



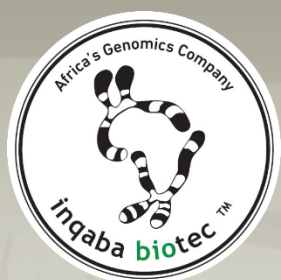
ICPOW2025

5TH INTERNATIONAL CONGRESS ON
PARASITES OF WILDLIFE

&

53RD ANNUAL PARSA CONFERENCE

14-18 SEPTEMBER 2025



PROGRAMME AND ABSTRACTS

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Congress Organising & Scientific Programme Review Committee

Prof. Sonja Matthee, Stellenbosch University, South Africa (Congress Chairperson)

Prof. Kerry Hadfield Malherbe, North-West University, South Africa

Prof. Wilmien Luus-Powell, University of Limpopo, South Africa

Dr Mamohale Chaisi, South African National Biodiversity Institute, South Africa

Dr Maxwell Barson, University of Botswana, Botswana

SAVETCON
EVENT MANAGEMENT

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Limited to no internet access
in the conference venue.
Stronger access at the
Skukuza Lodge Restaurant



MALARIA
AWARENESS



Welcome



Dear Fellow Parasitologists,

It is my great pleasure to welcome you to the 5th International Congress on Parasites of Wildlife (ICPOW) and the 53rd annual congress of the Parasitological Society of Southern Africa (PARSA), that is hosted at the Nombolo Mdhluli Conference Centre in Skukuza, the main congress centre of the world-famous Kruger National Park.

As Chairperson of this important event, I am honoured to host a global gathering of over 130 parasitologists and industry partners who share a commitment to advancing the field of wildlife parasitology. The congress aims to facilitate the exchange of research findings and fruitful engagement between delegates.

More importantly, the congress will act as platform to discuss and develop activities that will ensure capacity building in the field of parasitology in South Africa and Africa.

The 3rd African Parasite Network Meeting will be hosted as part of the ICPOW and this year the meeting will showcase the recently established “African Network” focus-group of the World Association for the Advancement of Veterinary Parasitology (WAAVP-AN). Further highlights include an information session on a global Wildlife Malaria Research Network. Presentations by researchers that have established successful Africa-Africa collaborations will form part of the programme.

Two post-congress workshops will be hosted as part of the congress programme.

I want to take this opportunity to thank the Organising Committee for all their hard work and time with organizing the congress. The organizing team made a huge effort to “pull out all the stops” to make this a truly memorable event.

Last but not least, a big word of thanks to all our partners and sponsors for contributing to the congress.

On behalf of the organizing committee, I extend our warmest welcome and encourage you to actively engage in all aspects of ICPOW2025. May your time at ICPOW2025 be both inspiring and enriching, filled with meaningful scientific dialogue and memorable social connections. We hope you enjoy every moment of your stay in the breathtaking surroundings of The Kruger.

Sincerely,

Prof. Sonja Matthee

ICPOW2025 ORGANISING COMMITTEE



**Prof. Kerry Hadfield
Malherbe**
North-West University,
South Africa



**Prof. Wilmien Luus-
Powell**
University of Limpopo,
South Africa



Dr Mamohale Chaisi
South African National
Biodiversity Institute,
South Africa



Dr Maxwell Barson
University of Botswana,
Botswana

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

Session Chairpersons

- | | |
|-------------------------------|-------------------------|
| 1. Annemarië Avenant-Oldewage | 10. Nico Smit |
| 2. Banie Penzhorn | 11. Nicola Collins |
| 3. Conrad Matthee | 12. Nkululeko Nyangiwe |
| 4. Edward Netherlands | 13. Raksha Bhoora |
| 5. Franck Prugnotte | 14. Russel Yong |
| 6. Kerry Hadfield Malherbe | 15. Susan Dippenaar |
| 7. Luther van der Mescht | 16. Virginie Rougeron |
| 8. Maxwell Barson | 17. Wilmien Luus-Powell |
| 9. Karien Labuschagne | 18. Zamantungwa Mnisi |

The oral and Poster adjudication committee

With appreciation to our partners and sponsors



International Congress on Parasites of Wildlife: A History

Based on the recollections of Professor Jo van As

In 1991 the local Parasitological Society of Southern Africa (PARSA) hosted the first “International Congress on Parasitology of Wildlife” in Kruger National Park. At that time, South Africa was going through political turmoil, and many scientists were isolated and excluded from the international scientific arena. The aim of the meeting was to provide a platform to engage with international scientists. Eighty-three international scientists, from 25 countries, presented 84 orals and numerous posters. Most of these scientists were in some way sponsored by the funds raised by the local organising committee. Professor Leon Fourie (an Elsdon-Dew medal laureate) played a significant role in fund-raising. Delegates started and ended the day with game drives as well as other social gatherings. On one particular evening, there was a spontaneous sing-song event, and many delegates could have been even more famous as singers/entertainers than as scientists (this was way before *Idols*).

During September 2014, PARSA hosted the 2nd International Congress on Parasites of Wildlife, in Kruger National Park. This meeting coincided with the 43rd Annual meeting of PARSA. Almost 150 delegates, from 19 countries (including South Africa), attended the meeting. The programme comprised 83 oral and 37 poster presentations. Kerstin Junker from Onderstepoort Veterinary Institute (South Africa), Serge Morand jointly from Centre Christophe Mérieux (Lao PDR) and CIRAD (France) and Ute Mackenstedt from University of Hohenheim (Germany) gave keynote addresses.

The days again ended with game drives and informal social events. At the 2014 meeting it was decided that PARSA will continue to host an International Congress on Parasitology of Wildlife every three years, with 2017 identified as the year for the 3rd International Congress on Parasites of Wildlife in Kruger National Park.

During the week of 24-27 September 2017 PARSA hosted the 3rd International Congress on Parasites of Wildlife, in Kruger National Park. Attended by more than 170 delegates, the programme consisted of 110 oral presentations and 51 poster presentations. Keynote presentations were delivered by Tom Cribb (University of Queensland), Franck Prugnolle (Infectious Diseases and Vectors: Ecology, Genetics, Evolution and Control Laboratory of the Centre National de la Recherche Scientifique (CNRS) in France) and Vanessa Ezenwa (University of Georgia, USA).

The 4th International Congress on Parasites of Wildlife was scheduled to take place during September of 2020. The congress was however postponed to 2021, and then again to 2022 due to the huge disruptions caused by the global pandemic, COVID-19.



Program Overview

DAY 1 – SUNDAY 14 SEPTEMBER

15h00-17h30	Registration
18h00-19h30	Welcome Reception @ Skukuza Safari Lodget

DAY 2 MONDAY 15 SEPTEMBER	07h30	Registration	
	08h00-09h00	Opening Plenary Session Welcome and Opening – <i>Prof. Sonja Matthee</i> Keynote 1 - Spatiotemporal variation in avian host-parasite communities (<i>Dr Jenny Dunn, Keele University, United Kingdom</i>)	
	09h00-10h00	Session 1.1.1 Special Session: Wildlife Malaria	Session 1.2.1 Aquatic Parasitology
	10h00-10h30	Mid-morning Refreshments & Poster Viewing	
	10h30-11h45	Session 1.1.2 Special Session: Wildlife Malaria and other Haemoparasites	Session 1.2.2 Aquatic Parasitology
	11h45-12h00	Networking and Posters	
	12h00-13h00	Lunch	
	13h00-13h35	Plenary Session 2 Gold Sponsor: Inqaba Biotech Guest Speaker 1 - Wildlife as carriers and transmitters of vectors, pathogens and diseases (<i>Dr Mamohale Chaisi, South African National Biodiversity Institute, South Africa</i>)	
	13h35-14h35	Session 1.1.3 Microbiomes, vectors and the environment	Session 1.2.3 Sand flies, midges and human perceptions
	14h35	End of Sessions	
	14h45-14h55	Cambridge University Press (<i>Prof. Russell Stothard, Liverpool School of Tropical Medicine, United Kingdom</i>)	
	14h55-17h00	African Parasite Network Meeting (for early-career and established researchers) (<i>Sponsored by Cambridge University Press</i>)	

DAY 3 TUESDAY 16 SEPTEMBER	07h30	Registration	
	08h00-08h45	Plenary Session 3 Keynote 2 - Old hosts as treasure troves of worms, worms as tags for new hosts: the overlooked potential of helminthology in invasion biology (<i>Prof. Maarten Vanhove, Universiteit Hasselt, Belgium</i>)	
	08h45-09h45	Session 2.1.1 Marine Parasitology	Session 2.2.1 Rodents and their parasites
	09h45-10h15	Mid-morning Refreshments & Poster Viewing	
	10h15-11h30	Session 2.1.2 Marine Parasitology	Session 2.2.2 Rodents, parasites and pathogens
	11h30-11h45	Networking and Posters	
	11h45-12h45	Lunch	
	12h45-13h10	Plenary Session 4 Guest Speaker 2 - Parasite conservation: A new frontier for the research on parasites of wildlife (<i>Prof. Nico Smit, North-West University, South Africa</i>)	
	13h10-14h25	Session 2.1.3 Schistosomes and other trematodes	Session 2.2.3 Trypanosomes
	14h25-15h30	Dedicated Poster Session	
	17h30-19h30	Boma-Braai - pre-booking required	

DAY 4 WEDNESDAY 17 SEPTEMBER	07h30	Registration	
	08h00-08h45	Plenary Session 5 Keynote 3 - On the trail of parasites: a journey through veterinary parasitology in southern African landscapes (<i>Prof. Luis Neves, University of Pretoria, South Africa</i>)	
	08h45-09h45	Session 3.1.1 Haemoparasite detection and diversity	Session 3.2.1 Medical Parasitology
	09h45-10h15	Mid-morning Refreshments & Poster Viewing	
	10h15-11h15	Session 3.1.2 Haemoparasite diversity and distribution	Session 3.2.2 Aquatic Parasitology
	11h15-11h45	Networking and Posters	
	11h45-12h45	Lunch	
	12h45-13h10	Plenary Session 6 Guest Speaker 3 - What can genetics teach us about the current taxonomic scheme for lice genera? (<i>Prof. Conrad Matthee, Stellenbosch University, South Africa</i>)	
	13h10-14h25	Session 2.1.3 Evolution and molecular ecology of parasites	Session 2.2.3 Parasites and pathogens associated with carnivores
	14h25	Close of Congress	
	14h45-16h00	PARSA AGM	
	18h00-22h00	Gala Dinner - pre-booking required	

DAY 5 – THURSDAY 18 SEPTEMBER			
07h45-08h00	Morning Refreshments		
08h00-12h00	Workshop 2 What species do I have in my eppendorf tube – a molecular approach (<i>Prof. Conrad Matthee</i>)	Workshop 3 The phenomena of radiation and co-evolution in parasites: what are we looking for? (<i>Prof. Maarten Vanhove</i>)	
12h00	Departure		

Programme Schedule by Day

Day 1 – Sunday, 14 September 2025

15h00-17h30	Registration @ Conference venue
18h00-19h30	Welcome Reception @ Safari Lodge Courtyard

Day 2 – Monday, 15 September 2025

07h30-08h00	Registration					
08h00-08h10	Plenary Session 1					
08h10-08h50	Welcome & Introduction (Prof. Sonja Matthee, Stellenbosch University - Congress Chairperson)					
	Keynote 1: Spatiotemporal variation in avian host-parasite communities (Dr Jenny Dunn, Keele University, United Kingdom)					
	Chair: Sonja Matthee					
	Venue 1 (Ndlopfu)			Venue 2 (Ndau & Nari)		
	Session 1.1.1			Session 1.2.1		
	Special Session: Wildlife Malaria			Aquatic Parasitology		
	Chair: Edward Netherlands			Chair: Wilmien Luus-Powell		
	Presenter	Title	Abstr	Presenter	Title	Abstr
09h00	Shimizu, Misa	Diversity and host impacts of <i>Haemoproteus</i> parasite infection from vultures in The Gambia	001	Yong, Russell Qi-Yung	Marine fish blood flukes (Aporocotylidae) of South Africa: an under-explored fauna	011
09h15	Mbou-Boutambe, Clark	Rodent malaria parasites detected in the invasive <i>Rattus rattus</i> in Gabon	103	Avenant-Oldewage, Annemarië	Purposeful design causes microhabitat restriction and enables reproductive success	101
09h30	Rivero, Ana	Plastic, fantastic: avian malaria plasticity in response to mosquito bites and co-infections	128	Benovics, Michal	Fish as potential non-host predators shaping trematode communities in a subarctic lake ecosystem	042
09h45	Stothard, Russell	Highlighting malaria in Uganda with an assessment of an associated risk of infection within semi-captive chimpanzees	143	Latief, Lutfiyya	Small particles, big impacts: exploring ionic and nano silver's influence on the reproduction of <i>Macrogryrodactylus congolensis</i>	051
10h00	Tea & Poster viewing (foyer and Plenary Hall)					

