, respectively for tsetse and Tabanids.

MONDAY, 16h00

35 - Occurrence and molecular detection of tick-borne pathogens in dogs from selected households at Ben Farm, Phalaborwa, Limpopo Province

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Ticks and tick-borne diseases impact both human and animal health. Domestic animals such as dogs play an important role as hosts of ticks and reservoirs of tick-borne pathogens by contributing to their maintenance and transmission within rural communities. However, studies focusing on tick borne pathogen surveillance in dogs remain limited, particularly in rural settings where dogs act as bridge hosts connecting wildlife, livestock, and human populations. The aim of this study was to identify the tick's infesting dogs and detect associated tick-borne pathogens in dog blood from selected households at Ben Farm, Phalaborwa, Limpopo Province, South Africa. A total of 39 dogs of mixed sex (23 females and 16 males) were randomly selected and examined for tick infestations, while blood samples were collected for DNA extraction and screened using reverse line blot (RLB) hybridization. The morphological identification of ticks confirmed only two tick species *Rhipicephalus sanguineus* and *Amblyomma hebraeum* infesting dogs. Overall, 48.7% (19/39) of the DNA samples tested positive for at least one pathogen, with higher infection level in females (56.5%, 13/23) than males (37.5%, 6/16), although not significantly different ($p=0.39$). Bacterial infections targeting the 16S rRNA gene were the most prevalent, detected in 43.6% (17/39) samples, dominated by *Anaplasma platys* and *Ehrlichia canis*. Protozoan infections targeting the 18S rRNA gene identified in 17.9% (7/39) of samples, primarily *Babesia vogeli*. Mixed infections involving both bacterial and protozoan pathogens were observed in 12.8% (5/39) of the samples. *Ehrlichia canis* and *A. platys*, which have zoonotic implications, were more prevalent, whereas *B. vogeli* is primarily associated with disease in puppies. The higher prevalence of *E. canis* and *A. platys*, both with zoonotic implications, suggests potential exposure risks for humans in the study area. These findings highlight the need for enhanced surveillance using both molecular and serological approaches to better understand the epidemiology and distribution of tick-borne diseases in this interface setting.

MONDAY, 16h15

56 - Unravelling the occurrence of *Sarcocystis* species in South African meat-producing animals: A multi-provincial molecular approach

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Sarcocystosis is a disease caused by the intracellular protozoan parasites of the genus *Sarcocystis*. The disease is prevalent in both humans and animals. Infected hosts manifest clinical signs such as inappetence, abdominal pain, nausea, emaciation, abortion and myositis which varies depending on whether the host acquires intestinal or muscular sarcocystosis. *Sarcocystis* species rely on two hosts to complete their life cycle. Over 200 species have been documented. Carnivores serve as definitive while herbivores as intermediate hosts. Omnivores fall under both categories. The epidemiology of the parasites involves determining their transmission cycles, spatial distribution, and the impact they have on animals and humans. *Sarcocystis* species have been identified in South Africa, but their diversity and ecosystems remain unexplored. This study investigates the occurrence of *Sarcocystis* species in livestock from abattoirs around Gauteng, Mpumalanga and Free State provinces. Tissue samples including the diaphragm, oesophagus and heart were collected from cattle, sheep and goat. COX-1 and 18S rRNA were used to screen and confirm the presence of *Sarcocystis* DNA using PCR. Positive amplicons were sent for Sanger sequencing. After sequence analysis the Maximum likelihood phylogenetic trees were constructed. The 18S rRNA *Sarcocystis* DNA isolated from the goat formed a monophyletic clade with *Sarcocystis capracanis* (87% bootstrap). The cattle sequences formed a clade with *S. heydorni*, a zoonotic species, *S. cruzi* and *S. levinei*. The sheep sequences formed a clade with *S. tenella*. COX 1 confirmed these results by detecting *S. cruzi* and *S. heydorni* in cattle and *S. tenella* in sheep, all with 100% bootstrap support. The same species could be detected in all infected tissues, indicating no predilection sites for the parasite species found within the respective host tissues. In South Africa, no published data has identified these species. Therefore, further parasitological and molecular investigations are required to elucidate the extent to which this parasite has spread within the country, its impact on the host and increase awareness to farming communities as the disease can have economic repercussions. The results provide interesting insights on possible species circulating in South African livestock and the need for further research on this topic.

MONDAY, 16h30

42 - More than meets the eye: OMICs-driven insights into the hidden epidemiology of *Anaplasma* in South African cattle

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Anaplasma species infect a wide range of ruminants, with cattle being naturally susceptible to *Anaplasma marginale* and *Anaplasma centrale*. In South Africa, bovine anaplasmosis is endemic in most cattle-rearing regions, except in low-rainfall areas where tick populations are limited, placing more than 99% of the national cattle population at risk. A surveillance study conducted between 2015 and 2016 in KwaZulu-Natal (KZN) Province, South Africa, analysed 109 cattle blood samples using duplex qPCR targeting the *msp1β* gene for *A. marginale* and *groEL* for *A. centrale*, revealing a 100% infection rate for both species. Subsequently, a follow-up study in 2022 examined 150 cattle (50 from KZN and 100 from the Free State Province) using a 16S rRNA next-generation sequencing approach. This analysis confirmed *A. marginale* as the most prevalent species across the provinces. Notably, *A. centrale* was the second most prevalent species in KZN with 22% prevalence, confirming infections from the earlier study conducted seven years prior. These observations raise important questions regarding the natural occurrence of *A. centrale* in the KZN region and the presence of tick vectors responsible for its transmission, particularly in the apparent absence of the known vector, *Rhipicephalus simus*. In addition, shotgun metagenomic analysis was performed to characterise the genome of *A. marginale* circulating in the Free State Province. Genome-wide comparative analysis revealed close similarity to the reference St. Maries and Florida strains, with further genomic characterisation ongoing. These findings highlight the widespread and stable circulation of *Anaplasma* species in South Africa.

Importantly, they suggest that the epidemiology of bovine anaplasmosis is more complex than currently understood, with potential knowledge gaps regarding transmission dynamics.

TUESDAY, 09h15

63 - Diversity of ticks and circulating tick-borne pathogens in selected farm at Namakgale Village, Limpopo Province, South Africa

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Ticks are hematophagous ectoparasites of domestic and wildlife animals and are recognised as important vectors of a wide range of pathogens. This study aimed to morphologically assess the diversity of tick species infesting livestock in Namakgale Village and to determine the prevalence and diversity of tick-borne pathogens using a 16S rRNA next-generation sequencing approach. Ticks (n = 910) and blood samples were collected in November 2025 from cattle (n = 110), sheep (n = 24), and goats (n = 96). Morphological identification revealed the presence of *Amblyomma hebraeum*, *Rhipicephalus evertsi evertsi*, *Rhipicephalus microplus*, and *Rhipicephalus simus*. *Amblyomma hebraeum* and *R. evertsi evertsi* were found across all host species, whereas *R. microplus* and *R. simus* were exclusively detected on cattle. Notably, *A. hebraeum* was the most prevalent species across all animal groups, highlighting its potential epidemiological significance in the study area. A total of 239 genomic DNA samples from livestock blood and tick tissues were screened by PCR targeting the 16S rRNA gene and sequenced using the PacBio Revio platform. Preliminary analysis of 12 cattle blood samples revealed a high prevalence of *Anaplasma centrale* and *Anaplasma marginale*, likely associated with the presence of *Rhipicephalus* species, known vectors of these pathogens. In addition, *Anaplasma phagocytophilum* was detected at low prevalence, indicating a potential zoonotic risk. These preliminary data provide insights into the diversity of tick species and their associated pathogens in Namakgale Village. Importantly, they highlight the need for continued surveillance to better understand tick–host–pathogen interactions and the potential risk of zoonotic transmission in the region.

TUESDAY, 09h30

18 – Genetic diversity of *Anaplasma marginale* in African buffalo (*Syncerus caffer*) from the Kruger National Park suggests host-specific divergence from cattle-associated strains

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The African buffalo (*Syncerus caffer*) is considered a reservoir host for *Anaplasma marginale*, the major causative agent of bovine anaplasmosis worldwide. Cattle-associated *A. marginale* strains have been molecularly characterized using genes such as *msp1α*, 16S rRNA, *msp4*, *msp5* and *GroEL*. However, the genetic diversity, population structure, and epidemiological role of *A. marginale* in buffalo remain largely unexplored. This study investigated the prevalence and genetic diversity of *A. marginale* strains in African buffalo from the Kruger National Park and cattle in a neighbouring rural community. A duplex real-time PCR assay, capable of detecting *A. marginale* and the closely related *A. centrale*, was used to screen 596 buffalo and 514 cattle samples. Among buffalo, 60.23% were co-infected with both *Anaplasma* species, while 17.95% and 4.87% had single infections with *A. marginale* and *A. centrale*, respectively. In contrast, cattle were predominantly infected with *A. marginale* alone (51.2%), with low levels of co-infections (2.5%) and *A. centrale* single infections (1.2%). Failure to amplify *msp1α* from *A. marginale*-positive buffalo samples necessitated the design of a forward primer specific for buffalo-associated *A. marginale*. A total of 22 *A. marginale*-positive buffalo samples were characterized using the modified *msp1α* genotyping method, followed by full-length 16S rRNA microbiome sequencing. Genotyping revealed 26 unique Msp1a repeats, clustering into two distinct sequence classes with sequences markedly divergent from previously described cattle-associated *A. marginale* repeats locally and globally. Analysis of Msp1a repeats revealed a conserved "VSSQS" motif present in both buffalo- and cattle-derived sequences. Notably, no cattle-associated Msp1a repeats, or *msp1α* genotypes were detected in the buffalo samples. 16S rRNA sequence analysis indicated that the buffalo-derived sequences showed 100% identity to known *A. marginale* sequences from cattle. Taken together, these results suggest host-specific divergence of *A. marginale* in buffalo and cattle. Genotyping of 23 *A. marginale*-positive cattle samples from the wildlife-livestock interface using the buffalo-specific forward primer revealed that 7% of *msp1α* genotypes identified were buffalo-type, suggesting that buffalo-type *A. marginale* does not persist in cattle, and further supporting host-associated divergence of these strains. These findings indicate that there is limited spillover of *A. marginale* between cattle and buffalo at the wildlife-livestock interface.