Day 2 – Monday, 15 September 2025

	Venue 1 (Ndlopfu)			Venue 2 (Ndau & Nari)		
	Session 1.1.2 Special Session: Wildlife Malaria and other Haemoparasites Chair: Raksha Bhoora			Session 1.2.2 Aquatic Parasitology Chair: Russell Yong		
	Presenter	Title	Abstr	Presenter	Title	Abstr
10h30	Rougeron, Virginie	Immune modulation and hidden costs of asymptomatic malaria in wild chimpanzees	141	Thobejane, Ketumile	Exploring parasite diversity in white-breasted cormorant (<i>Phalacrocorax lucidus</i>) from Loskop Dam, South Africa, with the first report of <i>Macrobilharzia</i> sp.	056
10h45	Boundenga, Larson	Evidence of <i>Plasmodium</i> parasite sharing between humans and non-human primates in confined Gabonese environments: implications for zoonotic malaria	094	Benovics, Michal	Population genetic structure and intraspecific variability in generalist fish parasites	057
11h00	Penzhorn, Banie	Haemoprotozoa of wildlife: the dilemma of "dead" names	132	Moema, Esmey	Protozoan parasites on the gills of <i>Oreochromis mossambicus</i> from Letlamoreng/Setumo Dam, Mahikeng, North-West Province	020
11h15	Netherlands, Edward	Reassessing the genus <i>Haemocystidium</i> (Apicomplexa: Haemoproteidae): insights from mitochondrial DNA genomes and morphological data	107	Coetzee, Francois	Taxonomic analysis of the parasitic community associated with Power's Clawed Frog, <i>Xenopus poweri</i> Hewitt, 1927 (Anura: Pipidae)	021
11h30	Barnard, Monique	Back to the future: Exploring the diversity of species of <i>Haemogregarina</i> in terrapins, with a focus on Southern Africa	061	Hüsken, Annabell	Beyond restoration: Environmental drivers of trematode dynamics in recovering streams	118
11h45	Networking and Posters (Ndlopfu)					
12h00	Lunch @ the Safari Lodge Restaurant					
13h00-13h10	Plenary Session 2 Gold Sponsor: Inqaba Biotech					
13h10-13h35	Guest Speaker 1: Wildlife as carriers and transmitters of vectors, pathogens and diseases (<i>Dr Mamohale Chaisi, South African National Biodiversity Institute, South Africa</i>) Chair: Maxwell Barson					
	Session 1.1.3 Microbiomes, vectors and the environment Chair: Zamantungwa Mnisi			Session 1.2.3 Sand flies, midges and human perceptions Chair: Nkululeko Nyangiwe		
13h35	Iddon, Alice	Survey of ticks and their microbiomes spanning national parks in Botswana	091	Ndwandwe, Khanyisani	Perceptions on anthelmintic resistance in goats under communal production systems	076
13h50	Mhlanga, Tapiwanashe	Global variations and implications of microbiome communities in ixodid ticks (Arachnida: Ixodidae): A systematic review	102	Labuschagne, Karien	Biting midges (Diptera: Ceratopogonidae: <i>Culicoides</i>) in South Africa: status and research	016
14h05	García-del Río, Marina	Environmental effects on nest microbiome-parasite interactions and bird condition: an experimental study	026	Kmentova, Nikol	From stigma to strategy: advancing the conservation and perception of metazoan parasites	104
14h20	Motloung, Rethabile	Predicting tick distributions in a changing climate: An ensemble approach for South Africa	018			
14h35	End of sessions					

Day 2 – Monday, 15 September 2025

14h45-14h55	Cambridge University Press (<i>Prof. Russell Stothard, Liverpool School of Tropical Medicine, United Kingdom</i>) Chair: Sonja Matthee
14h55-17h00	African Parasite Network Meeting (for early-career and established researchers) in Main Plenary Hall
14h55-15h00	African Parasite Network meeting <i>Embracing and advancing interdisciplinary research in parasitology on the African continent</i> Welcome - Prof. Sonja Matthee and Prof. Maxwell Barson Guest presentations on their experience of Africa-Africa collaborative research projects - <u>WAAVP-AN info session and Q&A</u> (<i>Dr Patrick Vudriko, Co-chair, WAAVP-AN (Makere University, Zimbabwe)</i>) - <u>WIMANET info session and Q&A</u> (<i>Dr Jenny Dunn, Keele University, United Kingdom & Dr Edward Netherlands, University of the Free State</i>) - <u>Examples of successful Africa-Africa collaborations</u> (<i>Prof. Wilmien Luus-Powell (University of Limpopo) & Prof. Maxwell Barson (University of Botswana)</i>) - Further engaging over refreshments - Group Photo  CAMBRIDGE UNIVERSITY PRESS 
17h00	Free evening

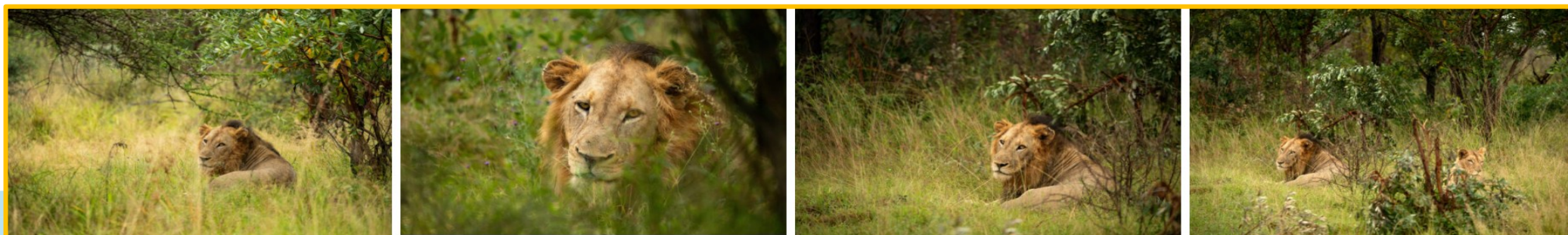


Day 3 – Tuesday, 16 September 2025

07h30-08h00	Registration					
08h00	Plenary Session 3 Keynote 2: Old hosts as treasure troves of worms, worms as tags for new hosts: the overlooked potential of helminthology in invasion biology (Prof. Maarten Vanhove, Universiteit Hasselt, Belgium) Chair: Wilmien Luus-Powell					
	Venue 1 (Ndlopfu) Session 2.1.1 Marine Parasitology Chair: Susan Dippenaar			Venue 2 (Ndau & Nari) Session 2.2.1 Rodents and their parasites Chair: Luther van der Mescht		
	Presenter	Title	Abstr	Presenter	Title	Abstr
08h45	Botha, Hesmarié	Reduce, reuse, recycle: redescription of one and description of two new <i>Gnathia</i> species (Isopoda: Gnathiidae) from historical museum material (1898–1976)	030	Krasnov, Boris	Clusters of regional flea and host assemblages: biogeography or ecology?	002
09h00	Cook, Courtney	Unravelling the taxonomy of fish haemogregarines, a few species at a time	071	Raubenheimer, Inge	Ectoparasites and gastrointestinal helminths associated with Smith's bush squirrel (<i>Paraxerus cepapi</i>) in South Africa	014
09h15	Lawton, Scott	Speciation in brachycladiid liver flukes, cryptic parasites of marine mammals, with applications for cetacean conservation	123	Schlemmer, Ernst	Nematode diversity associated with rodents and the extent of parasite sharing between sympatric rodents	093
09h30	Vermaak, Anja	Marine protected areas and parasite conservation: metazoan parasites of the Cape white seabream, <i>Diplodus capensis</i> , as case study	037	Kipling, Jessica	Parasite diversity of the Karoo bush rat (<i>Otomys unisulcatus</i>) in the Western Cape	012
09h45	Tea & Poster viewing (foyer and Ndlopfu)					
	Session 2.1.2 Marine Parasitology Chair: Nico Smit			Session 2.2.2 Rodents, parasites and pathogens Chair: Sonja Matthee		
10h15	Marchiori, Erica	A large-scale study on gastrointestinal helminth community of loggerhead sea turtles <i>Caretta caretta</i> : ecological drivers of diversity and insights into environmental changes	120	Little, Alyssa	Host and environmental factors influence ectoparasite infestations found on the Namaqua rock mouse, <i>Micaelamys namaquensis</i>	022
10h30	Dippenaar, Susan	The <i>Caligus</i> stumble block	035	Singo, Lola	Diversity and distribution of ectoparasites associated with <i>Rhabdomys</i> spp. (Muridae) in the Fynbos, Nama- and Succulent Karoo biomes	066
10h45	Cribb, Thomas	Monorchiid trematodes in Indo-Pacific butterflyfishes: enabling a biogeographical paradigm for fish parasites of the region?	114	Kruse, Nina	From park to periphery: haemoparasite infections in indigenous rodents at the wildlife-livestock-human interface in Greater Kruger	131
11h00	de Klerk, Linda	Characterising a new <i>Udonella</i> (Udonellidae: Monogenea) species: integrative taxonomy of an epibiont from South African waters	059	van der Mescht, Luther	Global latitudinal distributions of flea and small mammal host species richness, phylogenetic diversity, and functional diversity	032
11h15	Armstrong, Helen	Exploring the evolutionary history of the Cryptogonimidae	039	Matthee, Sonja	Host and parasite contribute to ectoparasite species assemblages on sympatric rodents	144

Day 3 – Tuesday, 16 September 2025

11h30	Networking and Posters (Plenary Hall)					
11h45	Lunch @ the Safari Lodge Restaurant					
12h45-13h10	Plenary Session 4 Guest Speaker 2: Parasite conservation: A new frontier for the research on parasites of wildlife (Prof. Nico Smit, North-West University, South Africa) Chair: Kerry Hadfield Malherbe					
	Venue 1 (Ndlopfu) Session 2.1.3 Schistosomes and other trematodes Chair: Annemarië Avenant-Oldewage			Venue 2 (Ndau & Nari) Session 2.2.3 Trypanosomes Chair: Franck Prugnolle		
	Presenter	Title	Abstr	Presenter	Title	Abstr
13h10	Kibet, Caroline	Diversity of avian schistosomes	046	Mulandane, Fernando	The national atlas of tsetse and trypanosomosis in Mozambique: preliminary results	079
13h25	Schols, Ruben	An innovative imaging tool and the impact of invasive snails on amphistomes of large African herbivores	099	Brito, Denise	Snacking preferences of tsetse flies: Identification of vector-host-parasite dynamics at the interface between agricultural and conservation areas	045
13h40	Lawton, Scott	Phylogeography of <i>Galba truncatula</i> and implications for the spread of fluke diseases of domestic animals and wildlife	121	Moyaba, Percy	Molecular detection of trypanosome parasite in <i>Stomoxys</i> flies from the northeastern KwaZulu-Natal Province of South Africa	010
13h55	Mukaratirwa, Samson	Geographical distribution, ecology and infection status of hosts of <i>Fasciola</i> species from selected localities in South Africa	127	Cossa, Nióbio	Evaluation of the vectorial competence of <i>Glossina brevipalpis</i> in the transmission of <i>Trypanosoma congolense</i> -savanna type, in the Matutuine District, Maputo Province, Mozambique	136
14h10	Schols, Ruben	<i>Schistosoma</i> species, parasite development, and co-infection combinations determine microbiome dynamics in the snail <i>Biomphalaria glabrata</i>	034	Mucache, Hermogenes	Prevalence of trypanosome species in the buffer zone of Maputo National Park, Matutuine District, Mozambique: preliminary results	074
14h25	Dedicated Poster Session					
15h30	End of Day 3 - Free evening					
17h30-19h30	Braai @ Cattle Baron Boma (Only guests who RSVP'd)					



Day 4 – Wednesday, 17 September 2025

07h30-08h00	Registration					
08h00	Plenary Session 5 Keynote 2: Keynote 3: On the trail of parasites: a journey through veterinary parasitology in southern African landscapes (Prof. Luis Neves, University of Pretoria, South Africa) Chair: Sonja Matthee					
	Venue 1 (Ndlopfu) Session 3.1.1 Haemoparasite detection and diversity Chair: Nicola Collins			Venue 2 (Ndau & Nari) Session 3.2.1 Medical Parasitology Chair: Virginie Rougeron		
	Presenter	Title	Abstr	Presenter	Title	Abstr
08h45	Sekgobela, Naledi	Multiplex real-time PCR for detecting <i>Theileria bicornis</i> and <i>Babesia bicornis</i> in rhinoceros	064	van Zyl, Robyn	Harnessing monoterpenoids for mosquito control and malaria transmission	090
09h00	Aphane, Karabo	Development of a method to extract high molecular weight DNA from a putative novel <i>Anaplasma</i> species identified in impala (<i>Aepyceros melampus</i>)	072	Samie, Amidou	The epidemiology and growth impact of microsporidia infections on children from low resources settings in the MaEd cohort	139
09h15	Fisher, Adam	Predicting heartwater spread using mechanistic models	047	Stothard, Russell	From baboons to vervets, with humans in between: Improving detection of <i>Strongyloides</i>	006
09h30	Davis, Erin	Prevalence and diversity of <i>Mycoplasma</i> , <i>Anaplasma</i> and <i>Bartonella</i> in captive and free-ranging black-footed cats (<i>Felis nigripes</i>) from South Africa	129	Mashatola, Boitumelo	Genetic diversity of <i>Entamoeba</i> species, and their impact on diarrhea occurrence among under five-year-old children in Vhembe, South Africa	140
09h45	Tea & Poster viewing (foyer and Ndlopfu)					
	Session 3.1.2 Haemoparasite diversity and distribution Chair: Banie Penzhorn			Session 3.2.2 Aquatic Parasitology Chair: Kerry Hadfield Malherbe		
10h15	Duarte, Marche	Prevalence of <i>Anaplasma marginale</i> and <i>A. centrale</i> in African buffalo (<i>Syncerus caffer</i>) in the Kruger National Park and characterization of <i>A. marginale</i> strains	070	Landman, Willie	Polystomatid flatworms in Africa: State of knowledge and the way forward	033
10h30	Mnisi, Zamantungwa	<i>Anaplasma platys</i> beyond canines: a systematic review of host range, zoonotic potential, and knowledge gaps in Africa	058	Erasmus, Anja	Making a comeback: a new perspective on gnathiid species described in the 1900s to early 2000s	050
10h45	Czirják, Gábor	Occurrence of vector-borne pathogens in Namibian herbivores: differences between Etosha National Park and freehold farmland	062	Schwelm, Jessica	Trematode infections in freshwater snails of South Africa: diversity, prevalence, and host interactions	078
11h00	Grillini, Marika	Investigating vector-borne protozoa in wild carnivores from northeastern Italy	124	Longstaff, Kelsey	Exploring the understudied biodiversity and taxonomy of corallanid isopods in Indonesian waters	029
11h15	Barnard, Monique					