TUESDAY, 09h45

43 - Patterns of *Rhipicephalus* tick infestation in commercial cattle herds of the Free State, South Africa

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Ticks are obligate blood-feeding ectoparasites of livestock that have a substantial economic impact on cattle production worldwide. The impact of these blood-sucking arthropods is intensified by human induced environmental and climatic changes, as well as by animal movement, which facilitates the dispersal of ticks and their associated pathogens. Accurate identification of tick species is essential for understanding their diversity and distribution to inform effective control strategies. This study aimed to investigate the prevalence, mean intensity and distribution of *Rhipicephalus* ticks infesting cattle across the Free State Province, South Africa. Adult ticks were collected monthly from 30 animals on 12 randomly selected commercial cattle farms, from April 2025 until February 2026. Specimens were then identified morphologically using published taxonomic keys. A total of 9 788 *Rhipicephalus* ticks belonging to 3 species were collected. A mixed-effect generalised linear model with a negative binomial distribution was used to investigate the effects of host-related factors (cattle breed type, age, and sex) and environmental factors (vegetation type) on tick prevalence and intensity. Tick prevalence was significantly influenced by both vegetation type ($\chi^2 = 7.34$, $p = 0.007$) and age group ($\chi^2 = 17.46$, $p < 0.001$), with animals on natural vegetation showing lower prevalence than those on cultivated pastures, and yearlings showing higher prevalence than adults. Furthermore, tick intensity was significantly influenced by age group ($\chi^2 = 19.36$, $p < 0.001$), with older cattle carrying the highest tick loads and yearlings the least. These findings highlight spatial and temporal variation in *Rhipicephalus* infestations across the province, reflecting the complex interplay between host characteristics and environmental conditions. This study provides valuable baseline data on the distribution of *Rhipicephalus* species in the Free State and contributes to a better understanding of tick diversity and distribution in commercial

cattle systems. These insights can enhance the development of more targeted and sustainable tick control strategies in the region.

TUESDAY, 10h30

10 - Battle for dominance: Invasion dynamics between the invasive Asiatic (*Rhipicephalus microplus*) and native African (*Rhipicephalus decoloratus*) blue tick in the Eastern Cape province, South Africa

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The invasive Asiatic blue tick (*Rhipicephalus microplus*) was first recorded in South Africa in 1908 and has since become widespread. This rapid expansion is concerning, as the species is a vector of both Asiatic and African bovine babesiosis. The expansion of *R. microplus* has reportedly occurred at the expense of the native African blue tick (*Rhipicephalus decoloratus*). Reports vary, with some indicating complete displacement of *R. decoloratus* within as little as two years. Conversely, other studies suggest that *R. microplus* causes a decline rather than complete displacement, resulting in sympatric tick communities. Many previous studies fail to consider long-term population dynamics, and consequently the drivers of displacement are often overlooked. The aim of this study was to quantify the displacement risk posed by the invasive *R. microplus* to the native *R. decoloratus*. A five-year dataset detailing all tick life stages, sampled monthly using drag sampling, was analysed. First, we examined whether larval abundance of *R. microplus* increased over time relative to *R. decoloratus*. Second, we assessed how the relative proportions of the two species shifted across the study period. Finally, we investigated the role of mean monthly temperature and relative humidity in shaping abundance patterns of both tick species. For both species, total abundance fluctuated among years, with similar interannual patterns, suggesting that temporal variation rather than displacement shaped overall species abundances. Model-predicted larval abundance differed significantly between species across all years and months, with *R. microplus* consistently outnumbering *R. decoloratus*. However, there was no evidence that *R. microplus* abundance directly influenced the consistently lower abundance of *R. decoloratus*. Support for environmental effects exceeding displacement effects was further evident in differing species responses to temperature and humidity, with relatively greater increases in *R. decoloratus* abundance compared to *R. microplus*. These results demonstrate that displacement of *R. decoloratus* by *R. microplus* is not universal but instead shaped by local environmental conditions that may permit sympatry between the two species. This study shows that claims of displacement alone shaping tick communities must be supported by long-term, robust analyses incorporating environmental and temporal effects rather than personal observations.

TUESDAY, 10h45

15 - Modelling the potential suitable habitats for blue ticks in the Free State Province, South Africa

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Rhipicephalus decoloratus and *Rhipicephalus microplus* are two of the most significant tick species affecting cattle, with major veterinary and economic impact. Both species are known vectors of protozoa that cause African babesiosis and anaplasmosis while *R. microplus* is also a vector for the Asiatic babesiosis. A recent surge in reports of Asiatic babesiosis coupled with new records of *R. microplus* in the Free State Province suggests that *R. microplus* could be more widespread than previously thought. Furthermore, studies have shown that *R. microplus* can displace *R. decoloratus* depending on local environmental conditions. However, environmental drivers of their distribution in the Free State Province remain poorly understood. This study aimed to identify key environmental factors that affect occurrence and model the potential suitable habitat of *R. decoloratus* and *R. microplus* in the Free State Province using Maximum Entropy (MaxEnt) models. Only 9 occurrence records were obtained for *R. microplus* none of which originated from the current sampling. In contrast, 174 records were obtained for *R. decoloratus* of which 17 were from sampling in this study. Habitat suitability modelling was thus only performed for *R. decoloratus* due to the small number of occurrence records for *R. microplus* within the province. Habitat suitability modelling was performed for *R. decoloratus* by including occurrence records as response variables while climate data generated by harmonic regression of long-term climate and livestock densities were included as predictor variables. Overall, the habitat suitability model for *R. decoloratus* performed moderately well with an Area Under the ROC Curve (AUC) value of 0.67 and True Skill Statistic (TSS) value of 0.29. Furthermore, the amplitude of maximum temperature (45.6%), cattle density (32.0%) and phase of vapour pressure deficit (20.8%) were identified as the most important predictors in the model. The model indicated high potential habitat suitability in the northern and northeastern regions, moderate suitability in the central and western parts and low suitability in the southern region for *R. decoloratus* in the province. These findings identify risk zones for *R. decoloratus* expansion and provide a spatial framework for targeted tick and tick-borne disease surveillance in the Free State Province.

TUESDAY, 11h00

47 - Analytical validation of novel xMAP assays for the detection of tick-borne haemoparasites in dogs

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Canine ehrlichiosis and anaplasmosis are globally distributed tick-borne infectious diseases that represent significant health concerns in domestic companion animal populations and have a potential zoonotic risk, yet accurate, rapid, and multiplexed diagnostic tools remain limited. Due to shared tick carriers, tick-borne pathogens often occur as co-infections in animals. Molecular diagnostics are sensitive and precise but limited in detecting multiple pathogens simultaneously. Multiplex assays are highly beneficial and preferred for rapid, sensitive, cost-effective, and specific testing of large numbers of analytes in a single biological sample. The Reverse Line Blot (RLB) hybridisation assay can identify several infections simultaneously, but it is time-consuming, labour-intensive, and prone to subjective results. The liquid array xMAP technology enables multiplexing of assays, thereby reducing turnaround time, labour, and costs compared to traditional methods. In this study, probes previously used for *Anaplasma/Ehrlichia* RLB detection and real-time PCR assays were adapted and optimised for xMAP assays, and the analytical diagnostic performance (accuracy, sensitivity, specificity, and reproducibility) was evaluated. The assays were tested against field samples collected from the Mnisi community in Mpumalanga and Gauteng samples collected at Themba Clinic, Mamelodi Animal Health Clinic, and Onderstepoort Veterinary Hospital (dogs). The study's success will enable accurate and rapid detection of the pathogens, thus aiding timely treatment and minimising antibiotic misuse. This will help prevent the emergence of resistant strains and reduce mortality.

TUESDAY, 11h15

02 - Phylogenetic and functional niche breadth in two taxa of arthropod ectoparasites: correlations with ecomorphological traits are scale-dependent

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The relationships between phylogenetic (PNB) and functional (FNB) niche breadth and abundance and body size in fleas and gamasid mites in multiple regions across the Palearctic were studied. The questions of the study were: whether (a) PNB or FNB correlated with abundance or body size; (b) the pattern of this correlation differed between the regional (within a region) and the continental (across regions) scales; and (c) the regional PNB and FNB of a parasite was affected by the phylogenetic and functional, respectively, diversity of all hosts in that region. The relationships between abundance and PNB or FNB were mainly manifested on the continental scale, but mostly not on the regional scale, being positive in both taxa. The effect of body size on PNB and FNB was found in only a few regions for fleas and in no regions for mites. On the contrary, continental PNB and FNB did not correlate with flea body size but decreased with an increase in mite body size. Regional PNB and FNB values of some, but not all, flea and mite species were positively associated with the phylogenetic and functional, respectively, diversity of hosts available in a region. In conclusion, the relationships between the abundance and body size of an ectoparasite and its PNB or FNB are scale-dependent. These relationships may differ from or be similar to the relationships between abundance or body size and niche breadth measured as the size of a host spectrum, depending on spatial scale and ectoparasite taxon.

TUESDAY, 13h00

44 - Blood parasites in Muridae from the Nama and Succulent Karoo, Fynbos, and Grassland biomes of South Africa

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Rodents play a critical ecological role across South Africa's diverse biomes, yet the diversity, prevalence, and distribution of their blood parasites remain poorly understood, particularly in arid and semi-arid regions. This study investigates haemoparasite infections in Muridae across four biomes, Succulent Karoo, Nama Karoo, Fynbos, and Grassland, to address key gaps in host–parasite ecology and potential zoonotic risk. Rodent blood samples were collected from multiple localities within each biome and screened for parasites using microscopy (Giemsa-stained blood smears) and molecular techniques (PCR-based identification). Preliminary results indicate the presence of *Trypanosoma* species across all sampled biomes, with confirmed identification of *Trypanosoma lewisi* in the Grassland biome. Microscopy screening revealed infections in several individuals across all regions, with variation of parasitaemia observed among sampling sites within each biome. Current data patterns suggest spatial heterogeneity in parasite occurrence, potentially linked to environmental conditions, host community structure, and vector dynamics. Notably, higher numbers of infected individuals have been observed in arid and heterogeneous environments, such as the Succulent Karoo. This study provides important baseline data on blood parasite occurrence in understudied South African biomes and demonstrates the value of integrating morphological and molecular approaches for parasite detection. Given the zoonotic potential of certain *Trypanosoma* species, these findings have implications for disease surveillance and biodiversity conservation. Continued sampling and analysis will further clarify patterns of parasite diversity and distribution, contributing to a better understanding of host–parasite interactions, ecosystem health, and emerging disease risks in changing environments.

TUESDAY, 13h15

40 - Human and climate drivers of helminth communities in wild canids: lessons for zoonotic surveillance in Southern African interfaces

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Climate change and human-driven landscape changes are reshaping host-parasite interactions, particularly at wildlife-livestock-human interfaces, amplifying zoonotic transmission risk. Understanding of how these drivers interact to structure helminth communities in mesocarnivores remains limited. This study applied a European model system to identify generalisable processes relevant to Southern African transmission dynamics, particularly for *Echinococcus* spp. A cross-sectional study of red fox (*Vulpes vulpes*, n=194) and golden jackal (*Canis aureus*, n=151) was conducted across peri-urban and rural gradients in Central and Eastern Europe. Host proximity to human settlements was quantified using GIS-derived distance buffers. Helminth infracommunities were evaluated using prevalence, abundance, diversity indices, and crowding metrics. Hosts sampled near (<1750 m) human settlements (61.2 %) exhibited significantly higher infracommunity crowding and parasite diversity. *Uncinaria* spp and *Ancylostoma* spp. were most prevalent (>60%), indicating strong environmental transmission at interface zones. Although *E. multilocularis* was less prevalent, infected hosts showed significantly higher infracommunity crowding, with abundant *Ancylostoma* spp and *Toxocara* spp., with a negative correlation between their abundances (Spearman's $\rho = -0.445$, $p < 0.001$). Human-modified landscapes concentrate hosts and interact with climate-sensitive parasite stages, where temperature and moisture regulate egg survival and larval development. Under climate variability, these processes are likely to intensify transmission at interface zones. This framework is directly applicable to Southern Africa, where peri-urban expansion may amplify *Echinococcus granulosus* transmission involving domestic dogs and wild canids. Human and climate drivers jointly structure helminth communities and zoonotic risk. A One Health approach incorporating wildlife, livestock, and human health sectors, supported by proactive climate-informed risk mapping, is essential for improving surveillance and control strategies in Southern African interface systems.

TUESDAY, 13h30

57 - Prevalence and first molecular characterization of *Gongylonema ingluvicola* in free-range chickens from eight localities in KwaZulu-Natal and Eastern Cape provinces of South Africa

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Gongylonema ingluvicola is a gastrointestinal nematode affecting both domestic and wild birds. This parasite causes local lesions in the form of burrows in the epithelial mucosa, which appear as white convoluted tracks. Despite the widespread occurrence of *G. ingluvicola* in poultry, genetic data of this gastrointestinal nematode infecting free-ranging chickens in South Africa remain scarce on genetic databases. This study determined the prevalence and characterized *G. ingluvicola* from free-ranging chickens in KwaZulu-Natal (KZN) and Eastern Cape (EC) provinces. Seventy-nine adult free-ranging chickens were randomly purchased from four localities per province, KZN (n=39) and EC (n=40). Chickens were humanely euthanized, and nematodes were recovered from the crop mucosa, then identified morphologically using stereo and scanning electron microscopy. Molecular confirmation was

performed using the mitochondrial *cox1* region. The overall prevalence of *G. ingluvicola* was 45.6% (36/79) across both provinces. The observed prevalence of infection was significantly higher in KZN as compared to the EC province ($p < 0.05$). Within the provinces, the prevalence ranged from 33.3% in Mtunzini to 90% in Shongweni areas in KZN, and 10% in Caguba to 60% in Umthatha in the EC. A total of 162 worms were collected, of which KZN accounted significantly more (78.4%) of the total worm count compared to the EC (21.6%) ($p < 0.05$). Molecular analysis clearly distinguished *Gongylonema* spp. from various hosts, with the isolates from this study forming a sister clade with *G. pulchrum* and *G. nepalensis*, species commonly infecting mammals. Furthermore, the studied isolates formed two strongly supported sister clades, with a low mean genetic variation of 1% between them. This clustering was further confirmed by the formation of two novel haplotypes (Hap_1 and Hap_2), exclusively representing the studied isolates, and were separated by five mutational steps. This study provides the first molecular characterization of *G. ingluvicola* in free-ranging chickens and highlights its genetic relationship with other species from various hosts. Thus, contributing essential baseline mitochondrial genetic data for this understudied parasite in South Africa.

TUESDAY, 13h45

06 - Prevalence and distribution of chewing lice in free-range chickens from selected rural localities of KwaZulu-Natal and Eastern Cape provinces, South Africa

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Chewing lice remains the most common ectoparasites affecting free-range chickens, particularly in rural communities where biosecurity and parasite control measures are limited. This study determined the prevalence, geographic distribution and species diversity of chewing lice infesting free-range chickens from selected rural localities of KwaZulu-Natal and Eastern Cape provinces of South Africa. Seventy-nine adult indigenous free-range chickens were purchased between September 2024 and November 2024. Following euthanasia, chewing lice were collected and scanned using scanning electron microscopy, then identified based on morphological characteristics. The prevalence and factors influencing the prevalences were analysed using descriptive and inferential statistics. The overall prevalence of chewing lice infestation was significantly ($p < 0.05$) higher in the Eastern Cape (95%) than in KwaZulu-Natal (64.1%), with marked variation among localities. Four chewing lice species were identified as *Menopon gallinae*, *Goniocotes gallinae*, *Goniodes dissimilis*, and *Menacanthus cornutus*. Among these, *M. gallinae* was the most prevalent (95%) and widely distributed species in both provinces while *M. cornutus* was the least prevalent species (7.5%), and it was reported only in one locality in the Eastern Cape province. Mixed infestations with two or more lice species were detected in both KwaZulu Natal (38.5%) and Eastern Cape (57.5%) chickens, this included combinations of *M. gallinae*, *G. dissimilis*, and *G. gallinae*. Prevalence of chewing lice was higher in coastal localities than inland areas. Prevalence rates were high in the KwaZulu-Natal south coast (Shongweni and Umzinto; 100%) compared to the north coast Mtunzini and Maphumulo, 0-60%), while consistently high rates were observed across both the south (Mthatha and Gcuwa; 100%) and north (Tsolo and Caguba; 71.43-100%) coasts of the Eastern Cape province. Male chickens were found to be more infected than females in both provinces, with higher prevalences observed in males in Mtunzini (60% compared to 25%), Maphumulo (50% compared to 0%), and Caguba (100% compared to 71.43%). Sexes had no significant effect ($p > 0.05$) on prevalence rates for chewing lice. These findings demonstrate that chewing lice infestation is widespread among free-range chickens in both provinces, highlighting the need for improved ectoparasite management strategies to enhance poultry health and productivity in rural farming systems.

TUESDAY, 14h00

30 - Digenean parasites and their influence on shaping the pullet carpet shell clams (*Venerupis corrugata*) aquaculture in Republic of South Africa

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Global aquaculture industry has experienced significant growth in recent decades, with bivalve molluscs in particular oysters, clams, scallops, and mussels being the main bivalve species cultured. Clams of the family Veneridae contribute almost 40% of the global marine bivalve fisheries. These clams are highly valued for their nutritional composition as well as their broad consumer appeal. In South Africa, the clam *Venerupis corrugata* is a potential aquaculture candidate species currently in the research and development phase with research efforts focusing on broodstock collection and conditioning, spawning and larval rearing. However, the high prevalence of digenean trematode parasites poses a significant challenge to reproductive success. These parasitic infections are hypothesised to impair gametogenesis and reduce fecundity, thereby threatening the viability of *V. corrugata* as an aquaculture candidate species. Histological analysis was used to examine gametogenesis in infected clams and revealed two predominant trematodes infecting the gonadal tissue i.e. *Gymnophallus* and *Bucephalus*. The prevalence of *Bucephalus* was highest between May and July, ranging from 25% to 30%, while *Gymnophallus* infections were more evenly distributed throughout the year due to the presence in multiple organs. The present study aims to quantify the impact of trematode infections on reproductive output, to develop effective early detection and screening protocols for parasite exclusion in broodstock selection. Experimental approaches will include assessments of cercaria shedding, feeding or clearance rates, application of anaesthetic procedures, and gonad biopsy techniques to support the development of strategies that enhance gonadal maturation and spawning success.

TUESDAY, 14h45

38 - Impala (*Aepyceros melampus*) as a potential reservoir host of a novel *Anaplasma* species in Mpumalanga Province, South Africa

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Over recent decades, there has been a global increase in the emergence and re-emergence of tick-borne rickettsial pathogens of significant public and veterinary health concern. Within a One Health context, these pathogens represent a growing threat at the human–animal–environment interface. In South Africa, expansion of the wildlife industry has extended this interface, increasing opportunities for tick-borne pathogen transmission between wildlife, livestock, and humans. Wildlife hosts play a critical role in the maintenance and diversification of *Anaplasma* species; however, the diversity of novel *Anaplasma* species and their epidemiological significance in African ecosystems remain poorly

understood. This study investigated impala (*Aepyceros melampus*) as a potential reservoir host of a novel *Anaplasma* species in Mpumalanga Province. A total of 51 blood samples collected in 2020 and 2025, from the Greater Kruger National Park, were screened for the presence of *Anaplasma* species using qPCR, followed by full-length 16S rRNA microbiome sequencing, and multilocus sequence analysis. Quantitative PCR confirmed the presence of *Anaplasma* DNA, with microbiome sequencing identifying *Anaplasma* as the dominant bacterial taxon (up to 70%). Two major sequence types (ST KNP-1a and ST KNP-1b) represented the predominant circulating lineages, alongside additional low-abundance variants (ST KNP-2, ST KNP-9 and sp. SAdog) suggestive of mixed infections with other *Anaplasma* species. Phylogenetic analyses based on the 16S rRNA and *groEL* genes consistently demonstrated that the KNP1 lineage forms a distinct clade, closely related to *Anaplasma ovis* but genetically divergent from it and other recognised species. The presence of two well-supported subclades (KNP-1a and KNP-1b) further indicates intra-lineage diversity. Ongoing *gltA*-based analyses will strengthen species delineation within a multilocus framework. These findings support the presence of a novel *Anaplasma* species circulating in impala and highlight the importance of wildlife reservoirs in the ecology of tick-borne pathogens. From a One Health perspective, the close phylogenetic relationship to livestock-associated species highlights the potential for spillover at the wildlife–livestock–human interface, warranting further investigation into its epidemiological and zoonotic significance.