Day 4 – Wednesday, 17 September 2025

11h15	Networking and Posters (Plenary Hall)					
11h45	Lunch @ the Safari Lodge Restaurant					
12h45-13h10	Plenary Session 6 Guest Speaker 3: What can genetics teach us about the current taxonomic scheme for lice genera? (Prof. Conrad Matthee, Stellenbosch University, South Africa) Chair: Sonja Matthee					
	Venue 1 (Plenary Hall) Session 3.1.3 Evolution and molecular ecology of parasites Chair: Conrad Matthee			Venue 2 (Ndau & Nari) Session 3.2.3 Parasites and pathogens associated with carnivores Chair: Karien Labuschagne		
	Presenter	Title	Abstr	Presenter	Title	Abstr
13h10	Najer, Tomas	Mitochondrial genome fragmentation in parasitic lice	023	Ferraro, Elisabetta	Cardiopulmonary parasites in Golden Jackals from Italy	063
13h25	Kuchta, Roman	Diversity and biology of <i>Spirometra</i> tapeworms, zoonotic parasites of wildlife	043	Ferraro, Elisabetta	Parasite infections in wolves: a study on health risks and zoonotic implications	065
13h40	Smit, Aneliza	Unravelling the evolution of <i>Amblyomma</i> : The case of <i>Amblyomma splendidum</i>	073	Beraldo, Paola	Mapping intestinal parasites in golden jackals in Italy to track health risks	083
13h55	Sheykhkanloo, Nona	Diversity and evolutionary history of <i>Pneumocystis fungi</i> in their New Guinean rodent hosts	019	Cassini, Rudi	Parasitic infections in Golden Jackals: a comparative analysis of diagnostic methods	081
14h10	Hernández-Orts, Jesus	Molecular data reveal a complex of cryptic species within <i>Corynosoma australe</i> Johnston, 1937 (Acanthocephala: Polymorphidae), a parasite of pinnipeds from both the Northern and Southern Hemispheres	111	Wachter, Bettina	Characterisation of vector-borne pathogens in brown and spotted hyenas from Namibia and Tanzania reveals high frequency of infection and genetic variability	048
14h25	Close of Congress					
14h45	PARSA AGM					
18h00-22h00	Gala Dinner & Presentation Awards @ Cattle Baron Restaurant (Only guests who RSVP'd)					

Day 5 – Thursday, 18 September 2025

07h45-08h00	Morning Refreshments	
08h00-12h00	Workshop 1 What species do I have in my eppendorf tube – a molecular approach <i>(Prof. Conrad Matthee)</i>	Workshop 2 The phenomena of radiation and co-evolution in parasites: what are we looking for? <i>(Prof. Maarten Vanhove)</i>
12h00	Departure	

Posters

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P1	Nyangiwe, Nkululeko	Acaricide resistance of <i>Rhipicephalus decoloratus</i> ticks collected from communal grazing cattle in South Africa	005
P2	Merino, Santiago	Changes in nest microclimate affect concentration of gases and ectoparasite abundance in nests of Eurasian blue tits (<i>Cyanistes caeruleus</i>)	008
P3	Serage, Naledi	Molecular detection of <i>Trypanosoma congolense</i> savannah infecting cattle in north-eastern KwaZulu-Natal Province, South Africa	009
P4	Raubenheimer, Inge	Mitochondrial DNA phylogeography of a species-specific sucking louse, <i>Johnsonphirus heliosciuri</i> , act as a proxy to provide insights into the population connectivity of its host, Smith's bush squirrels, <i>Paraxerus cepapi</i>	015
P5	García-Velasco, Javier	Is that a bedbug? First record of <i>Cimex lectularius</i> L. inside Eurasian Blue Tit (<i>Cyanistes caeruleus</i> L.) nests	027
P6	Nkosi, Mmatlala D.	Trypanosome infection prevalence in <i>Glossina brevipalpis</i> collected from the communal areas of north-eastern KwaZulu-Natal, South Africa	031
P7	Yssel, Roney	Gastrointestinal nematodes and <i>Enterobacteriaceae</i> bacteria infecting horses in Potchefstroom town of North-West Province, South Africa	036
P8	Jamesboy, Eunice	The role of the Medical Entomology Museum in advancing vector-borne disease research and parasite surveillance	041
P9	Plank, Kamogelo	Detection of <i>Trypanosoma equiperdum</i> antibodies from South African horses and donkeys using complement fixation test	052
P10	Jordán, Lilla	Physiological costs of sub-clinical haemoparasite co-infections in Namibian cheetahs (<i>Acinonyx jubatus</i>)	054
P11	Jordán, Lilla	Movement costs of sub-clinical babesiosis in free-ranging Namibian cheetahs (<i>Acinonyx jubatus</i>)	055
P12	Czirják, Gábor Á.	Estimating <i>Toxoplasma gondii</i> exposure in Swedish wolverines (<i>Gulo gulo</i>) – a retrospective study	060
P13	Jamesboy, Eunice	Potential applications of <i>Toxorhynchites</i> mosquitoes in integrated pest management (IPM) strategies	067
P14	Fagir, Dina M.	Ectoparasite diversity and distribution in <i>Rattus rattus</i> and <i>Rattus tanezumi</i> from rural communities in the Savanna biome, South Africa	068
P15	Sekujika, Okuhle	Diversity of <i>Sarcocystis</i> in wildlife from the Greater Kruger, South Africa	075
P16	Nel, Mikyla	Occurrence of <i>Anaplasma marginale</i> in cattle from villages in the Mnisi Community, Mpumalanga province, South Africa	077
P17	Collins, Nicola E.	Assessment of quantitative real-time PCR assays to detect a novel <i>Anaplasma</i> species in dogs	080
P18	Dejmková, Tereza	Unravelling the development of anuran trypanosomes in mosquito vectors	087
P19	Gounden, Sarina	Molecular detection and risk factors of fasciolosis in sheep, snails and the environment in the Eastern Cape, South Africa	088
P20	Schlemmer, Ernst	New species of <i>Gastronodius</i> Singh, 1934 (Nematoda: Spirocercidae) discovered in a South African rodent	095
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Keynote Presentations

K1 - Spatiotemporal variation in avian host-parasite communities

Jenny C. Dunn

Keele University, Newcastle, Staffordshire, United Kingdom - j.c.dunn@keele.ac.uk

Avian haemosporidians are a relatively well-studied group of wildlife parasites, but systems within which we understand community-level associations across multiple host and parasite species remain rare. We generally assume that host-parasite associations remain stable across time and space, but studies that allow us to test these hypotheses can be logistically challenging to establish.

Here, I will introduce you to a seven-year community-level host-parasite study, exploring temporal variation in host-parasite associations in a passerine-haemoparasite system. I will discuss generalism and specialism in different parasite lineages and how this varies between years, as well as the implications of each strategy for host immune response. Finally, I will discuss spatial variation in host-parasite interactions and the need for co-ordinated large-scale studies across space and time.



Biography: Jenny obtained her PhD in avian ecology from the University of Leeds in 2010, working on anti-predator behaviours and their consequences in farmland birds. During her PhD she spent a brief time working with Prof John Quinn (now at UCC) at Oxford University working on avian personality and parasite infection. She then left academia, moving to the Royal Society for the Protection of Birds, where she worked as a Conservation Scientist for 6 years, focussing on developing management solutions for the conservation of European Turtle Dove. Until this point, she had been focussed on avian ecology, working on haemoparasites as side projects. In 2016 she took up a lectureship at the University of Lincoln, where her lab worked on the ecology and diversity of parasite infection in avian systems.

She moved to Keele University in summer 2024, where her lab works on a range of projects involving avian parasite and pathogen ecology, and the impacts of humans on these systems. Since the end of 2023 she has been Action Chair for the Wildlife Malaria Network, an EU COST-funded global network focussed on uniting research efforts of those working on malaria parasites in wildlife.

Monday 15 September - 08h10 (Ndlopfu)

K2 - Old hosts as treasure troves of worms, worms as tags for new hosts: the overlooked potential of helminthology in invasion biology

Maarten Vanhove

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Introduced alien species are major threats to biodiversity worldwide. Potential reasons include parasite co-introduction and transmission, aspects that are often understudied. Origins and identity of introduced species or strains are often unknown, let alone of their parasite fauna. Monitoring only provides partial answers for lack of baseline data. Especially in the Global South, native parasite biodiversity is often scarcely studied. We studied introduced fishes and amphibians in Central and Southern African inland waters, and the monogenean parasites infecting them. Given their direct lifecycle, these flatworms are hypothesized to be easily co-introduced with their hosts, and to be useful “tags” for host populations. Monogeneans were collected from hosts retrieved from biodiversity collections and through recent fieldwork. Parasites were morphologically identified to species level, and characterised genetically using nuclear and mitochondrial markers, including some mitochondrial genomes. We demonstrate the potential of historical host collections to establish pre-translocation baselines for parasite communities, enabling distinguishing between native and co-introduced parasite species. Monogeneans can help trace origins and pathways of aquatic invasions. For Nile tilapia and African clawed frog, two notorious invaders, parasite mitochondrial markers provide higher resolution than host genetics. We offer proof-of-concept of biodiversity infrastructure and helminths as sources of information in a One Health context. However, closer scrutiny of the parasitology of Nile tilapia, a fish of global economic and ecological importance, indicated that a One Health approach is mostly lacking. We recommend more scientific consideration to the parasites of invasive species, using a more integrative approach than currently often taken.



Biography: Maarten P.M. Vanhove, associate professor at Hasselt University (Centre for Environmental Sciences, Research Group Zoology: Biodiversity & Toxicology) and invited lecturer at the University of Liège (Faculty of Veterinary Medicine, Department of Morphology and Pathology), holds master's degrees in biology (2006) and social-cultural anthropology (2007), and a PhD in sciences (2012) from KU Leuven (Belgium). He was a researcher at the Royal Museum for Central Africa (Belgium), the Hellenic Centre for Marine Research (Greece), and Masaryk University (Czech Republic); policy scientist focusing on capacity development about African biodiversity at the Royal Belgian Institute of Natural Sciences; and curator of worms at the Finnish Museum of Natural History (University of Helsinki, Finland). He studies parasite diversity and genetics in evolutionary and

conservation-relevant contexts, and biodiversity policy, especially in Africa and the Mediterranean. He was involved in starting the Belgian One Health Network, is active in the boards of the Royal Belgian Zoological Society and of the Belgian Society of Parasitology and Protistology and is Steering Committee Member for Europe of the IUCN SSC Parasite Specialist Group. He received the 2002 Jacques Kets Prize for Biology (Royal Zoological Society of Antwerp), the best young researcher presentation award (2013 International Congress on Monogenea), and the 2013 Henri Schouteden Prize (Royal Flemish Academy of Belgium for Science and the Arts). In 2024, a proposal he co-created in response to the Young Academy of Belgium's call for inspiration “The aftermath of an educide: how to rebuild knowledge?” was awarded a prize.

Tuesday 16 September - 08h00 (Ndlopfu)

K3 - On the trail of parasites: a journey through veterinary parasitology in southern African landscapes

Luis Neves

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Parasites are mesmerizing for their ecological plasticity, their complex adaptive biochemistry and especially for their diversity and beauty. I would like to tell you a story “of parasites and men”, which unfolds in the southern African landscapes, bridging generations of parasitologists, their dreams, questions and memories. In my pursuit of insights into the complex lives of these fascinating organisms, parasitology has become an incredibly important part of my life. As a result, I have been exposed to a vast diversity of experiences and adventures, making it extremely difficult to decide on the stories that best represent my trajectory as a veterinary parasitologist. Based on the main areas covered throughout my research path, I opted to highlight three key topics in the context of African parasitology; tsetse flies, trypanosomes and ticks. The southernmost distribution of trypanosomes and tsetse flies on planet Earth spreads across a belt, which includes parts of Mozambique, South Africa and Eswatini. Studies in these areas have made major contributions to trypanosome and tsetse fly research. Over 25 years, I have used a combination of parasitological and molecular techniques in this area to thoroughly evaluate the diversity, distribution and prevalence of trypanosomes. Furthermore, I contributed to developing and applying genetic markers to elucidate the genetic structure and gene flow between tsetse fly populations. Our research group conducted similar studies in other locations of southern Africa, some of which, led to the development of molecular diagnostic assays for African trypanosomes. Moreover, in studies involving mainly wildlife trypanosome isolates, we evaluated genetic markers for their suitability for diagnosis, genotyping and phylogenetic inferences in *Trypanosoma vivax* and *Trypanosoma congolense* populations. Additionally, studies focusing on diversity and evolutionary links between African and South American trypanosome populations were conducted in these isolates. Another key component of our research has been trypanocidal drug resistance and its possible association to mechanical transmission of trypanosomes in southern Africa. After many years of apprenticeship with the renowned African tick taxonomist, Prof. Ivan Horak, I have embarked on a journey across southern Africa to find answers to a major taxonomic controversy on the validity of the species status of *Amblyomma pomposum* (Dönitz 1909). For this, thousands of *Amblyomma* ticks were collected, several molecular markers were analysed and hundreds of DNA sequences were generated. We do not have the answer yet, but we are excited to follow on these promising new trails, “giving science a chance”.



Biography: Professor Luis Neves is a leading expert in Veterinary Parasitology, specializing in vector-borne diseases, with a career spanning over three decades. Born in Beira, Mozambique, he completed his veterinary degree at Eduardo Mondlane University, Maputo. He advanced his academic pursuits at the University of Liverpool, earning an MVSc in Applied Parasitology (1991) and a PhD focusing on *Babesia* culture and immunodiagnostics (1999). For 25 years, Prof. Neves contributed extensively to veterinary education and research at Eduardo Mondlane University, where he served as Dean of the Faculty of Veterinary Science (1999–2005). He was instrumental in establishing the university's Biotechnology

Center, fostering interdisciplinary collaboration in molecular biology and cell biology and applied immunochemistry, integrating the Faculties of Agriculture and Forestry, Natural Sciences, Veterinary Science, and the Medical School. Prof. Neves was the Director of the Biotechnology Center from its inception in 2005 until 2013. Moreover, Prof. Neves was the recipient of the National Prize of Research and Innovation in Veterinary Science, awarded in



November 2023, by the Mozambican Veterinary Council. Since joining the Faculty of Veterinary Science at the University of Pretoria, South Africa in 2013, Prof. Neves has focused on understanding the intricate interactions between parasites, hosts, and vectors. His research includes ticks and tick-borne diseases, such as babesiosis, and ehrlichiosis, as well as the epidemiology and control of tsetse flies and trypanosomoses. He is also deeply involved in zoonotic disease studies, such as toxoplasmosis and rickettsial infections. A recent focus has been unravelling the genetic and phenotypic distinctions within *Amblyomma* populations across southern Africa, addressing taxonomic controversies, tick species diversity, distribution and their ecology. Prof. Neves has been a coordinator for high-impact initiatives, such as the Southern African Centre for Infectious Disease Surveillance (SACIDS) and regional projects for tsetse fly and trypanosomiasis control. As part of the Enhancing Research for Africa Network (ERFAN), he played a pivotal role in regional and international capacity-building programmes. With over 80 publications and numerous presentations at national and international conferences, Prof. Neves's scientific contributions have shaped and continue to shape veterinary parasitology and vector-borne diseases research. In the course of his academic career, he established an extensive international collaboration network, which includes scientists and institutions from Africa, America and Europe. Furthermore, his mentorship of postgraduate students and younger academics reflects his dedication to developing the next generation of scientists and scholars to this amazing but important field, of veterinary parasitology.

Wednesday 17 September - 08h00 (Ndlopfu)

Guest Speaker Presentations

G1 - Wildlife as carriers and transmitters of vectors, pathogens and diseases

Mamohale Chaisi

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South Africa is a megadiverse country, with an exceptional variety of wild animals, some of which are endemic to the region. Some of these animals are endangered and threatened with extinction due to various anthropological factors, thus necessitating their placement in different facilities for conservation purposes. However, the vast diversity of vectors and parasites poses significant challenges to conservation efforts through disease transmission. Furthermore, there is limited information on the role of wild animals in the transmission of vectors and pathogens of economic and zoonotic importance as well as on the distribution trends of hosts, vectors and pathogens. This presentation highlights our studies on the surveillance of vectors and vector-borne pathogens and neglected zoonoses in threatened and endangered wildlife using an integrated taxonomy approach. The findings reveal a high diversity of vectors and pathogens across various animal taxa and new host-vector-pathogen relationships, highlighting their potential threat to biodiversity conservation, food security and public health.



Biography: Dr Mamohale Chaisi completed her PhD in Veterinary Parasitology at the Department of Veterinary Tropical Diseases, University of Pretoria and MSc in Parasitology at the University of Natal (now KwaZulu-Natal). She is currently a Principal Scientist in Zoological Research at the South African National Biodiversity Institute and an Extraordinary Lecturer at the University of Pretoria. She further leads the South African Living Collections Cluster and is a member of the Wildlife Malaria Network (WIMANET). Her current research focuses on molecular

diagnostics, ecology, epidemiology and systematics of vectors and vector-borne pathogens in wild and domestic animals in South Africa. These studies are essential for the management and control of infections, identifying possible hotspots for disease emergence, developing specific diagnostic tools, and monitoring trends in the distribution of pathogens, vectors and hosts. She has published many articles in accredited and peer-reviewed journals and has acted as a reviewer for various international journals including Parasitology International, PLoS One, Ticks and Tick-borne Diseases, Parasitology Research, Tropical Medicine and Infectious Disease, International Journal of Acarology, Pathogens, Infectious Disease Reports and Journal of Zoo and Wildlife Medicine.

Monday 16 September – 13h10 (Ndlopfu)

G2 - Parasite conservation: A new frontier for the research on parasites of wildlife

Nico Smit

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Global biodiversity has been in decline for several decades, marked by species extinctions and population losses that have cascading negative impacts on ecosystems. Despite the growing list of described species, much of the actual threatened biodiversity remains unknown, particularly among invertebrates, including the ones with a parasitic mode of life. Parasites, which may outnumber free-living species and constitute a significant proportion of ecosystem biomass, remain largely neglected in conservation efforts. The extinction of free-living host species often leads to co-extinction events, where parasite species may face extinction even prior to their host species. This presentation highlights the need to incorporate parasites into broader conservation agendas and management plans and practices. It provides an overview of the evolution of species conservation from a focus solely on free-living species to one that includes symbiont assemblages. However, several obstacles continue to hinder the inclusion of any parasitic species in conservation, and these will be discussed in detail. Furthermore, two case studies from our recent work on aquatic parasite conservations will be presented. The first focus on the parasites of threatened freshwater fish species of the south African cape fold freshwater ecoregion and the second look at the role of marine protected areas in the conservation of fish parasite diversity. In conclusion the presentation outlines future research directions to better understand and conserve parasites of wildlife, advocating for their inclusion in biodiversity monitoring programs and conservation agendas. Addressing these gaps is essential for maintaining the integrity of natural systems and the biodiversity they support.



Biography: Prof. Nico Smit is a Professor of Ecology in the School of Biological Sciences at North-West University, Potchefstroom Campus, South Africa. Nico's research focuses on the biodiversity, taxonomy and ecology of marine and freshwater parasites and he has authored and co-authored more than 250 scientific papers and three edited books on these and other related topics. To date 23 PhD and 39 MSc students have graduated under his supervision. His research and teaching excellence has internationally been recognised through visiting Professor appointments at University of Duisburg-Essen, Germany, University of Queensland, Australia and Masaryk

University, Czech Republic, and through his current appointment as Adjunct Professor of Marine Biology and Ecology at the Rosenstiel School of Marine, Atmospheric and Earth Science, University of Miami, USA. National recognition for his research excellence includes a Honorary Medal from the South African Academy for Science and Arts' Faculty of Natural Science and Technology for a significant contribution towards the advancement and development of Science in South Africa and the Elsdon-Dew Medal from the Parasitological Society of southern Africa (PARSA) in recognition of a significant contributions to the advancement of Parasitology in Africa. Nico has also contributed to the management of national and international academic societies as president of the Parasitological Society of Southern Africa (PARSA), president of the South African Society of Aquatic Scientists (SASAqS) and committee member of the International Congress on Fish Parasites (ISFP). He currently serves as a Steering Committee Member of the International Union for Conservation of Nature (IUCN) Species Survival Commission (SSC) Parasite Specialist Group. During the past 8 years he has refereed papers for 17 international journals, served as associate editor of three international journals and was guest editor for two special issues of the International Journal for Parasitology: Parasites and Wildlife. He is currently rated by the South African National Research Foundation (NRF) as an internationally acclaimed scientist (B1) in the field of aquatic parasitology.

Tuesday 17 September – 12h45 (Ndlopfu)

G3 - What can genetics teach us about the current taxonomic scheme for lice genera?

Conrad A. Matthee^{1*}, Nina du Toit-Heunis^{1,2}, Sonja Matthee³, Lance A. Durden⁴, Jessica E. Light²

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Sucking lice represent a species rich parasite group that shares an intimate evolutionary relationship with their mammalian hosts. Two genera, *Polyplax* and *Hoplopleura*, primarily parasitize rodents and their taxonomy is mainly based on morphological characters. To determine the systematics and the evolutionary mechanisms that gave rise to *Polyplax* and *Hoplopleura* species diversity, four genes were used to generate a phylogeny for 105 individuals representing ~56 identified species. The monophyly of neither *Polyplax* nor *Hoplopleura* was supported and topological conflict among individual gene trees resulted in a

non-tested hypothesis that ancestral hybridization may have shaped the evolution of some *Polyplax* species. Several species complexes or cryptic divergences were detected within the hoplopleurid species *H. acanthopus*, *H. arizonensis*, *H. hesperomydis*, *H. oryzomydis*, *H. pacifica*, and *H. sciuricola*, and the polyplacid species *P. arvicantis*, *P. auricularis*, *P. biseriata*, *P. myotomydis*, *P. otomydis*, *P. reclinata*, and *P. spinulosa*. Four morphological and genetically distinct taxa were sampled from Gerbillinae or Deomyinae and these probably represent new species. The taxonomy of *Polyplax* and *Hoplopleura* needs a thorough revision, and the species diversity of these lice can be attributed to an interplay between host associations, host switching and geographic locations of host species.



Biography: Conrad Matthee is a Professor in Evolutionary Genetics in the Department of Botany and Zoology at Stellenbosch University. He performs multidisciplinary research in Ecology, Systematics and Evolution with a focus on African fauna. In the field of parasitology, he is best known for his contributions towards parasite host co-evolution and phylogenetics of ticks. More recent research also includes microbiome diversity of fleas and ticks in particular.

Wednesday 17 September – 12h45 (Ndlopfu)

Workshops

Workshop 1 - What species do I have in my eppendorf tube – a molecular approach

Presented by Prof. Conrad Matthee

This will be an interactive workshop where the presenter will present content and then require participants to do some analyses online – practical experience is the best way to learn. Prof. Matthee will provide you with sequence data, and a problem to solve.

Workshop 2 - The phenomena of radiation and co-evolution in parasites: what are we looking for?

Presented by Prof. Maarten Vanhove

Co-speciation, co-evolution, cophylogeny...: words that sound like music in the ears of many parasitologists. However, what are we actually saying if we use these words, and what are their different meanings? Just like for the term (adaptive) radiation, denoting a phenomenon to which parasites are also said to be prone, we need to be careful, as parasitologists, not to use these words lightly. It remains highly worthwhile to explore these aspects of parasite diversity, as they may shed light on fascinating patterns of diversification in our favourite organisms, and can also help us understand aspects of parasite ecology, like transmission between hosts. This workshop will combine theoretical lectures interspersed with "journal club"-style moments. Using case studies, many of which centred on African host-parasite systems, we will explore together what we are actually looking for when searching for co-evolution and radiation in parasites and perhaps agree on how we can find it.

Oral Presentations

001 - Diversity and host impacts of *Haemoproteus* parasite infection from vultures in Gambia

Misa Shimizu¹, Carolina Romeiro Fernandes Chagas¹ & Jenny C. Dunn²

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Haemoproteus (Haemosporida: Haemoproteidae) is an avian haemosporidian parasite and is known for its genetic diversity and avian host-specificity. Their distribution remains largely unexplored in Africa, particularly among non-passerine birds. The impact of *Haemoproteus* infections on avian hosts is also poorly understood, posing a potential threat to endangered species. The sub-Saharan area, including The Gambia, a biodiversity hotspot, is home to several endangered species of vultures. Six out of the eight vulture species are listed on the IUCN Red List, requiring urgent conservation measures. However, research about avian haemosporidian parasites has never been conducted in this country nor for the vulture species in this area. This research aims to evaluate *Haemoproteus* parasite diversity in The Gambia and morphologically describe the parasite species. From 2019 to 2025, vultures including Hooded Vultures (*Necrosyrtes monachus*) and White-Backed Vultures (*Gyps africanus*) were captured by using cannon nets and mist nets, and blood samples were taken via venipuncture of the brachial veins. All the samples underwent polymerase chain reaction (PCR) targeting parasite mitochondrial DNA cytochrome b gene (*CytB*), and positive samples were sequenced and phylogenetic analysis carried out. Morphological identification of the avian haemosporidian parasites and evaluation of immunological reaction to estimate the impact of the parasite infection were conducted. We identified *Haemoproteus* species in these two vulture species, marking the first record of avian haemosporidian parasites in vultures from The Gambia. Our findings contribute to the understanding of *Haemoproteus* distribution and highlight the necessity for further research on non-passerine birds in the sub-Saharan region.

Monday 15 September – 09h00 (Ndlopfu)

002 - Clusters of regional flea and host assemblages: biogeography or ecology?

Boris R. Krasnov

Mitrani Department of Desert Ecology, Swiss Institute for Dryland Environmental and Energy Research, Jacob Blaustein Institutes for Desert Research, Ben-Gurion University of the Negev, Sede Boqer Campus, 8499000 Midreshet Ben-Gurion, Israel - krasnov@bgu.ac.il

Step-down factor analyses (SDFA) and cluster analyses were used to identify biogeographic (across the entire globe) and ecological (within a realm across the main terrestrial biomes) clusters of regional assemblages of fleas and their small mammalian hosts from six biogeographic realms. At the global scale, the clusters of regional assemblage loadings on SDFA axes reflected well the assemblage distribution, according to the biogeographic realms to which they belong except for fleas and hosts from Madagascar (belonging to the Afrotropics but clustered with the Indo-Malay and the Australasian assemblages, respectively) and hosts from Morocco and Egypt (both belonging to the Palearctic, but clustered with the Afrotropical assemblages). The cluster topology, corresponding to the biogeographic realms, was similar between flea and host assemblages, but the topology of subtrees within realm-specific clusters

substantially differed between fleas and hosts. At the scale of biogeographic realms, the distribution of regional flea and host assemblages did not correspond to the predominant biome types. Assemblages with similar loadings on SDFA axes were often situated in different biomes and vice versa. The across-biome, within-realm distributions of flea versus host assemblages suggested weak congruence between these distributions. These results indicate that dispersal is a predominant mechanism of flea and host community assembly across large regions.