TUESDAY, 15h00

45 - The South Africa *Theileria parva* population is unique

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There is limited knowledge of the different types of *Theileria parva* genotypes circulating across South Africa and of how disease outbreaks can be linked to particular genotypes. In view of this, and due to the widespread use of microsatellite characterisation, 96 isolates from endemic areas (KwaZulu-Natal, Limpopo, and Mpumalanga provinces), and non-endemic (Free State province) were analysed using 10 simple sequence repeat markers. Samples from outbreak areas, diagnostic, research, and archived material were also included. There was no host differentiation between buffalo-type and cattle-derived buffalo-type isolates. Geographic differentiation was moderate, except for Free State province isolates collected between 2024 - 2025, which had a unique genotype. The high genetic identity of Free State isolates collected from 2012 - 2018 with KwaZulu-Natal populations indicates that KwaZulu-Natal may be a possible outbreak source. The 2024-2025 Free State isolates were only related to one another with regard to the genetic distance and genetic identity, which meant that the source could not be reliably identified. Our results indicate that microsatellite markers can be routinely used to identify unique genotypes and genetic changes that may be linked to genetic drift and/or gene flow.

TUESDAY, 15h15

52 - Molecular characterization of *Theileria* parasites in horses and zebras: Comparative analysis of the 18S rRNA, *ema* and *cox-1* genes for species discrimination.

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Equine theileriosis is an infectious tickborne disease of equids caused by the apicomplexan parasites *Theileria equi* and *Theileria haneyi*. The disease has significant implications for international horse movement, and accurate diagnosis is essential, particularly since these two parasites differ in drug susceptibility and serological cross-reactivity. In this study, we aimed to molecularly characterise both parasites in South African horse and zebra blood samples using comparative phylogenetic analysis across four genetic markers. DNA isolated from blood samples were screened using established quantitative real-time (qPCR) assays to confirm *Theileria* infections. Conventional PCR assays targeting the 18S rRNA, equi merozoite antigen-1 (*ema-1*), equi merozoite antigen-11 (*ema-11*) and mitochondrial cytochrome oxidase-1 (*cox-1*) genes were subsequently performed on qPCR positive samples and the amplicons were sequenced. Analysis of the qPCR results indicated that mixed *T. equi* and *T. haneyi* infections were present in most horse (71%) and zebra (90%) samples. Interestingly, *T. equi*-exclusive infections were detected only in horses (29%), whereas *T. haneyi*-exclusive infections were detected only in zebras (10%). Analysis of the 18S rRNA gene identified four of the five globally recognised genetic *T. equi* groups (A-D). Genotypes A, C and D were detected in both horses and zebras, whereas genotype B occurred exclusively in zebras. Genotype E was not detected. The *ema* gene family was targeted because *ema-1* and *ema-11* are exclusive to *T. equi* or *T. haneyi* respectively. Analysis of the *ema-1* gene identified three distinct clades (A-C), whereas *ema-11* analysis identified two main clades with greater sequence diversity than observed in *ema-1*. This finding is consistent with previously described *ema* clustering patterns respectively. Comparison of the *ema-1* and 18S rRNA phylogenetic trees showed that sequences were randomly distributed across different clades. Importantly, construction of a tree based on the *cox-1* gene sequences placed sequences associated with all studied *T. equi* genotypes into a single monophyletic clade, clearly separating them from *cox-1* sequences associated with *T. haneyi*, supporting the current view that *T. equi* genotypes and *T. haneyi* represent distinct parasite species. Multi-locus analysis, particularly of the *cox-1* gene, supports the classification of *T. haneyi* as a separate species from *T. equi*.

TUESDAY, 15h30

13 - Subtype distribution of *Blastocystis* among animals in Vhembe District, Limpopo, South Africa

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Blastocystis is a ubiquitous microscopic parasitic microorganism that belongs to the phylum Stramenopila. Globally, the subtype's distribution of *Blastocystis* in both humans and animals has been reported, but such studies have never been done in South Africa. The present study aims to determine the subtype distribution of *Blastocystis* among animals in Northern South Africa. A total of 364 stool samples were used (wild mice, cattle and pigs). Conventional PCR was performed in order to amplify the DNA segment of *Blastocystis* 18S SSU rRNA gene. The positive PCR products (83) were sequenced. The sequences for *Blastocystis* were assembled and the subtype's identification was performed using DNA barcoding. The phylogenetic tree was constructed using MEGAX software. The results of the study reveal that 186 (51.7%) samples were positive for *Blastocystis*. Nine different subtypes were obtained which included ST1, ST4, ST5, ST6, ST8, ST10, ST12, ST13, and ST17. The subtype distribution of *Blastocystis* was as follows, subtype 5 was the most dominant one with 28.3% while ST13 was 2.2%. The relationship of *Blastocystis* subtypes were observed and the subtypes that were identified in Vhembe are the same as the subtypes that were identified in different parts of the world. This is the first report of *Blastocystis* subtypes distribution in wild mice, cow and pig samples from South Africa. It further highlights the zoonotic potential of *Blastocystis* which could be transmitted between humans and animals.

END ORAL PRESENTATIONS

POSTER SESSION 1, 31 August 2026

04 - Haemoparasite infections in free-range chickens from rural communities of KwaZulu-Natal and Eastern Cape provinces of South Africa

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Haemoparasites infections have been associated with high morbidity and mortality rates in poultry species, and this remains a burden and severe threat in poultry production. Regardless of this challenge, there is a paucity of information on the burden of haemoparasites in free-ranging chickens in South Africa. This study aimed to determine the prevalence and identity of haemoparasites infecting free-ranging chickens in the KwaZulu-Natal (KZN) and Eastern Cape (EC) provinces of South Africa. Free-ranging chickens from selected villages in EC ($n = 39$) and KZN ($n = 39$) were purchased, and blood samples were collected from wing vein using syringe. Giemsa stained thin and thick blood smears were prepared to identify haemoparasites using morphological identification keys. Results showed that all 78 chickens (100%) were infested with haemoparasites. *Leucocytozoon schoutedeni* was the only species detected both as a single infection and in mixed infections, while other species were observed only in mixed infections. The highest infection prevalence of *L. schoutedeni* were recorded in KZN (17.9%) compared to EC (2.6%). Furthermore, mixed infections between two or more haemoparasites were observed in chickens from both provinces. These included double infection of *Plasmodium* spp., and *L. schoutedeni* with a prevalence of 56.4 % in chickens in KZN and 41.0 % in EC. Triple infections with *Plasmodium* spp., *Haemoproteus* spp., and *L. schoutedeni* with a prevalence of 28.2% and 17.9% were documented in free-range chickens from EC and KZN. The lowest prevalence of infection was recorded in chickens infested with a triple infection of *Plasmodium* spp., *L. schoutedeni* and *Trypanosoma avium* in KZN (2.6%). Interestingly, quadruple infections with *Plasmodium* spp., *Haemoproteus* spp., *L. schoutedeni* and *T. avium* were documented with a prevalence of 10.3% and 5.1% in chickens from EC and KZN respectively. The occurrence of these mixed infections may be attributed to the environmental conditions that prompted their survival and occurrence of their vectors in the localities which these chickens were roaming. The study results contribute significant knowledge on the distribution of these haemoparasites species in South Africa, which could be useful in developing effective haemoparasites control measures in South Africa.

23 - Molecular characterization of *Taenia* species infecting domestic animals collected from different abattoirs in Zimbabwe

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Taenia species have a significant effect on both humans and animals. Taeniasis is an important zoonotic disease caused by various *Taenia* species which reside in the intestines of their definitive hosts. In addition, cysticercosis, also caused by the same parasites in intermediate hosts, results in considerable economic losses due to impacts on livestock and the condemnation of carcasses at abattoirs. This study aimed to determine the genetic characterisation and diversity of *Taenia* species from different localities in Zimbabwe. A total of 34 cysts were collected from the muscles of pigs and cattle during routine inspections at abattoirs in Kwekwe and Bulawayo. These comprise 30 isolates from pigs and 4 from cattle. DNA was extracted from all isolates, and 18S PCR amplification was performed. Molecular identification of the cysts was carried out through sequencing the 18S genes, and two species were positively identified. All isolates from pigs except one were identified as *Taenia solium*, and those from cattle were identified as *Taenia saginata*. One isolate from pigs was identified as *Taenia saginata*, which may represent an accidental infection. Phylogenetic analysis of isolates in this study with other isolates from different regions across the world clustered them into two major clades, showing species separation. Most of the *Taenia solium* isolates from this study formed their own clade, whilst *Taenia saginata* isolates formed a separate clade and clustered closely with a *Taenia asiatica*, a human isolate from China. These results highlight the importance of conducting a comparative genetic diversity study of these parasites, as there is limited molecular data currently available. This could also improve our understanding of nature and significance of intra-specific variation within *Taenia* species of medical and veterinary importance.

27 - Parasite diversity of *Oreochromis mossambicus* and *Clarias gariepinus* in the water bodies within the Mankweng rural area, Limpopo Province

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Understanding the parasite composition of indigenous fish species is crucial for assessing ecosystem health, as the information gathered can serve as a baseline for conserving diverse biota. Mozambique tilapia, *Oreochromis mossambicus* Peters, 1852 (Cichlidae), and *Clarias gariepinus* (Burchell, 1822), the sharp-tooth catfish (Clariidae), are native to South Africa and have been studied as parasite hosts from fish mainly sampled from large reservoirs. As a consequence, the parasite composition of *O. mossambicus* (n = 37) and *C. gariepinus* (n = 14) was determined from specimens sampled from four sites in the Mankweng area, that is, the neighbourhood to the campus of the University of Limpopo. Standard methodologies for fish handling, fish euthanasia, and parasite collection were followed. From the data collected, epidemiological indices, i.e., prevalence (P), intensity of infection (IF), and mean intensity (MI), were calculated. A total of 478 parasites representing five species and 74 parasites comprising 11 species were collected and identified from *O. mossambicus* and *C. gariepinus*, respectively, and included one and two new species of monopisthocotylans, respectively. In *O. mossambicus*, the most prevalent and abundant parasites were the metacercariae, *Neogryporhynchus lasiopeus* (P = 100%, IF = 2–63, MI = 24.6), followed by metacercariae of the genus *Neodiplostomum* sp. (P = 53.3%, IF = 3–11, MI = 6.6). From *C. gariepinus*, Monopisthocotyla *Quadriacanthus* spp., and *Gyrodactylus* spp. were the most abundant parasites, having a P = 57%, IF = 2–14, and MI = 8.13, followed by nematodes with a P = 14.29%, IF = 1, MI = 1, and MA = 0.143 recorded. The parasite's diversity reflects the ecological conditions of the localities sampled.

The study was supported by DSTI-NRF SARChI Chair (No.101054).

32 - Prevalence of serum antibodies of tick-borne diseases and the presence of *Rhipicephalus microplus* in communal grazing cattle in the north-eastern region of the Eastern Cape Province of South Africa

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In Africa, the impact of ticks is ranked high, and they transmit diseases such as cowdriosis, anaplasmosis, bovine babesiosis and theileriosis. A survey to determine the prevalence of tick-borne diseases (TBDs) and ticks infesting cattle was conducted in the communal areas of the north-eastern region of the Eastern Cape Province (ECP). Tick counts, packed cell volume (PCV), body condition scores (BCS), and serological test for TBDs were seasonally conducted in communally grazed cattle (n = 240) in Joe Gqabi district in two local municipalities (Elundini and Senqu). A standard indirect fluorescent antibody test (IFAT) was used to determine antibodies to *Babesia bigemina*, *Babesia bovis*, and *Ehrlichia ruminantium* and indirect enzyme-linked immunosorbent assay (ELISA) was employed for antibodies to *Anaplasma marginale* detection. The highest tick loads were observed on cattle during the hot-wet and post-rainy seasons and lowest during the cool-dry season. The *E. ruminantium* prevalence in Elundini was 16% and 14% in post-rainy and hot-dry seasons respectively and 15% at Senqu during the post-rainy season. *Babesia bigemina* prevalence was highest at Elundini (18%) and Senqu (16%) during the post-rainy season and hot-wet season respectively. Cattle BCS was negatively correlated with *E. ruminantium* ($P < 0.01$; $r = -0.203$), *B. bovis* ($P < 0.01$; $r = -0.125$), and *A. marginale* ($P < 0.01$; $r = -0.122$) seroprevalence. The PCV was negatively correlated with *B. bigemina* ($P < 0.01$; $r = -0.138$) seroprevalence. On the other hand, *E. ruminantium* was positively correlated with *Amblyomma hebraeum* ($P < 0.05$; $r = 0.112$) infestation, while *B. bovis* ($P < 0.05$; $r = 0.134$) and *B. bigemina* ($P < 0.05$; $r = 0.188$) were positively correlated with *Rhipicephalus microplus* infestation, and *B. bigemina* ($P < 0.05$; $r = 0.077$) was positively correlated with *Rhipicephalus decoloratus* infestation. Our study reports for the first time the presence of *R. microplus* in the study area. Further research is, however, needed to better understand seroprevalence and the transmission mode of TBDs to cattle so that effective disease control measures can be developed.

33 - Hidden *Rickettsia* diversity at the human-animal-environment interface in rural Mpumalanga

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Tick-borne rickettsioses caused by bacteria of the genus *Rickettsia* are emerging zoonotic infections of growing public health importance worldwide. In South Africa, several *Rickettsia* species have been associated with tick vectors and human disease; however, the diversity and circulation of these pathogens within rural communities remain poorly understood. Ticks feeding on wild; domestic and peri-domestic animals as well as humans may play an important role in maintaining and transmitting *Rickettsia* species at the human-wildlife–livestock interface. Despite the presence of competent tick vectors in rural areas of the Mpumalanga Province, limited molecular characterisation has been conducted on circulating *Rickettsia* species. This study aims to screen and molecularly characterise *Rickettsia* species in ticks collected from cattle and dogs, as well as blood collected from rodents and humans from a rural community in Mpumalanga, South Africa, to better understand pathogen diversity and prevalence. DNA from these samples was screened for the presence of rickettsia using a real-time PCR assay targeting the *gltA* gene region. Previously identified positive samples, based on 16S microbiome sequencing) were re-analysed, focusing specifically on *Rickettsia* genus reads. A cycle threshold (Ct) cut-off of 35 was applied to define positivity. Samples that tested negative by qPCR despite prior 16S detection showed a strong correlation with a low proportion of *Rickettsia* reads in the microbiome dataset. Among 21 previously positive dog tick samples, all were qPCR-positive, with 17 showing strong *gltA* amplification and 5 exhibiting non-specific *gltA* amplification. Screening of an additional 676 dog tick samples yielded 263 positives (Ct<35), while 415 samples had CT values above the positivity threshold. Of 40 previously positive cattle tick samples, 31 were positive (Ct<35), while 16 yielded CT values above 35. Preliminary Sanger sequencing of selected dog tick samples (Ct<30) was analysed using BLAST for tentative species identification. This indicated 9 sequences matching

Rickettsia africae and 1 matching *Rickettsia conorii*. One sequence could not be conclusively resolved between *Rickettsia sibirica* and *Rickettsia barbariae* due to identical reference gene regions. Further characterisation using additional gene targets (*ompA* and *ompB*) is underway to improve species-level resolution.

34 - Assessment of parasite diversity in fish species occurring in selected dams around Gauteng and North West provinces of South Africa

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Freshwater ecosystems in South Africa are increasingly threatened by biological stressors, including parasite fauna, which compromise fish health through impaired growth, reduced fitness, behavioural alterations, and associated economic impacts [1]. This study adopted a two-pronged approach and was conducted across three major impoundments in the Gauteng and North-West provinces: Hartbeespoort, Roodekoppies, and Roodeplaas Dams. A questionnaire survey was administered to local fishermen to evaluate their knowledge, attitudes, and practices regarding fish parasites. Additionally, freshly caught fish were randomly purchased from fishermen at the study sites on a seasonal basis to assess variations in parasite diversity. Parasites were first morphologically identified and then confirmed by Polymerase Chain Reaction targeting the 18S rRNA gene (protozoa), cytochrome c oxidase subunit I (COI) gene (arthropods), and internal transcribed spacer (ITS) regions (helminths). The survey respondent demographic (N = 106) comprised 16% females and 84% males. Approximately 95% of the fishermen reported no knowledge of fish parasites, and 85% indicated that they do not clean fish immediately after capture and before selling. Furthermore, all respondents (100%) were unaware of zoonotic parasites associated with freshwater fish. A total of N = 92 fish were obtained across all dams over four seasons, comprising *Clarias gariepinus* (n = 21/92; 23%) and *Cyprinus carpio* (n = 71/92; 77%). Overall, n = 29 (32%) of the fish were infected, including 5 *C. gariepinus* and 24 *Cy. carpio*. Among *C. gariepinus*, the parasites identified included *Contracaecum* spp. (14%), *Dactylogyrus* spp. (5%), and *Proteocephalus* spp. (5%). In contrast, *Cy. carpio* was infected with *Argulus japonicus* (21%), *Atractolytcestus huronensis* (4%), *Dactylogyrus* spp. (7%), and *Cryptosporidium* spp. (1%). The occurrence of *Contracaecum* and *Cryptosporidium* spp. highlights potential public health concerns, given their zoonotic significance and association with waterborne transmission. These findings contribute to a broader understanding of parasite diversity in South African freshwater systems, with important implications for biodiversity conservation, aquaculture management, and disease surveillance.

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37 - Gut microbes of *Stomoxys* flies from different ecological settings northeastern KwaZulu-Natal province, South Africa

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Stomoxys flies (Diptera: Muscidae) are significant parasitic hematophagous insects that act as mechanical vectors for a wide range of pathogens affecting both humans and livestock globally. These flies maintain a complex relationship with gut microbes that is essential for their survival, development, and role as disease vectors. The current study utilised high-throughput sequencing of the 16S rRNA gene to profile gut microbiota associated with different *Stomoxys* species namely: *S. calcitrans*, *S. niger niger*, *S. niger bilineatus*, *S. sitiens*, *S. taeniatus* and *S. boueti*. collected from different land use (communal, commercial and protect land) settings in northeastern KwaZulu-Natal Province, South Africa. From analysed 31 fly DNA samples, a total of 704 OTUs were generated representing microbial diversity of medical and veterinary significance as well as those of symbiotic and parasitic association. The results identified six dominant genera that were shared from *Stomoxys* flies across all locations which included namely: *Escherichia-Sigella*, *Acinetobacter*, *Pseudomonas*, *Enterobacter*, *Staphylococcus* and *Streptococcus*. This study contributes to the limited knowledge on microbiota associated with different species of *Stomoxys* flies from different ecological settings and provides data that will be useful in symbiont-based strategies to control and reduce the spread of vectors and vector-borne diseases.

39 - Hidden germ of the University of Limpopo: *Cichlidogyrus* spp. (Monopisthocotyla: Dactylogyridae) from *Oreochromis mossambicus* (Peters) in the artificial pond on the Turfloop campus

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Mozambique tilapia, *Oreochromis mossambicus* (Peters) (Cichlidae), occurs naturally in Southern Africa, including the Limpopo River basin. Due to its widespread presence in various water bodies, it has become a popular model for ecological and ecotoxicological studies. As an object of interest, 58 parasitic species across eight parasitic groups have been recorded on *O. mossambicus*, including 10 species from four monopisthocotylan genera. Those of *Cichlidogyrus* Paperna, 1960 are *C. dossoui* Douëllou, 1993, *C. sclerosus* Paperna & Thurston, 1969, and *C. tilapiae* Paperna, 1960. In April 2025, five specimens of *O. mossambicus* (TL = 13.8–17 cm) were collected from an artificial pond on the Turfloop campus of the University of Limpopo. Examination of the gills revealed infection with monopisthocotylans of the family Dactylogyridae. An integrated approach combining morphometrical evaluation of the haptor hard parts and male copulatory organs, along with sequencing of two rDNA fragments (28S and 18S+ITS), confirmed the presence of two *Cichlidogyrus* species. *Cichlidogyrus sclerosus*, with a prevalence (P) of 100%, intensity of infection (IF) of 3–21, and mean intensity (MI) of 12.2, dominated the infection, while *Cichlidogyrus* sp. (*halli*-like type) was recorded in fewer numbers (P = 40%, IF = 1–2, MI = 1.5). The newly generated molecular data of *C. sclerosus* supported its identity, with the 18S+ITS1 rDNA sequence found to be identical with the five entries available in the database. An identical hit was identified for *Cichlidogyrus* sp. using BLAST, corresponding to an unidentified *Cichlidogyrus* species from *Oreochromis niloticus* L. sampled in Zimbabwe. The species represents a new species to science, as it differs substantially in the genetic data from *Cichlidogyrus halli* (Price & Kirk, 1967), with a divergence of 2.1–2.4% in 18S+ITS1 rDNA (14–16 bp) and 1.8–2.1% in 28S rDNA (14–16 bp). The present study confirms the importance of applying an integrated approach to taxonomy and shows that even well-studied host fish can yield exciting findings.