Tuesday 16 September – 08h45 (Ndau & Nari)

006 - From baboons to vervets, with humans in between: improving detection of *Strongyloides*

J Russell Stothard

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Control of human threadworms presents a considerable challenge, complicated in part by zoonotic transmission of certain species within non-human primates. Current molecular epidemiological surveillance for zoonotic strongyloidiasis is confounded by routine use of a genus-specific TaqMan[®] probe assay that conflates *Strongyloides fuelleborni fuelleborni* with *Strongyloides stercoralis*. To improve surveillance, we developed then validated a novel duplex species-specific TaqMan[®] probe assay, screening a representative collection of available clinical samples, alongside isolates from baboons and vervets. Our assay was highly discriminatory, evidencing no cross-reactivity, and had a lowest DNA detection limit of 1 pg/μL. However, as the genus-specific DNA assay has greater detection ability, we propose a two-step protocol where samples are first screened with this assay then if positive, are screened with our species-specific assay, discriminating (co)infections between each threadworm species. We demonstrate the use of this improved diagnostic assay during attempts to elucidate the transmission of threadworms within a UK semi-captive colony of baboons and human-vervet encroachment in Malawi.

Wednesday 17 September – 09h15 (Ndau & Nari)

010 - Molecular detection of trypanosome parasite in *Stomoxys* flies from the northeastern KwaZulu-Natal Province of South Africa

Percy Moyaba^{1,2}, Johan Esterhuizen¹, Oriel Thekisoe² & Moeti O. Taioe^{1,2}

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Stomoxys flies (Diptera: Muscidae) are blood-feeding insects which are known as mechanical vectors of trypanosome parasites. African animal trypanosomiasis (AAT) causes significant morbidity and mortality among livestock. The aim of this study was to determine the species and prevalence of trypanosomes transmitted by *Stomoxys* flies from the historical AAT foci in the northeastern KwaZulu-Natal (KZN) Province. Fly collection was carried out using H-traps. A total of 160 *Stomoxys* consisting of four spp., namely, *S. niger niger*, *S. calcitrans*, *S. sitiens* and *S. niger bilineatus* were screened using ITS PCR assay for the presence of *Trypanosoma* spp. DNA. Of the four *Stomoxys* spp. screened, trypanosome DNA was detected from two

species, namely, *S. n. niger* and *S. calcitrans*. Our results showed that *T. congolense* was most prevalent (11%) followed by *T. theileri* (8.2%). The least prevalent, *T. brucei*, was only detected from *S. n niger* (1.6%). To our knowledge this is the first study to report on detection of *Trypanosoma* spp. DNA from *Stomoxys* flies collected from the northeastern KZN. Results of this study, highlights that any vector control programme for AAT in this area should consider *Stomoxys* flies along with tsetse flies, the biological vectors of AAT.

Tuesday 16 September – 13h40 (Ndau & Nari)

011 - Marine fish blood flukes (Aporocotylidae) of South Africa: an under-explored fauna

Russell Q-Y. Yong¹, Olena Kudlai², Anja Vermaak¹ & Nico J. Smit¹

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The marine teleost-infecting blood fluke family Aporocotylidae has rapidly grown in the number of recognised species, more than doubling in both number of genera and species described since the turn of the 21st century. Regional bias in attention, however, means large parts of the world are under-studied for fish blood flukes; the entire continent of Africa, for example, does not have a single record of a marine aporocotylid. Our recent work in South Africa has uncovered the first reported instances of aporocotylid infections from marine fishes for the country. We report three new species from seabreams (family Sparidae), one from the heart of Hottentot or bronze seabream, *Pachymetopon blochii* (Valenciennes) from off Cape Town, another from the eyes of the musselcracker, *Sparodon durbanensis* (Castelnau) from off Garden Route (Tsitsikamma) National Park, Western Cape, and a third from the heart of zebra seabream, *Diplodus hottentotus* (Smith) from De Hoop Nature Reserve, Western Cape. We propose a new genus for the species which infects *P. blochii*; the remaining two species respectively conform to the genera *Skoulekia* and *Cardicola*. Finally, we provide a record of a species of *Deontacylix* Linton, 1910 from blue seachub, *Kyphosus cinerascens* (Forsskal) (Kyphosidae) from Sodwana Bay, KwaZulu-Natal, and contextualise it in the global understanding of species of that genus.

Monday 15 September – 09h00 (Ndau & Nari)

012 - Parasite diversity of the Karoo bush rat (*Otomys unisulcatus*) in the Western Cape

Jessica Kipling¹, Conrad Matthee², Alexandr A. Stekolnikov³, Eddie A. Ueckermann⁴, Cang Hui^{5,6}, Ernst Schlemmer¹ & Sonja Matthee¹

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The Karoo bush rat (*Otomys unisulcatus*) is endemic to the Western and Northern Cape provinces of South Africa where it lives in groups, eats succulents, and constructs unique stick nests. The species currently lacks a consolidated and quantitative parasite list. To address this, 159 *Otomys unisulcatus* (62 males and 97 females) were trapped across ten localities in the Western Cape of South Africa during the late spring, and summer periods of 2023-2025. All parasites were removed. A total of 7929 parasites (6025 ectoparasites and 1904 endoparasites) were recorded across seven taxonomic groups: lice, ticks, fleas, mesostigmatan mites, trombiculid mites, nematodes, and cestodes. The most abundant parasite taxa were lice (18.22 ± 2.76) followed by mites (15.03 ± 1.42). Chiggers were the most diverse taxon (five genera and fifteen species), followed by nematodes (five genera and five species) and fleas (four genera and nine species). Novel data include at least 20 new host-parasite records of which eight are undescribed chigger species. From these findings it is evident that *O. unisulcatus* hosts a relatively rich diversity of parasites. It is predicted that future studies which include the Northern Cape would likely add to the parasite profile of this rodent.

Tuesday 16 September – 09h30 (Ndau & Nari)

014 - Ectoparasites and gastrointestinal helminths associated with Smith's bush squirrel (*Paraxerus cepapi*) in South Africa

Inge Raubenheimer¹, Conrad A. Matthee², Alexandr A. Stekolnikov³, Jeanette Wentzel^{4,5}, Lourens Swanepoel⁶ & Sonja Matthee¹

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Paraxerus cepapi is an arboreal tree squirrel that occurs in the Savanna biome of Africa and information on its parasite diversity is limited and mostly qualitative. The aim of the study was to record the diversity and abundance of ecto- and helminth parasites associated with *P. cepapi* across its distribution in South Africa. *Paraxerus cepapi* individuals (n=94) were opportunistically obtained from eight localities during 2020-2024. In total, 21 parasite species (19 ectoparasites and two nematodes) and one tick species group were identified. This included three species of lice, five ticks, two *Xenopsylla* flea individuals, one mesostigmatic mite, nine chiggers and two nematodes. The two recovered cestode individuals remained unidentified. Nematodes were the most prevalent (93.67%) followed by lice (80.85%). *Syphatineria cepapi* was recorded in 92.41% of *P. cepapi*, while an unknown *Strongyloides* species, resembling *S. robustus*, was recorded in 21.52% squirrels. The lice species displayed variation in parasitope preference, while chiggers were primarily recorded in the ears. This study provides new country records for the lice species *Werneckia paraxeri* and *Enderleinellus heliosciuri*, for the chigger species *Microtrombicula polymorpha* and *Walchia* and the nematode *S. cf. robustus*. New locality records were documented for the nematode *S. cepapi* in South Africa and *P. cepapi* is a new host record for the nine chigger species and *S. cf.*

robustus. It is evident that *P. cepapi* in South Africa hosts a considerably larger diversity of parasite taxa than previously recorded. These findings warrant future studies on the parasite diversity of *P. cepapi* in Africa.

Tuesday 16 September – 09h00 (Ndau & Nari)

016 - Biting midges (Diptera: Ceratopogonidae: *Culicoides*) in South Africa: status and research

Karien Labuschagne

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Worldwide, *Culicoides* biting midges are implicated in the transmission of disease-causing agents to livestock, wildlife and man. The most important viruses transmitted by *Culicoides* in South Africa are African horse sickness (AHS), bluetongue (BT) and equine encephalosis (EE) viruses. Despite the significant impact on the equine and livestock industries, very few institutions are actively working on *Culicoides* taxonomy, monitoring and control. The ARC-OVR is a WOA reference centre for *Culicoides*-transmitted diseases, as well as the leading research centre on *Culicoides* species distribution and mapping, species identification and description of new species. Changes in farming practices and the environment necessitates pro-active monitoring to track changes in *Culicoides* species and disease distribution. DALRRD funding was obtained to monitor species distribution across South Africa. All *Culicoides* species collected through field surveys and other activities are identified to species level and the data added to the database to update distribution records and species maps. Collected specimens are also added to the National Collection of Insects of Veterinary Importance (NCIVI) that are housed at the ARC-OVR. These samples can be utilised for other research activities such as genetic studies on specific *Culicoides* species as well as the description of new species. To optimize field collections, trap evaluations are done to compare new trap designs and materials for collection of *Culicoides* species, as well as for other blood feeding Diptera. This presentation will highlight and discuss the research activities currently being conducted on *Culicoides* species and trap evaluations at the ARC-OVR.

Monday 15 September – 13h50 (Ndau & Nari)

018 - Predicting tick distributions in a changing climate: An ensemble approach for South Africa

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There are concerns that climate change may increase the habitats of ticks and impact animal and human health in the future. Understanding the distribution of ticks in relation to climate change is essential for both vector and pathogen management. Therefore, knowledge of the current and future spatial distributions of ticks is becoming critical to pathogen transmission and disease control. This study produced the baseline (2021-2040) and future (2041-2060) species distribution models for 10 tick species for South Africa, of which one is alien and nine are indigenous. Specifically, this study used ensemble models in the Biomod2 package with a suite of physical and anthropogenic covariates against ticks-presence-only location data submitted by the expert to the SANBI Integrated Publishing Toolkit. All species are projected to gain significant portions of suitable ranges in the future. Notably, an alien species, *Rhipicephalus microplus* is predicted to gain the most, with a 14% increase in its suitable range in South Africa. This expansion could potentially disrupt ecological balances in the ecosystems it is likely to occupy. Native species such as *Amblyomma hebraeum* and *Hyalomma rufipes* are expected to expand their ranges by 10 and 9%, respectively, and others with less than 6%. The predicted expansion of ticks could introduce new disease dynamics and potentially higher incidences of diseases in humans and animals in currently unaffected areas. The study provides baseline information to support ongoing monitoring and adaptive management strategies to mitigate the negative impacts associated with ticks on ecosystems, public health, and agriculture.

Monday 15 September – 14h20 (Ndlopfu)

019 - Diversity and evolutionary history of *Pneumocystis* fungi in their New Guinean rodent hosts

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Pneumocystis is a genus of fungal parasites that live in the lungs of mammals. They are described as having strong host specificity, but recent studies question this long-standing paradigm. In rodents, *Pneumocystis* evolutionary history showed patterns of co-evolution alongside numerous host switches, divergent lineages infecting specific hosts, and, in South-East Asia, lineages infecting multiple closely related species. In New Guinea, a unique system of two spatially overlapping but temporally separated radiations occurred following the colonisation of the island by two closely related rodent tribes, The Hydromyini ('Old Endemics,' 8 million years ago) and the Rattini ('New Endemics,' 1 million years ago). More recently, invasive *Rattus* species, *R. exulans*, and *R. rattus* have colonised the island through human dispersal. This mix of recent invaders and long-term residents provides a unique opportunity to explore how *Pneumocystis* adapts to hosts with very different evolutionary and ecological histories. We investigated the prevalence and genetic diversity of *Pneumocystis* using molecular screening and sequencing of the *Cytochrome b* gene from over 460 samples collected from two elevational transects (Mount Wilhelm and Finisterre Range) to maximise rodent species diversity. *Pneumocystis* prevalence was similar in the two endemic rodent

tribes but significantly lower in invasive *Rattus* species. Our phylogenetic analysis revealed clear contrasts compared to the evolutionary history of *Pneumocystis* in African and Southeast Asian rodents. We discuss how the unique radiation of New Guinea rodents can shed light on the evolutionary history of this important parasitic group.

Wednesday 17 September – 13h55 (Ndlopfu)

020 - Protozoan parasites on the gills of *Oreochromis mossambicus* from Letlamoreng/Setumo Dam, Mahikeng, North-West Province

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The Mozambique tilapia (*Oreochromis mossambicus*) is an ecologically and economically important species, especially in aquaculture. Recent mass mortality events, particularly in Letlamoreng/Setumo Dam, Mahikeng, South Africa, have raised concerns about the health of these populations. This study investigated the parasitic infestations affecting *O. mossambicus* during the June 2023 mortality event, focusing on protozoan parasites found on the gills, an organ essential for respiration. Fish samples were collected and necropsied, with gills, skin, and intestines examined for parasites using Haematoxylin staining and Silver Nitrate impregnation. Four protozoan species were identified: *Trichodina centrostrigeata*, *Ambiphyra neobolae*, *Chilodonella hexasticha*, and *Apiosoma piscicola*. These parasites co-existed on the gills, contributing to respiratory distress, and potentially exacerbating the mortality event. Comparisons with previous studies revealed variations in size and morphology, suggesting the need for further research to understand the role of these parasites in tilapia health dynamics. This study underscores the importance of protozoan parasites as a factor influencing tilapia health and survival in natural and aquaculture environments. The findings contribute to understanding parasitic infestations in tilapia and provide insights into managing and mitigating mass mortality events. Continued research on parasite-host interactions is crucial for developing better fish health management practices and policies in South Africa and other aquaculture settings worldwide.

Monday 15 September – 11h00 (Ndau & Nari)

021 - Taxonomic analysis of the parasitic community associated with Power's Clawed Frog, *Xenopus poweri* Hewitt, 1927 (Anura: Pipidae)

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With the exception of *Xenopus laevis*, the parasite fauna of *Xenopus* species is poorly known. This is especially true for *Xenopus poweri* as both its internal and external parasites remain largely unexplored. *Xenopus poweri* has a conservation status of least concern and a broad distribution, ranging from western to southern Africa, including countries such as Botswana, Namibia, Cameroon, Nigeria, and Angola. This study aims to investigate the parasite diversity of Power's Clawed Frog (*Xenopus poweri*). Frogs were collected from the Okavango swamps of Botswana and the Caprivi Strip of Namibia using baited bucket traps. A comprehensive

parasitic survey identified eight distinct parasite species across four invertebrate groups. These included two monogeneans (*Protopolystoma xenopodis* and *Gyrdicotylus gallieni*), four digeneans (*Dollfuscella* sp., *Oligolecithus elianae*, *Progonimodiscus doyeri*, and *Tylodelphys xenopodis*), one cestode (*Cephalochlamys namaquensis*), and two nematodes (*Batrachocamallanus slomei* and *Tanqua tiara*). The findings reveal a notable overlap between the parasite fauna of *Xenopus poweri* and that of *Xenopus laevis*, suggesting potential host-parasite similarities across *Xenopus* species. To deepen the understanding of these parasites the research explored the molecular and morphological aspects of these parasites. In conclusion, this research marks a significant advancement in broadening our understanding of parasite diversity in *Xenopus poweri* and elucidating host-parasite interactions.

Monday 15 September – 11h15 (Nda & Nari)

022 - Host and environmental factors influence ectoparasite infestations found on *Micaelamys namaquensis*

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Rodents and their parasites play an important role in ecosystem functioning, yet limited information exists on how abiotic and biotic features interact and influence ectoparasites associated with rodents in South Africa. The Namaqua rock mouse, *Micaelamys namaquensis*, is a widely distributed rodent found throughout southern Africa. This study investigated the ectoparasite infestations on this small rodent and particularly the influence of abiotic and biotic features across three biomes in South Africa. Machine learning elastic net regression was used in the analyses and the outcome was analysed with a mixed negative binomial generalized linear model. In total, 7412 ectoparasites were removed from 142 *M. namaquensis* from four Succulent Karoo, three Nama-Karoo and three Fynbos sites. Male hosts harboured higher abundances for overall ectoparasites (grouped to higher taxa). In addition, larger bodied hosts had higher mite and tick infestations. The overall ectoparasite; flea and tick abundance were significantly higher in the Nama-Karoo as opposed to the Fynbos and Succulent Karoo biome. Further, mite and tick infestations were found to be positively related to soil moisture, temperature, leaf area index and normalized difference vegetation index. These findings underscore the importance of both abiotic and biotic features in shaping ectoparasites infestation and advances the understanding of these interactions in explaining the mechanisms that influence ectoparasite diversity on rodents.

Tuesday 16 September – 10h15 (Nda & Nari)

023 - Mitochondrial genome fragmentation in parasitic lice

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Mitochondrial genome organization is diverse across Eukaryotes but remarkably stable across animals. Most bilaterian animals have mitochondrial genomes (mitogenomes) with highly conserved gene order and organization, encoded on a single circular chromosome. Parasitic lice (Insecta: Phthiraptera) exhibits a notable exception from this conservation, having highly variable mitogenomes in terms of gene order, heteroplasmy, and mitogenome fragmentation. From currently recognized groups of parasitic lice, the ecologically most diverse parvorder Amblycera also has the largest diversity of mitogenome organization, including single chromosome mitogenomes, highly fragmented and many possible intermediate states. In more specialized lice, mitogenome organization seems more phylogenetically conserved. In avian feather lice (Ischnocera), mitogenomes are single-chromosome or highly fragmented, without intermediate states discovered to date. In mammalian lice (Rhynchophthirina, Trichodectera, Anoplura), all known mitogenomes are highly fragmented. In our study, we analyzed an evolutionary pattern and temporal dynamics of mitogenome fragmentation across the most diverse group, Amblycera. We inferred some fragmentation events to have occurred less than five million years ago, and fragmentation rate to have changed multiple times in the course of amblyceran evolution. We compared the rates of DNA substitution and gene rearrangement within mitogenome fragmentation events and found that lineages with fragmented mitochondrial genomes had significantly higher rates of mitochondrial sequence evolution. The genes in these mitogenomes were likely to be more rearranged than those on single circular chromosomes. Combining phylogenomics, mitochondrial genomics and temporal analyses provides a portrait of mitogenome evolution, showing the importance of multilateral approach for improving the understanding of mitogenome fragmentation.

Wednesday 17 September – 13h10 (Ndlopfu)

026 - Environmental effects on nest microbiome-parasite interactions and bird condition: an experimental study

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The microclimate inside avian nesting cavities provides suitable growth conditions for microbial communities and ectoparasites, which in turn may play a crucial role in influencing the well-being of the host. In this study, we investigated the microbiome of Blue Tit (*Cyanistes caeruleus*) nests subjected to experimental manipulations of temperature and humidity, aiming to evaluate the impact of these factors on fungal and bacterial communities and on the associations between these microbial communities, parasitism, and nesting birds' condition. Our results indicated that while bacterial alpha diversity remained unaffected by the experimental manipulation, beta diversity differed significantly, particularly between nests with increased humidity and control nests. Similarly, elevated temperature and humidity increased fungal alpha diversity and altered fungal beta diversity. In addition, pathogenic fungi, including dermatophytes, proliferated in humidity nests, potentially contributing to poorer nestling body condition compared to other nest treatment groups. Furthermore, alterations in the microclimate influenced the interactions between microbes, ectoparasites and nestling body condition. We found positive relationships between microbes and parasites in the nests where they were more abundant or were not negatively affected by changes in the microclimate, therefore indicating that there were the necessary conditions to promote the development of those microbes that coexist with parasites. On the other hand, we identified strong associations between certain bacteria and fungi and ectoparasites such as fleas, mites and blood-sucking dipterans, which can facilitate microbial growth due to the effects of their parasitism. These findings highlight the complex interactions between nest microclimate, microbial diversity, ectoparasites, and nestling development.

Monday 15 September – 14h05 (Ndlopfu)

029 - Exploring the understudied biodiversity and taxonomy of corallanid isopods in Indonesian waters

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Corallanidae Hansen, 1890, is a small isopod family comprising six genera and 79 species. Most corallanids function as temporary parasites (micropredators) or commensalists, but *Argathona* Stebbing, 1905 species are distinct in their temporary parasitism of fish, feeding on blood before detaching. With only 16 described species dating back to 1857, much of the taxonomic knowledge of *Argathona* is outdated, with uncertainties regarding species validity and synonymy due to inadequate historical descriptions. While primarily distributed in tropical and subtropical waters, their biodiversity, biogeography, and host associations remain poorly understood. This study aimed to enhance knowledge of Corallanidae biodiversity in Central-Indo Pacific waters and clarify taxonomic uncertainties within the family. Morphological and molecular analyses were conducted on collected and preserved specimens from Australia and Indonesia. Australian samples were collected from Heron Island, Wistari Reef (Queensland), and Darwin (Northern Territory), while Indonesian specimens originated from the South China Sea and Java Sea, specifically Sarawak and South Kalimantan (Borneo). Morphological analysis confirmed all specimens belonged to *Argathona*, with multiple species present, including two new to science. This study provided new host records, including the first documented case of corallanids parasitising elasmobranchs, new morphological data for known species, the first records of *Argathona* spp. in Borneo, and the first molecular analysis of *Argathona* species. These findings improve understanding of Corallanidae host

associations and highlight the overlooked biodiversity of these isopods, emphasising the need for further research on their ecological roles and distribution.

Wednesday 17 September – 11h00 (Ndau & Nari)

030 - Reduce, reuse, recycle: redescription of one and description of two new *Gnathia* species (Isopoda: Gnathiidae) from historical museum material (1898–1976)

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Research on marine parasites, such as gnathiids (family Gnathiidae), has been overshadowed by terrestrial and freshwater parasites studies due to the challenges of offshore sampling. These temporary ectoparasites, found from tide pools to the open ocean, exhibit diverse morphological differences between their parasitic juvenile stages and free-living adults, which has complicated past taxonomy. Historically, taxonomic descriptions have focused on males due to their more distinguishable morphology. Although morphological standards for gnathiids were established in 1926 and refined over the past two decades, many early descriptions remain inadequate, necessitating redescrptions. However, obtaining fresh specimens requires specialised equipment, expertise, and funding, making museum collections invaluable for taxonomy. This study originally aimed to redescrbe *Gnathia spongicola* Barnard, 1920, described from the Temperate Southern Africa marine realm. The initial description was limited to a single drawing with outdated terminology and generic characters. During the examination of *G. spongicola* specimens from the Iziko Museum of South Africa, two additional species were identified and described as new to science. Morphological analyses were conducted using a Nikon SMZ1500 light microscope, with micrographs captured via a Nikon DS-Fi3 camera. Scanning electron microscopy (SEM) was performed following standard protocols. Illustrations were created using a camera lucida and finalised in Adobe Illustrator. All taxonomic information was entered into the DEscriptive Language for TAXonomy (DELTA) program to generate a standardised description. This study highlights the importance of museum collections in reducing the need for new sampling, reusing previously collected material to redescrbe species and recycling museum collections to describe new species.

Tuesday 16 September – 08h45 (Ndlopfu)

032 - Global latitudinal distributions of flea and small mammal host species richness, phylogenetic diversity, and functional diversity

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A latitudinal gradient in species richness (SR) is one of the most pervasive biogeographic patterns. SR is just one aspect of biodiversity, but equally important facets like phylogenetic (PD) and functional diversity (FD) received less attention. We investigated latitudinal patterns in SR, PD and FD of fleas and hosts using data of 1022 flea and 900 mammal species across the world. First, we asked whether latitudinal patterns in SR, PD and FD of fleas and hosts follow a latitudinal gradient. Then, we asked whether these patterns vary geographically, and differ between fleas and hosts. Our last objective was to determine whether latitudinal patterns in PD and FD follow the same as SR. Broken-stick regression models were used to analyse latitudinal variation of each diversity facet as well as patterns in fleas and hosts in each geographic quadrant. A classical latitudinal pattern was not found in fleas or hosts for any diversity facet or geographic quadrant, except for flea PD in the southeast and host FD in the southwest. Latitudinal patterns in diversity facets differed geographically but patterns of flea and host SR were similar in most quadrants whereas these patterns in flea and host PD were only similar in the southwest. No similarity was apparent in flea vs host FD and latitudinal patterns of flea and host PD and FD generally did not follow the pattern of SR. In conclusion, latitudinal gradients of SR, PD and FD are not universal but instead represent an interplay of ecological and historical processes.

Tuesday 16 September – 11h00 (Ndau & Nari)

033 - Polystomatid flatworms in Africa: State of knowledge and the way forward

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Polystomatid flatworms (Monogenea, Polystomatidae) are known from various hosts, including the Australian lungfish, all three orders of amphibians (salamanders, frogs, and caecilians), freshwater turtles, and even the eyes of the common hippopotamus. Of the 30 currently identified polystome genera, 19 are associated with amphibians, nine with freshwater turtles, one with the lungfish, and one with the hippopotamus. In Africa, four polystome genera - *Eupolystoma*, *Metapolystoma*, *Polystoma*, and *Protopolystoma* - have been recorded in amphibians, while two additional genera, *Kankana* and *Madapolystoma*, are known from Madagascar. A single genus, *Uropolystomoides*, has been found in freshwater turtles, and *Oculotrema* is the only known genus parasitizing the eye of the hippopotamus. In Africa, amphibian polystomes appear to be strictly host specific. However, in other regions, such as the Nearctic Realm, they exhibit a lower degree of host specificity. Similarly, polystomes

infecting freshwater turtles show less strict host specificity, especially in zoological gardens, where multiple turtle species are often kept in shared water bodies. Molecular evidence indicates that the cosmopolitan genus *Polystoma* is polyphyletic. This taxonomic cluster needs revision, as the African species differ significantly from *Polystoma integerrimum*, the European type species. Consequently, the African cluster requires reclassification and renaming.