The study was supported by the DSTI-NRF SARCHI Chair (No. 101054). The WRG at North-West University is acknowledged for granting access to the molecular laboratory.

50 - Molecular Characterization of *Echinococcus granulosus* of Cattle from the Matebeleland Region, Zimbabwe

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Cystic Echinococcosis (CE) caused by *Echinococcus granulosus* sensu lato (s.l.) is a neglected helminth zoonosis affecting humans and various animal species. CE has been reported in almost all countries of sub-Saharan Africa but its prevalence and public health impact is subject to large geographical variations. The reasons for these differences are not well understood. Occurrence of different species/genotypes of *E. granulosus* s.l. has been suggested. CE is very common in all livestock species in Sub-Saharan Africa, though it is poorly documented in Zimbabwe. The aim of this study was to molecularly characterize hydatid cysts collected from cattle at the Cold Storage Company (CSC) Ltd in Bulawayo, Zimbabwe. A total of 15 hydatid cysts were collected from cattle that were slaughtered on different days. DNA extraction from all the 15 samples was successfully carried out using a kit after which 18S rDNA was amplified using PCR producing a 603bp fragment. A restriction digest was performed on the amplified fragment using the enzymes *Bam*H1, *Eco*R1 and *Hinf*1. The results of the restriction digest showed that one isolate was different from the other isolates. However, the 18S fragments were sequenced and chromatograms obtained were manually edited and analysed using the Basic Local Alignment Search Tool (BLAST). The species identified were mostly *E.canadensis* (5), *E. ortleppi* (2) and another species, which is 96% identical to *E.canadensis* (1), making it an unknown strain. The results obtained show the importance of cattle in the transmission of *E. canadensis*, the “camel strain”. The current study showed the presence of *E.canadensis* and *E.ortleppi* cysts in cattle of Zimbabwe. The presence of these strains and especially the fact that the zoonotic *E.granulosus* is dominant, make CE an important public health concern in Zimbabwe.

51 - Communal sheep farmer's knowledge and attitudes on the incidence of gastrointestinal parasites in the Eastern Cape, South Africa

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In many African countries, agriculture plays an essential economic role in improving many livelihoods and understanding specific limiting factors for emerging farmers is vital in the development of their agricultural activities. This study aimed to investigate communal sheep farmer's knowledge and attitudes toward Gastro-Intestinal Parasites (GIPs) in the Eastern Cape Province, South Africa. A cross-sectional survey was conducted between September and November 2018 from three agro-ecological zones, namely, arid region, semi-humid, and humid. Of the total of 107 farmers who participated in the study, 69% were males, and 38% were females. Most livestock owners (85%) were aged >46 years old across all the study areas. Most farmers (83%) perceived that their animals are susceptible to wireworm (*H. contortus*) during the hot-wet season, followed by the hot-dry season (14%), with relatively low

during the cold season (2%). Most farmers (85%) interviewed revealed that lambs are more exposed to parasitic infection, than mature sheep (15%) across all agro-ecological zones. An insignificant number of farmers (8%) with knowledge about GIPs life cycle and its biology (92%) across all agro-ecological zones. This study reveals a significant increase in the occurrence of GIPs over the past few years across all agro-ecological, with largely (67%) attributed to the resistance of the strain to deworming remedies and changes in climatic weather patterns (33%). The farming experience was strongly ($p < 0.05$) associated with the farmer's gender and age. Helminths were reported significantly higher ($p < 0.05$) in humid zones than in other agro-ecological zones. This study concludes that most farmers perceived lambs as more susceptible to GIPs than old sheep.

54 - First insights into the parasite diversity of the critically endangered cichlid *Chetia brevis* from the Mlumati River, Eswatini

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Freshwater fish parasites are important indicators of ecosystem health and biodiversity, yet parasite communities of many threatened fish species in southern Africa remain poorly documented. This study presents preliminary observations on the parasite diversity of the critically endangered, orange-fringed large-mouth river bream *Chetia brevis* from the Mlumati River at the Matsamo weir, Eswatini. Due to conservation constraints and low encounter rates, only three specimens were available for parasitological examination; results are therefore exploratory and baseline in nature. Standard parasitological techniques included external examination, gill dissection, and internal organ inspection under stereomicroscopy. Recovered parasites were isolated, fixed, and identified morphologically to the lowest possible taxonomic level. Four parasite groups were recorded. A monogenean, *Enterogyrus* sp., was recovered from the stomach of one specimen, consistent with the gastrointestinal association of this group in cichlids. Digenean larval stages were present in all specimens, occurring as encysted forms within black pigmented cysts in the skin and fins, as well as in the body cavity and gill arches. Although not identifiable to species level, these larvae will be subjected to molecular analysis to resolve their identity and clarify transmission pathways. Their presence indicates active transmission of complex digenean life cycles and suggests that *C. brevis* functions as an intermediate or transport host. Nematode larvae, *Contracaecum* sp., was found in the body cavity and stomach wall. An ergasilid copepod, *Neoergasilus japonicus*, was recorded from the gills of one fish. This represents the first record of this species in Eswatini and confirms its spread beyond its native range into southern African freshwater systems. Given the limited sample size, findings remain preliminary. However, they highlight a conservation concern: parasite diversity is linked to host persistence, and the critically endangered status of *C. brevis* may imply parallel risks of parasite loss (co-extinction), except for opportunistic or invasive taxa that may increase under altered ecological conditions. Expanded surveys across seasons and sites are required to better understand parasite diversity, transmission dynamics, and conservation implications for this host.

POSTER SESSION 2, 01 September 2026

58 - An overview of foot and mouth disease in the Eastern Cape Province: The invisible danger to animal trade and national growth Eastern Cape Province, South Africa

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Foot-and-mouth disease virus commonly known as (FMDV) is one of the limited veterinary pathogens that distinguishes guidelines and international export in animal products. Its prominence forces methods to control that incorporate numerous causes is contributing to the disease's biology and spread characteristics. This study presents an integrated overview of FMDV of livestock production associated with communal and commercial farming systems in six district municipalities (DMs) of the Eastern Cape Province. There is no control of FMDV in communal and commercial farming systems of the Eastern Cape Province. A sampling of six districts with vigorous weekly surveillance and testing followed by of vaccination of positive farms. Confirmed positive farms were quarantined and vaccinated. During the FMDV outbreak in 2024 at least 97% of farms in Sarah Baartman district (SBD) was infect with FMDV and 3% of farms in Amathole district (AD) was also confirmed. In 2025 due to uncontrolled animal movement the FMDV managed to spread across the province to other four districts. The distribution was recorded as follows: 45 % farms from (AD), followed by Alfred Nzo (AND) with 41 %, Chris Hani (CHD) with 6 %, Joe Gqabi (JGD) had 4 %, SBD with 3 % and the OR Tambo (ORTD) was having the least infections with 1%. The control measures through vaccinations around the province was a need to slow the spread of the FMDV. About 85 542 and 20 070 animals were vaccinated by government veterinarians and private veterinarians, respectively. The highest numbers were from AND and CHD at 65 % and 19 % respectively. Other districts recorded small numbers of animal vaccinations by government. AMD was leading with 7 % followed by JGD with 5 %. The least numbers of animals vaccinated were in ORTD and SBD with 3 % and 2 % respectively. This study demonstrates that unreliable monitoring, inefficient implementation of control policies and unrestricted movement of cattle across the Eastern Cape, other provinces and ultimately the international borders are all factors that contribute to the persistence of the disease in Eastern Cape.

59 - Host-associated patterns of ectoparasite infestation in sympatric *Rattus rattus* and *Rattus tanezumi* in rural communities, Mpumalanga Province, South Africa

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Rodents of the genus *Rattus* are important reservoirs of ectoparasites of medical and veterinary significance. This is particularly relevant in rural landscapes where close proximity between rodents, livestock and humans may facilitate parasite transmission. This study investigated ectoparasite infestations associated with two commensal rat species, *Rattus rattus* and *Rattus tanezumi*, in rural communities in Mpumalanga Province, South Africa. Rodents were captured as part of a broader surveillance project conducted between 2014 and 2022. Each animal was examined for ectoparasites (ticks, lice, mites and fleas), which were collected and enumerated. Capture sites were classified as village (inside and around houses) or grazing (areas where crops are cultivated) habitats to assess potential differences in the distribution of *Rattus rattus* and *Rattus tanezumi* between habitat types. A total of 126 rodents were examined, comprising 67 *R. rattus* and 59 *R. tanezumi*. Both species were primarily associated with village habitats, with only a few individuals recorded in grazing areas. In total, 1,234 ectoparasites were recovered, comprising 32 ticks, 605 lice, 264 mites and 333 fleas. Lice represented the dominant ectoparasite group overall, followed by fleas and mites, while ticks were rare across both host species. Clear host-associated patterns in ectoparasite assemblages were observed. Lice occurred more abundantly on *R. rattus*, including several high-intensity infestations, whereas mites were more frequently associated with *R. tanezumi*. Fleas were shared between both host species, although higher infestation peaks were occasionally recorded in *R. rattus*, while ticks showed no apparent host specificity. These patterns suggest partial partitioning of ectoparasite communities between sympatric *Rattus* species, likely reflecting differences in host ecology, behaviour and microhabitat use. Mean abundance of each ectoparasite group was compared between host species and habitat types to further evaluate ecological drivers of infestation. Overall, the findings highlight the role of commensal *Rattus* species as important hosts of diverse ectoparasite communities in rural South African environments and underscore their potential relevance in the maintenance and transmission of parasites of veterinary and public health importance.

60 - Assessing ecosystem health in Loskop Dam using fish health and parasite diversity of *Oreochromis mossambicus*

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The Mozambique tilapia (*Oreochromis mossambicus*) is a native fish species recently classified as vulnerable on the IUCN Red List, primarily due to anthropogenic pressures and hybridisation with invasive species. Despite its physiological resilience, this species is sensitive to environmental changes, making it an effective bioindicator for assessing aquatic ecosystem health and human impacts. The aim of this study was to evaluate the health and parasite diversity of *O. mossambicus* as indicators of ecosystem health and to correlate them with the water quality of Loskop Dam, Mpumalanga, South Africa. Water samples were collected from two localities within the dam (the river inflow and the dam wall) and analysed for nutrients and selected metals. Ten fish specimens were collected per locality using gill nets. The Health Assessment Index (HAI) was applied to evaluate fish condition, while parasitological examinations assessed parasite diversity and intensity. Fish from the river inflow site were generally larger but showed signs of poorer health, including higher incidences of pansteatitis (yellow fat disease), compared to those from the dam wall. Ectoparasites identified included the monogenean *Cichlidogyrus halli* and the branchiuran *Argulus japonicus*, while endoparasites included *Contracaecum* larvae and gryporhynchid cestode larvae. Notably, parasite intensity was higher in fish from the dam wall site. Water quality analysis revealed elevated nitrate levels (0.6 mg/L) at the inflow compared to the dam wall (0.1 mg/L), reflecting upstream anthropogenic pollution from the Olifants River catchment. As water moves through the dam, dilution and sedimentation help reduce contaminant levels, contributing to observed differences in fish health and parasite burden. These findings highlight the usefulness of *O. mossambicus* as a biological indicator and demonstrate the interconnectedness of water quality, fish health, and parasite diversity. Ongoing monitoring of systems such as the Loskop Dam is vital for aquatic conservation and water resource management.

61 - Exploring the microbial communities of *Rhipicephalus* tick species parasitizing domestic animals in South Africa

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Tick infestation and tick-borne diseases are a major concern for domestic animal health. The aim of this study was to document microbiota of veterinary important *Rhipicephalus* tick species collected from domestic animals including cattle, sheep, goats, horses, dogs and the vegetation in comparison to colony reared ticks using 16S rRNA metabarcoding on the Illumina MiSeq platform. Field-derived ticks were identified as *Rhipicephalus evertsi evertsi*, *R. appendiculatus* and *R. sanguineus*, whilst colony reared ticks included *R. e. evertsi*, *R. appendiculatus*, *R. decoloratus* and *R. microplus*. A total of 689 ASV amplicon sequence variants (ASVs) were generated. These were composed of 27 bacterial phyla; 64 classes; 145 bacterial orders, 234 bacterial families and 580 bacterial genera. The dominant phyla included Proteobacteria (30.8%), Firmicutes (18.3%), Actinobacteria (14.9%) and Bacteroidetes (13.8%). The remaining 23 phyla in this study contributed to 22.2% of the overall ASV sequences and each were in low abundance. Amongst the detected microbiota, 580 genera were detected. These comprised of genera that are known to contain pathogenic species. Genera known to contain potential tick-borne zoonotic pathogens (TBZ) detected included *Rickettsiae*, *Coxiella*, *Francisella*, *Ehrlichia* and *Anaplasma*. This study further identified genera known to contain commensal/symbionts from the environment, these included *Coxiella*, *Francisella*, *Rickettsiae*, *Proteus*, *Aerococcus*, *Micrococcus*, *Cloacibacterium*, *Rhodococcus* and *Fusobacterium*. Other potential pathogenic genera detected include *Escherichia-shigella*, *Staphylococcus*, *Pseudomonas*, *Streptococcus*, *Campylobacter* and *Clostridium-Sensu_stricto_1*. The tick microbiota data generated in this study provides baseline knowledge of the microbiome of *Rhipicephalus* tick species infesting domestic animals in South Africa.

64 - Monopisthocotylan diversity of threatened Anabantidae and Cyprinidae, and an invasive cichlid, from the Cape Fold Ecoregion

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To understand South Africa's aquatic biodiversity, there has been an increased effort for the inclusion of less well-known taxonomic groups. Previously, the very diverse and ecologically significant freshwater fish parasites have been neglected and unrecognised in biodiversity studies. However, growing efforts to understand this component of aquatic biodiversity, their contribution to ecosystems and how they can subsequently be incorporated into evidence-based conservation and management planning, prompted the focus on characterising parasitic communities of endangered and threatened freshwater fishes in South Africa. During parasitological surveys in July-August 2025, individuals of the endangered *Pseudobarbus vulneratus* (n = 22) (Cyprinidae) and data-deficient *Sandelia capensis* (n = 9) (Anabantidae) from the Eerste River, Stellenbosch, Western Cape, and the critically endangered *Pseudobarbus burchelli* (n = 25) and invasive *Tilapia sparrmanii* (n = 6) (Cichlidae) from the Huis River, Barrydale, Western Cape, were screened for metazoan parasites. The fish parasitic communities from

the Eerste River and Huis River were represented by species of the Monopisthocotyla (Dactylogyridae and Gyrodactylidae), Cestoda, Digenea (Diplostomidae and Sanguinicolidae), and Nematoda. Here, the findings on the Monopisthocotyla are presented, where identification to the lowest taxonomic level was done by combining morphometrics, morphology and molecular inferences with congeners using the 18S rDNA, 28S rDNA, ITS1-5.8S-ITS2 and COI mtDNA gene regions. *Pseudobarbus vulneratus* and *S. capensis* from the Eerste River were parasitised with *Gyrodactylus* sp. 1 [Prevalence (P) = 50%, Intensity of Infection (IF) 1–7] and *Gyrodactylus* sp. 2 (P = 89%, IF 1–8) on the fins and gills, respectively. *Pseudobarbus burchelli* from the Huis River was parasitised with *Dactylogyrus* sp. 1 (P = 60%, IF 1–12) on the gills and *Gyrodactylus* sp. 3 (P = 80%, IF 2–43) on the fins, while *Cichlidogyrus* sp. 1 (P = 67%, IF 1–2) and *Enterogyrus* sp. 1 (P = 100%, IF 3–13) were respectively found on the gills and in the intestine of the invasive *T. sparrmanii*. Documenting the parasitic diversity associated with threatened freshwater fish species helps fill critical biodiversity knowledge gaps and provides a foundation for integrating parasite data into conservation planning for South Africa's threatened freshwater ecosystems.

65 - Who lives inside the parasite? A first look at the microbiome of the temporary fish parasitic isopod *Gnathia pantherina* (Isopoda: Gnathiidae)

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Gnathiid isopods are obligate blood-feeding temporary ectoparasites of marine fishes and keystone species in coastal ecosystems. Despite their ecological importance and recognised role as vectors of fish haemogregarines, nothing is currently known about gnathiid microbiota. This is a significant gap in our understanding of parasite-associated microbial communities in South African marine systems. Establishing a reliable extraction protocol is therefore a critical first step. This preliminary study, embedded within a larger National Research Foundation (NRF)-funded project on the endosymbionts of parasitic isopods and leeches, evaluates specimen-preparation methods for whole-body microbiome extraction from the larval form of *Gnathia pantherina* Smit & Basson, 2002. Zuphea (unfed larvae) and praniza (fed larvae) collected from elasmobranchs at Boknesstrand were subjected to a range of preservation and surface-washing approaches, including freezing, chemical fixation, and treatment with ethanol, sodium hypochlorite, and Tween 20. DNA was extracted, followed by 16S rRNA amplicon sequencing, to characterise the internal microbial communities. Scanning electron microscopy confirmed decontamination efficacy across treatments, with sodium hypochlorite and Tween 20 yielding the most effective surface decontamination while preserving sufficient internal DNA for downstream analyses. Sequencing revealed low-diversity microbiomes in both larval stages, with Vibrionaceae among the dominant taxa recovered, consistent with patterns reported for cymothoid isopods. Microbial community composition differed markedly between zuphea and praniza, suggesting stage-specific dynamics associated with blood-meal acquisition. These results establish a reproducible methodological foundation for comparative microbiome studies across gnathiid developmental stages and host species. These findings open a new frontier in our understanding of microbial symbioses in marine blood-feeding crustaceans and will inform future comparative investigations into how microbiome composition shifts across host species and life stages in South African coastal ecosystems.

66 - Repurposing Drugs as Acetylcholinesterase Inhibitors Against the Malaria Vector *Anopheles*: An Integrated In Vitro and In Silico Study

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Malaria remains a major global health challenge, with vector control serving as a cornerstone of disease prevention. Insecticides targeting acetylcholinesterase (AChE) in *Anopheles* mosquitoes are widely used; however, the emergence of insecticide resistance necessitates the identification of novel chemical scaffolds. Repurposing existing compounds offers a cost-effective strategy for accelerating insecticide discovery. This study aimed to identify and evaluate repurposed therapeutic agents as potential inhibitors of *Anopheles* AChE through an integrated *in vitro* and *in silico* screening approach. A library of 62 therapeutically used drugs and compounds from the Wits Pharmacology Division Compound Library was screened at 5 μ M for inhibition of *Anopheles* AChE using a standardised Ellman's assay. The library comprised a diverse collection of compounds, including antiparasitic, antifungal, antibacterial, antioxidant, metal-chelating, and benzimidazole-derived agents, as well as several miscellaneous therapeutics. Molecular docking was employed to characterise ligand-enzyme interactions using Schrödinger Maestro (2023-2, version 13.6.122), while *in silico* analyses assessed pharmacokinetic properties, mammalian toxicity, and predicted environmental impact. Propoxur, the positive control, demonstrated strong AChE inhibition ($77.12 \pm 1.86\%$) but was associated with high predicted human toxicity. Several compounds displayed promising inhibitory activity with improved selectivity profiles. Among these, quinine demonstrated low inhibition of *Anopheles* AChE ($27.05 \pm 4.64\%$), while pyrazinecarboxamide achieved moderate inhibition ($37.26 \pm 2.83\%$) with favourable safety characteristics. Camptothecin exhibited comparable inhibition ($37.11 \pm 2.13\%$) but was predicted to have greater mammalian toxicity. Notably, butylated hydroxyanisole emerged as the most promising candidate, demonstrating moderate inhibition ($45.00 \pm 0.52\%$), selectivity towards *Anopheles* AChE, and a favourable mammalian safety profile. Docking analyses identified Tyr282, Tyr493, Tyr494, His600, and Ser360 as key residues contributing to ligand stabilisation within *Anopheles* AChE. The findings highlight that successful insecticide repurposing requires balancing enzyme inhibition with environmental and non-target organism safety. Several chemical scaffolds, including pyrazines, pyrans, indolizines, benzimidazoles, and quinolines, represent promising starting points for lead optimisation and may contribute to the development of next-generation vector control agents to support sustainable malaria control and resistance management. Collectively, these findings demonstrate how integrated experimental and computational approaches can accelerate the discovery of novel insecticidal leads for malaria vector control.