Wednesday 17 September – 10h15 (Ndau & Nari)

034 - Schistosome species, parasite development, and co-infection combinations determine microbiome dynamics in the snail *Biomphalaria glabrata*

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Schistosomiasis is a snail-borne disease affecting over 200 million people worldwide. Despite dedicated control efforts and effective diagnostic tools, schistosomiasis remains prevalent. Novel and sustainable control measures are urgently needed. Bacteria might offer such a solution as links between bacteria, disease resistance and transmission potential of intermediate hosts have been established in other systems. To better understand the tripartite interaction potentially driving snail-schistosome compatibility patterns, microbial communities must be investigated throughout and across various parasite exposure conditions. Therefore, we studied *Biomphalaria glabrata* snails exposed to a high- and low-shedder population of *Schistosoma mansoni* and *Schistosoma rodhaini* in single and co-exposure experiments. Snails were sacrificed at different time points post-exposure and their bacterial communities and trematode (co-)infection status were determined through metabarcoding tools. Snails infected by low- and high-shedder *S. mansoni* populations were more likely to have bacterial community dysbiosis than those infected by *S. rodhaini* but this was also affected by miracidial load. Moreover, the single-infection hierarchical effect on the bacterial component of the microbiome is not maintained under co-infection with *S. rodhaini*, which appears to stabilize the snail's bacterial profile even after being outcompeted by high-shedder *S. mansoni*. Finally, alpha diversity differed significantly between infected and uninfected snails around the onset period of shedding at 30 days post-miracidial exposure. The timing of this bacterial shift suggests an intricate parasite-snail interaction around key parasite development moments. Future studies investigating the tripartite interaction are advised to consider the effect of outcompeted or prepatent infections on the snail's microbiome.

Tuesday 16 September – 14h10 (Ndlopfu)

035 - The *Caligus* stumble block

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Caligus (Caligidae: Siphonostomatoida) consists of about 280 species of copepods that are mostly infecting the external surface or the oral/gill cavities of marine fish hosts with a few also reported from fresh and brackish waters. Additionally, some were reported from plankton samples with no host records. The presence of *Caligus* species in plankton samples may be due to the host moving from marine to freshwater that will dislodge the parasites and force them to find a new host or due to competitive interaction with other ectoparasites that force them to leave the host and find another. Of the known species, only 52 were reported off southern Africa. Collected *Caligus* specimens are fairly easily recognized as a *Caligus* species due to a set of distinguishing features, but a specific species identification is more complicated. To assist with the species identification, many species were grouped based on shared features into eight species groups. Species collected off South Africa will be used to illustrate the shared features of the applicable species group as well as features of some species not attributed to any of the species' groups.

Tuesday 16 September – 10h30 (Ndlopfu)

037 - Marine protected areas and parasite conservation: metazoan parasites of the Cape white seabream, *Diplodus capensis*, as case study

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Whereas the community composition of fishes has been vastly studied, research examining the community composition of parasites that live within fishes is limited. Even more sparse are data that can work towards describing what drives parasite community composition and distribution. To collect such baseline data, we examined the metazoan parasite communities of *Diplodus capensis* (Smith) (Teleostei: Sparidae), a fish endemic to the coast of southern Africa, and which is heavily relied on for subsistence and sport angling. We were also curious to know if metazoan parasite communities of *D. capensis* varied between marine protected areas (MPAs) and non-MPAs, to assess whether parasites are also inadvertently being protected by these conservation efforts. Accordingly, we collected sixty specimens of *D. capensis* across two MPAs and three non-MPAs and performed parasitological dissections of the fish. The parasites were identified using morphological and molecular analyses. Using these data, we analysed the alpha and beta diversity of the parasites among fish, among localities, and between protection statuses using Shannon-Wiener and Simpson's diversity metrics, and Bray Curtis dissimilarity metrics, respectively. Thirty parasite taxa were identified, and the proportional abundance of parasite taxa varied greatly across fish. Non-MPAs had a slightly higher richness of parasitic taxa with fewer dominant families than MPAs, albeit a less even richness compared to the MPAs. This study is among the first in South Africa to explore the link between protection status and parasite biodiversity, providing foundational data for understanding how marine protected areas might influence the distribution of parasitic taxa.

Tuesday 16 September – 09h30 (Ndlopfu)

039 - Exploring the evolutionary history of the Cryptogonimidae

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The Cryptogonimidae is a large family of trematodes found circumtropically in freshwater and marine ecosystems. Their definitive hosts are piscivorous fishes or reptiles, transmitted through fish second intermediate hosts. In this talk, I will explore the evolutionary and biogeographical narrative of the Cryptogonimidae, attempting to infer whether the directionality and frequency of switching between freshwater and marine ecosystems and between reptile and fish definitive hosts. Recent increases in taxa coverage have greatly improved our capacity for insights into the history of this family, but important gaps and uncertainties remain.

Tuesday 16 September – 11h15 (Ndlopfu)

042 - Fish as potential non-host predators shaping trematode communities in a subarctic lake ecosystem

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Predation is an important ecological force structuring parasite populations, and trematodes (Digenea), with their complex life cycles involving multiple hosts, play an integral role in aquatic food webs. However, the role of non-host predators in the formation of trematode communities is still largely unexplored. As dead-end hosts, fish may disrupt trematode transmission by removing infected hosts, thus limiting the spread and dynamics of the parasite population within the already challenging short transmission window in high-latitude ecosystems. Given the relatively low species diversity and well-documented trophic interactions in the food web, Lake Takvatn (Norway) is an ideal natural laboratory to study seasonal predator-prey-parasite dynamics. We investigated the influence of Arctic charr (*Salvelinus alpinus*) and brown trout (*Salmo trutta*) as non-host predators of trematodes by studying their consumption of infected intermediate hosts, snails (*Ampullaceana balthica*) and amphipods (*Gammarus lacustris*). We conducted seasonal sampling (July, August and October) to assess trematode community composition in both free-living and predated hosts, including ecological factors that influence the strength of predator-parasite interactions (mechanistic and behavioral traits). By addressing this critical knowledge gap, our results will improve understanding of the ecological role of non-host predators in parasite population dynamics, particularly in subarctic ecosystems where environmental constraints may amplify these effects.

Monday 15 September – 09h30 (Ndau & Nari)

043 - Diversity and biology of *Spirometra* tapeworms, zoonotic parasites of wildlife

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Tapeworms of the genus *Spirometra* (Cestoda: Diphyllbothriidea) are well-known intestinal parasites of carnivores, with their larval stages (spargana) occurring in various vertebrates. However, their species diversity, host associations and geographical distribution remain poorly understood. Molecular data support the validity of *Spirometra*, which has often been synonymised with *Diphyllbothrium*. Although the species of both genera share morphological similarities, they are not closely related and their life cycles are different. This review presents five species currently recognised as valid (*S. asiana*, *S. decipiens*, *S. erinaceieuropaei*, *S. mansoni* and *S. theileri*) and two additional genetic lineages representing two undescribed species. A certain geographical pattern can be observed in the distribution of the individual *Spirometra* species that have been genetically characterised. Molecular data on *Spirometra* tapeworms in Africa are scarce and genetically characterised specimens are available only for two, possibly three species (the African endemit *S. theileri*, the cosmopolitan *S. mansoni* and possibly the recently described *S. asiana*, which should be confirmed). The comparison of genetically identified specimens using the complete *cox1* marker with corresponding morphological vouchers (hologenophores) is of crucial importance for clarifying the distribution and host associations of *Spirometra* tapeworms.

Wednesday 17 September – 13h25 (Ndlopfu)

045 - Snacking preferences of tsetse flies: Identification of vector-host-parasite dynamics at the interface between agricultural and conservation areas

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African trypanosomosis (AT) has long plagued Africa, affecting both humans and animals. The disease, caused by *Trypanosoma* parasites, depends on complex interactions involving tsetse flies (*Glossina* sp.) as vectors and mammalian hosts. Understanding the interactions between parasites, vectors, and hosts is crucial for devising strategies to control AT, particularly in areas where agriculture and conservation intersect. This study aimed to identify these interactions in interface and conservation regions in central and southern Mozambique. We collected 200 tsetse flies from two national parks and their buffer zones. Flies were identified following taxonomic keys. We then identified their blood meal sources, the trypanosome species infecting them, and the composition of their microbiome, using a metabarcoding

approach: we amplified selected genetic markers for these different components and sequenced the amplicons on a high-throughput platform. Sequence data was processed using mbctools and FROG. Overall, we identified 4 fly species: *G. austeni*, *G. brevipalpis*, *G. morsitans* and *G. pallidipes*. Our metabarcoding approach revealed five trypanosome species, with *T. brucei*, *T. congolense*, and *T. godfreyi* being the most prevalent. Blood meal analyses identified 18 animal species; in the central region, warthog was the dominant blood source, followed by human, while in the southern region, human was most common, followed by bushbuck. The tsetse fly microbiome was dominated by *Wigglesworthia glossinidia* and *Wolbachia* sp. Findings showed a high diversity of host and parasite species, where blood meal preference and bacterial diversity were influenced by geographical location and tsetse fly species, highlighting the complexity of AT dynamics.

Tuesday 16 September – 13h25 (Ndaou & Nari)

046 - Diversity of avian schistosomes

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Schistosomes are parasites of birds and mammals, including humans. Some of them are the causative agents of cercarial dermatitis, with more and more cases being reported worldwide. Despite their common occurrence, their diversity is poorly understood. We have molecularly characterised schistosomes from aquatic snails and birds from different freshwater ecosystems in Europe using three genetic markers, *cox1*, ITS1-5.8s-ITS2, and 28S rDNA, complemented with all molecular data available in GenBank. *cox1* appears to be the most suitable marker for species identification. Based on the available molecular data, 25 species and 50 unidentified lineages were found worldwide. From our study, four species were found in birds from the Czech Republic (*Allobilharzia* sp. I, *Dendritobilharzia pulverulenta*, '*Trichobilharzia*' *filiformis* and *Trichobilharzia regenti*), while 16 species were found in snails from the Czech Republic, Germany, Norway and Poland. Of these, 14 were previously reported species (*Anserobilharzia* sp. I, *Bilharziella polonica*, *T. anseri*, '*T.*' *filiformis*, *T. franki*, *T. mergi*, *T. regenti*, *T. szidati*, *Trichobilharzia* sp. VIII, Schistosomatidae gen. sp. VIII, X, XVIII, XIX, and XXI), while two new genetic lineages were discovered (Schistosomatidae gen. sp. XXII and XXIII). In addition, cryptic species were discovered within the populations of *Allobilharzia visceralis*, *Anserobilharzia brantae*, *D. pulverulenta*, *T. szidati*, and *Nasusbilharzia melancorhypha*. Despite the great diversity discovered, the taxonomic classification is still unclear, as there are no adults suitable for an appropriate morphological description.

Tuesday 16 September – 13h10 (Ndlopfu)

047 - Predicting heartwater spread using mechanistic models

Adam Fisher¹ & Hannah Rose Vineer¹

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Heartwater is a fatal tick-borne disease (TBD) affecting wild and livestock ruminants throughout much of Africa. Furthermore, the geographic range of heartwater is expanding and is predicted to continue doing so. Despite this, our understanding of heartwater dynamics lags far behind that of many other TBDs. We are therefore limited in our ability to predict disease spread and design effective control strategies. In this study, we derive and analyse a mathematical model of heartwater dynamics. We analyse our model to predict the most influential parameters for disease risk, both in terms of new outbreaks, and in heartwater-endemic regions. We show that the host finding efficiency of ticks is the most influential parameter affecting outbreak risk. Also, outbreak risk is highly sensitive to the impact of the heartwater pathogen on tick fitness – a previously unexplored concept for any TBD system. In areas where heartwater is established, we show that disease can be controlled via enzootic stability (prolonged host immunity attained via frequent pathogen exposure). However, the maintenance of enzootic stability was dependent on several ecological and physiological parameters. Regarding practical output, we suggest prioritising tick control measures during periods when ticks are most active in terms of dispersing towards hosts, so as to mitigate heightened outbreak risk. In addition, given the specificity of conditions required for enzootic stability, we caution against relying solely on enzootic stability for long-term heartwater protection. More broadly, our study highlights important tick life history parameters that have been neglected by previous TBD models.

Wednesday 17 September – 09h15 (Ndlophu)

048 - Characterisation of vector-borne pathogens in brown and spotted hyenas from Namibia and Tanzania reveals high frequency of infection and genetic variability

Jürgen Krücken¹, Gabor Á. Czirják², Sabrina Ramünke³, Maria Serocki⁴, Heribert Hofer⁵, Georg von Samson-Himmelstjerna⁶, Marion L East⁷ & Bettina Wachter⁸

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Wildlife species are often infected with vector-borne pathogens (VBPs). Here, we examined samples with PCR and sequencing from brown hyenas (*Parahyaena brunnea*) from Namibia (BHNA, n = 17), and spotted hyenas (*Crocuta crocuta*) from Namibia (SHNA, n = 19) and Tanzania (SHTZ, n = 25). We targeted Onchocercidae, Piroplasmida, Hepatozoidae, Anaplasmataceae and *Rickettsia* spp. and conducted maximum-likelihood phylogenetic analyses. Evidence of filaroid infection was detected in 47.1% BHNA, 47.4% SHNA and 36.0% SHTZ. Phylograms suggested presence of several undescribed *Acanthocheilonema* species. *Babesia lengau*-like piroplasms were identified in 70.6% BHNA, 88.9% SHNA and 32.0% SHTZ, and their sequence variability was high compared to *B. lengau* from cheetahs (*Acinonyx jubatus*). *Hepatozoon felis*-like parasites were found in 64.7% BHNA, 36.8% SHNA and 44.0% SHTZ. Phylogenetic analysis revealed high diversity with hyena sequences located outside the major *H. felis* cluster from wild and domestic felids. Anaplasmataceae infection was high with 82.4% in BHNA and 100.0% in SHNA and lower in SHTZ (32%). For the first time in Sub-Saharan Africa, *Rickettsia raoultii* was detected in one BHNA and three SHTZ. In BHNA and SHNA, co-infections occurred significantly more often than in SHTZ. Despite high VBPs frequencies, knowledge regarding pathology caused by single- and co-infections in mammalian hosts, and vectors of new parasite species is missing. Characterisation of VBP genotypes in wild and domestic host species, and potential vectors from overlapping habitats will help clarify the ecology of VBPs and their impact on wildlife and domestic animals.