67 - An Integrated Computational and Experimental Framework for Investigating Atovaquone Resistance and Discovering Novel Antimalarial Leads

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Atovaquone is an antimalarial agent targeting the mitochondrial cytochrome *bc1* complex of *Plasmodium falciparum*. However, the emergence of resistance-associated mutations within the target protein threatens its clinical effectiveness. A deeper understanding of the structural determinants of resistance and the identification of compounds capable of maintaining activity against resistant variants are essential for the development of improved antimalarial therapies.

This study aimed to establish a comprehensive knowledge base of cytochrome *bc1* inhibitors, investigate molecular basis of atovaquone-resistance through computational modelling, evaluate a

series of naphthoquinone-triazole hybrids compounds using integrated experimental and *in silico* approaches, and apply these insights to the rational designing of chalcone compounds with potential to overcome resistance. A database of 616 unique compounds reported in the literature against the cytochrome *bc1* complex was developed, incorporating structural and biological activity data. Structure-based computational models representing both atovaquone-sensitive and resistant forms of the target were generated to examine ligand binding modes and resistance-associated changes within the binding pocket. Novel hybrid compounds were evaluated through a combination of laboratory-based antimalarial testing and molecular modelling studies, including docking and interaction analyses. Building on the mechanistic insights obtained, additional chalcone compounds were rationally designed and assessed computationally for their ability to interact favourably with the resistant target model. Analysis of the curated database revealed that only 135 of the 616 collated inhibitors demonstrated activity against resistant strains, with quinolones emerging as the most potent and extensively studied scaffold. Comparative modelling identified resistance-associated alterations in ligand binding, providing insights into reduced atovaquone efficacy. Two naphthoquinone-triazole hybrid compounds were identified with promising antimalarial activity and favourable binding characteristics. Furthermore, structure-guided ligand design led to the identification of three additional chalcone compounds predicted to retain key interactions within the resistant binding site, suggesting potential strategies to overcome resistance. This work demonstrates the value of combining data curation, molecular modelling, experimental validation, and rational drug design in addressing antimalarial drug resistance, providing a foundation for the continued discovery and optimisation of cytochrome *bc1* inhibitors with the potential to combat atovaquone-resistant malaria.

68 - Evaluation of Phenylhydrazone Quinoline Hybrids as Selective Inhibitors of *Anopheles* Acetylcholinesterase

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Malaria remains a global health challenge, with 282 million cases and over 610,000 deaths reported in 2024. The growing resistance of *Plasmodium* and *Anopheles* to antimalarial drugs and insecticides underscore the urgent need for novel compounds with selective activity. Quinoline scaffolds have historically provided valuable pharmacological agents, therefore fifteen phenylhydrazone quinoline hybrids (PHYD) were designed, synthesized and evaluated for their biological activity, focusing on inhibition of *Anopheles* acetylcholinesterase (AChE), alongside *in silico* pharmacokinetic and toxicological profiling. *In vitro* assays revealed that the PHYD compounds exhibited antimalarial activity towards the NF54 strain of *Plasmodium falciparum* resulting in parasite viability ranging from 20.92% to 79.44% at 50µM. The compounds exhibited poor inhibitory activity towards *Anopheles* larvae (1.6%-10%) and low AChE (inhibition 20.88% to 31.34%). Derivative PHYD-10 (31.34±2.34%) exhibited the most AChE inhibition however this was less potent than propoxur (77.32±2.22%). Molecular docking revealed favourable binding affinities, with scores surpassing that of propoxur. Key interactions included hydrogen bonding and π-π stacking with residues including Tyr282 and Tyr489, indicating that PHYD hybrids may exhibit a multipoint stabilisation mechanism within the AChE catalytic groove. Structural variations at the 7-position (chloro, bromo, fluoro) and differences in phenylhydrazone fluorination patterns influenced binding orientation and strength. Pharmacokinetic predictions indicated that all PHYD compounds cross the blood-brain barrier, a trait desirable for CNS drug development but problematic for insecticidal repurposing due to risks of unwanted neurotoxicity in non-target organisms. Lipophilicity values were higher than propoxur, with PHYD-10 (LogP_{o/w} 3.39) raising concerns about bioaccumulation. Predicted LD₅₀ values were higher than propoxur (PHYD-10: 900mg/kg vs. propoxur: 24mg/kg), suggesting reduced acute human toxicity. However, hepatotoxicity, neurotoxicity, and severe aquatic toxicity remained concerns, with PHYD-10 showing greater toxicity to fish and daphnids than propoxur. Overall, these findings highlight the trade-offs in repurposing quinoline hybrids as insecticides.

While the PHYD series demonstrates selective inhibition of mosquito AChE and reduced human toxicity compared to carbamates, their CNS penetration and environmental liabilities limit immediate applicability. Careful structural optimization is required to balance efficacy, safety, and sustainability in the development of next generation vector control agents.

69 - Assessing community knowledge and preventative practices for *Plasmodium* infections in the Vaal Triangle, Gauteng, South Africa

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Malaria remains a major public health concern in Southern Africa, necessitating robust vector control strategies and community awareness to prevent transmission. In South Africa, particularly in rural communities, traditional phytomedicines derived from indigenous knowledge are widely used for mosquito repellence. However, despite general awareness of malaria, knowledge gaps and misconceptions persist, especially in non-endemic areas such as the Vaal Triangle, Gauteng, South Africa. This study aimed to assess community knowledge, attitudes, and perceptions toward malaria prevention, treatment, and the use of traditional mosquito repellents. Following WITS human ethic clearance approval (M221039), a descriptive cross-sectional study was conducted using a semi-structured questionnaire (n=419) among residents of the Vaal Triangle. The data was analysed using descriptive/inferential statistics analysis (SPSS). Despite high malaria awareness (86.9%), misconceptions about transmission and treatment were prevalent. Most participants (70.2%) believed malaria could spread through contact with an infected person, and 86.9% believed malaria could be managed without medical treatment. Regarding prevention, 89.9% reported using mosquito repellents, though only 48.9% recognised the effectiveness of sleeping under mosquito nets. Traditional medicine was commonly used for malaria prevention. With 49.4% of respondents referencing unnamed remedies, plants species such as Imbiza (*Lippia javanica*/*Cyrtanthus obliquus*) and Umsenge (*Cussonia sphaerocephala*/*C. spicata*), amongst others, were reportedly used in the treatment of malaria infections and/or to control mosquitoes. This study highlights the need for targeted, culturally sensitive educational interventions to correct misconceptions and improve malaria prevention practices. Collaborative integration of traditional knowledge with evidence-based malaria control strategies may strengthen public health interventions.

70 - Global phylogeny of *Gyrodactylus* (Monogenea) revealing origin and diversification of Nearctic species

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The evolutionary history and biogeographic origin of Nearctic *Gyrodactylus* remain poorly understood despite the remarkable diversity of these viviparous monogeneans in North American freshwater fishes. We investigated the phylogeny, historical origin, host-parasite associations, and morphological evolution of attachment organ in Nearctic *Gyrodactylus* at the global level. Freshwater fishes in North America and Europe were sampled for *Gyrodactylus* species. Partial ITS1–ITS2 sequences representing 189 *Gyrodactylus* species and four *Swingleus* species and including *Gyrodactylus* species obtained from field sampling and those retrieved from GenBank were used for the study. Phylogenetic relationships were inferred using Bayesian Inference and Maximum Likelihood approaches, and

ancestral state reconstructions of geographic distribution, host associations, and haptoral morphology were performed in Mesquite. Both BI and ML analyses recovered highly congruent topologies and showed that Nearctic *Gyrodactylus* represents a paraphyletic assemblage. Reconstruction of geographic origin revealed multiple independent evolutionary origins of Nearctic lineages. Nearctic taxa occurred in basal, intermediate, and derived positions throughout the phylogeny. Basal and intermediate Nearctic lineages were interspersed with Western and Eastern Palearctic taxa, suggesting historical biogeographic connections between North American and Eurasian parasite faunas, whereas the terminal portion of the tree contained a well-supported monophyletic Nearctic lineage interpreted as a secondary diversification event within North America. Ancestral host reconstruction revealed Cypriniformes as the principal ancestral host group for *Gyrodactylus*, whereas parasites infecting Cyprinodontiformes formed a more derived and phylogenetically structured assemblage. Other host groups appeared sporadically throughout the phylogeny, indicating repeated host-switching events and possible fish translocations rather than host-associated radiations. Mapping of haptoral traits into phylogeny revealed multiple independent character acquisitions and losses during *Gyrodactylus* history. The morphological characters of haptor, specifically, plate-like ventral bar membrane, ventral bar median knob, and terminal hook filament were restricted mainly to derived Nearctic and Neotropical lineages, suggesting that these diagnostic haptoral features evolved secondarily within derived American taxa rather than representing ancestral states. The study highlights a complex evolutionary history of *Gyrodactylus* shaped by repeated dispersal, historical interchange from Palearctic to Nearctic, host switching, regional diversification, and convergent morphological evolution.

This study was supported by the Ministry of Education, Youth and Sports of the Czech Republic, project no. LUAUS23080.

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