Wednesday 17 September – 14h10 (Nda & Nari)

050 - Making a comeback: a new perspective on gnathiid species described in the 1900s to early 2000's

Anja Erasmus¹, Kerry A. Hadfield¹, Matt D. Nicholson², Gina C. Hendrick², Paul C. Sikkell^{1,2} & Nico J. Smit^{1,2}

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The functional integrity of coral reefs depends on a variety of organisms, including gnathiid isopods, which play a crucial ecological role. However, many species of gnathiid isopods, first described in the 1900s, have remained poorly characterised due to limited data. Focusing on recent surveys conducted across 15 islands within the Tropical Atlantic Realm (TAR), this study revisits species of the genus *Gnathia* from this region. Using light traps, emergence traps, and benthic substrata washing techniques, larval and adult gnathiid specimens were collected for detailed analyses. Larval specimens were kept alive for observation in the laboratory until moulting into adult males to ensure accurate identification. Six previously described species with varying levels of information available were collected, namely *Gnathia calsi* (1993), *Gnathia jimmybuffetti* (2023), *Gnathia magdalenensis* (1988), *Gnathia marleyi* (2012), *Gnathia micheli* (2012), and *Gnathia virginalis* (1926). Of these, only *G. jimmybuffetti* and *G. marleyi* have been molecularly characterised and have descriptions of the female and juvenile stages. In an attempt to standardise the information available on all species of *Gnathia*, newly collected material was subjected to scanning electron microscopy and genetic sequencing for all life stages, and new distribution ranges were recorded. These techniques identified key distinguishing features, linked different life stages and reinforced morphological findings with selected molecular markers. Furthermore, these surveys led to the discovery of several new species, emphasising the presence of yet-to-be-described gnathiid species in the Tropical Atlantic region. This research underlines the importance of revisiting historical

species data with modern techniques to better understand biodiversity, distribution, and ecological roles in marine ecosystems.

Wednesday 17 September – 10h30 (Ndau & Nari)

051 - Small particles, big impacts: exploring ionic and nano silver's influence on the reproduction of *Macrogyrodactylus congolensis*

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The monogenean ectoparasite, *Macrogyrodactylus congolensis*, rapidly reproduces and has an opportunistic transmission on *Clarias gariepinus*. In aquaculture facilities, it reaches high intensities and causes severe pathology. Silver is a recognised therapeutic remedy due to its antimicrobial properties and a few recent reports discuss its potential in controlling parasitic infections in/on fish. This study aims to evaluate the effects of ionic silver (AgNO₃) and engineered nano-silver (nAg) on the reproductive dynamics, spatial distribution, and tegument integrity of the ectoparasite *M. congolensis*. Parasite reproduction was assessed off-host (exposed to a range of concentrations of AgNO₃ and nAg) and on-host (fish individually infected with parasites and exposed to LC₁₀ concentrations of AgNO₃ and nAg for *M. congolensis*). The spatial distribution of parasites was analysed using heat maps and pixel counts to identify preferred attachment sites. Scanning electron microscopy (SEM) and energy-dispersive X-ray spectroscopy (EDS) were used to examine parasite tegument morphology and elemental composition following exposures. Off-host exposures showed concentration-dependent effects, with higher concentrations ($\geq 50 \mu\text{g/L}$ AgNO₃, $\geq 20 \text{ mg/L}$ nAg) inhibiting parasite reproduction. On-host exposures resulted in moderate inhibition of parasite reproduction. Spatial distribution analyses of *M. congolensis* highlighted a preference for the host's head, which suggests targeted microhabitat selection. SEM revealed tegument disruptions in parasites exposed to both forms of Ag, with AgNO₃ causing more observable damage compared to nAg. EDS analyses confirmed Ag accumulation on the parasite's tegument following exposures. These findings suggest the potential of Ag treatments for monogenean management in aquaculture; however, additional research is required.

Monday 15 September – 09h45 (Ndau & Nari)

056 - Exploring parasite diversity in white-breasted cormorant (*Phalacrocorax lucidus*) from Loskop Dam, South Africa, with the first report of *Macrobilharzia* sp.

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Parasites are prevalent in wildlife, with trematodes commonly infecting piscivorous birds, including cormorants. However, research on trematode parasites in southern Africa, particularly those infecting piscivorous birds, is limited. This study investigated the trematode parasites infesting the white-breasted cormorant, *Phalacrocorax lucidus* (Lichtenstein, MHC, 1823) at Loskop Dam, Mpumalanga Province, South Africa using morphological techniques. Cormorants (n=14) were collected by members of the Mpumalanga Tourism and Parks Agency (MTPA), and parasitological examination revealed endoparasites in their digestive systems. Several trematodes were identified, including *Macrobilharzia* sp., *Clinostomum* sp., and *Petasiger* sp. Molecular characterisation is underway for species confirmation. *Macrobilharzia* sp. represents the first recorded occurrence of this parasite in South Africa. All cormorants examined were infected with at least one trematode species, therefore, having a 100% prevalence of trematodes. *Petasiger* sp. had the highest prevalence of 100%, while *Clinostomum* sp. had the lowest prevalence of 7%. The parasite fauna exhibited a high diversity, with additional species awaiting identification. Phylogenetic analysis will help clarify the relationships among these species. The presence of zoonotic species highlights the ecological and health significance of the host-parasite system. This study significantly expands the understanding of parasite diversity in Loskop Dam, South Africa and provides a baseline for future research on trematode infections in piscivorous birds.

Monday 15 September – 10h30 (Ndau & Nari)

057 - Population genetic structure and intraspecific variability in generalist fish parasites

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Monogenean parasites often exhibit strict host specificity and are commonly used in cophylogenetic studies due to their close evolutionary associations with their hosts. However, generalist species, which infect a broad range of hosts, provide valuable insights into population structure and dispersal patterns. Some monogenean species have been recorded from remarkably diverse host ranges, making them ideal models for assessing host and geographic influences on parasite population structure. Only in the last decade have population genetic and taxonomic studies of monogeneans begun incorporating mitochondrial genes and whole mitogenomes. While these markers have proven highly effective, mitochondrial data for monogeneans remain scarce and are currently available for only a few species. In contrast, microsatellites (one of the most widely used population genetic markers) have been relatively underutilized in monogenean research. Our application of microsatellite markers to monogeneans yielded surprisingly consistent results, revealing population genetic patterns similar to those observed in vertebrates. However, unexpected subpopulation structuring at the local level suggests that parasite population structure is closely linked to the population structure of their hosts. Nonetheless, this relationship is not universal, as our data also indicate that anthropogenic factors significantly shape parasite population structure at both local and broad geographic scales. Our large-scale genotyping of monogeneans repeatedly revealed exceptional intraspecific mitochondrial variability, with the patterns

intimately linked to phylogeography of their fish hosts. However, the high mutation rate in mitochondrial regions, often not reflected in commonly used ribosomal markers, must be considered in future taxonomic studies.

Monday 15 September – 10h45 (Ndau & Nari)

058 - *Anaplasma platys* beyond canines: A systematic review of host range, zoonotic potential, and knowledge gaps in Africa

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Tick-borne pathogens pose a significant threat to animal and human health, particularly in Africa, where emerging and neglected pathogens are identified incidentally. *Anaplasma platys* is a causative agent of canine cyclic thrombocytopenia, transmitted by *Rhipicephalus sanguineus* sensu lato. However, reports of *A. platys* in Africa remain scarce and fragmented, with most detections occurring as co-infections in broader *Anaplasma* surveys. Consequently, no dedicated studies have comprehensively assessed its epidemiology, host range, and zoonotic potential in the region. A systematic review was conducted from February to May 2025, analysing all English-language publications available in PubMed, ScienceDirect, and Scopus. Following several screening processes, 122 peer-reviewed studies published from 1997 to 2024, were deemed eligible. The findings indicate that *A. platys* have been detected in 24 of the 54 African countries across multiple host species. While its prevalence in dogs ranged from 100% to 1%, it was also identified in cattle (84%–0.2%), sheep (66.7%–1%), goats (34.7%–4%), camels (39.62%–1%), impalas (7%), and buffaloes (2%). Additionally, *A. platys* were detected in various tick species, including *R. sanguineus* (52%), *Rhipicephalus pulchellus* (24%), *Rhipicephalus annulatus* (5.6%), *Hyalomma leachi* (18.9%), and *Hyalomma excavatum* (24.5%). A documented human case involved a veterinarian who had travelled to South Africa, raising concerns about zoonotic potential, though the infection source remains unclear. These findings highlight *A. platys*' broad host range and association with multiple tick vectors. However, critical knowledge gaps remain regarding host-specific genotypes and tick species' roles in transmission.

Wednesday 17 September – 10h30 (Ndlopfu)

059 - Characterising a new *Udonella* (Udonellidae: Monogenea) species: Integrative taxonomy of an epibiont from South African waters

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The marine ecosystem hosts a complex network of parasites, including the intriguing genus *Udonella*. These epibionts use parasitic copepods as substrates to indirectly feed on their fish hosts. Despite their widespread presence, only ten species are documented globally. Historically, classification was challenging due to the lack of key morphological traits, but molecular research has clarified their taxonomy, confirming Udonellidae as a monophyletic group. New species discoveries play a crucial role in refining their phylogeny. The present study describes a new *Udonella* species found on *Caligus tetradontis*, a parasite of the Evileye blaasop, *Amblyrhynchote honckenii*, from South Africa's coast. Twelve udonellids were found on three *C. tetradontis* collected from a single *A. honckenii* specimen caught at Mossel Bay. The udonellids were morphologically analysed and molecularly sequenced (partial 18S and 28S rDNA genes). Morphology revealed distinct characteristics in body size, pharynx, ovary, and testis that clearly differentiate the new species from existing *Udonella* taxa. The phylogenetic analysis of 18S rDNA revealed a close relationship between the newly discovered *Udonella* species and *Udonella fugu*, the only other udonellid known to be an epibiont on a caligid parasite of the family Tetraodontidae. This connection highlights the significance of host specificity in udonellid biology. *Udonella* species notably exhibit stronger host specificity to fish rather than copepods, with both fish host and phylogeography playing crucial roles in species identification. This research demonstrates how combining morphological and molecular data enhances species delimitation. Moreover, it underscores the evolutionary significance of host-parasite interactions in shaping udonellid diversity and distribution.

Tuesday 16 September – 11h00 (Ndlopfu)

061 - Back to the future: exploring the diversity of species of *Haemogregarina* in terrapins, with a focus on southern Africa

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Species of *Haemogregarina* Danilewsky, 1885 (Apicomplexa: Haemogregarinidae) are some of the most common and widely distributed obligate apicomplexan blood parasites of primarily aquatic ectothermic vertebrates. Approximately 40 species of *Haemogregarina* have been described infecting terrapin species globally, however, only two, *Haemogregarina maputensis*, Diaz 1950 and *Haemogregarina pelusiensi*, Pienaar 1962, have been described in Southern Africa. Most initial descriptions of species of *Haemogregarina*, including *H. maputensis* and *H. pelusiensi*, were based on the morphology of peripheral blood gamont stages. As the gamonts of species of *Haemogregarina* display high morphological similarity, the integration of morphological and molecular techniques is essential in the study of these parasites. This study assesses the species diversity of species of *Haemogregarina* infecting freshwater terrapin hosts using both morphological and molecular approaches. Additionally, blood samples from *Pelu. sinuatus*, *Pelu. subniger*, *Pelu. castenoides*, *Pelomedusa subrufa* and *Pelo. galeata* were screened for species of *Haemogregarina*, with more than 95% of terrapins infected. Three genotypes were identified, with one species of *Haemogregarina* infecting all host

species screened. Two genotypes conform morphologically with *H. maputensis* and *H. pelusiensi*, warranting the redescription and molecular characterisation of these species. The findings of this study reveal that a) the diversity of this group is higher than previously thought and that these parasites are not host-specific and b) highlight the need for further research to fully understand the evolutionary and ecological dynamics of these parasites.

Wednesday 17 September – 11h15 (Ndlopfu)

062 - Occurrence of vector-borne pathogens in Namibian herbivores: differences between Etosha National Park and freehold farmland

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The study of vector-borne pathogens (VBPs) in Southern Africa has a long history due to the importance of these microorganisms for both human and veterinary medicine. Wildlife species are important reservoirs for VBPs and mortality events have been reported in various herbivores. Considering the Southern African biodiversity of both hosts and pathogens, our aim was to screen opportunistically collected samples of blood and liver from different herbivore species with PCR for Piroplasmida, *Bartonella* and Trypanosomatida. We screened 75 samples from herbivores from the Etosha National Park (ENP) in Namibia and 154 samples (140 wildlife species, 14 livestock) from the Namibian freehold farmland. In line with previous research, 37.1% of the animals were infected with piroplasms. The frequency of infection in ENP was lower than in freehold farmland (16% and 47.4%, respectively). Besides known piroplasms such as *Theileria equi*, our sequencing data suggested the presence of several unclassified species. *Bartonella* were detected in ENP in wildebeests only (n=12, 16%), whereas on freehold farmland, predominantly oryx and wildebeests were *Bartonella* positive (10%). All are unclassified *Bartonella* but one kudu was positive for *B. bovis*. *Trypanosoma* were only detected in two kudu and one cattle sample from freehold farmland, while another kudu was positive for *Leishmania*. Translocations associated with game industry and conservation programs as well as the expansion of livestock production revealed an increase in the risk of transmission within wildlife and between wildlife and livestock in recent years. Thus, understanding the ecology and epidemiology of these pathogens is becoming even more crucial.

Wednesday 17 September – 10h45 (Ndlopfu)

063 - Cardiopulmonary Parasites in Golden Jackals from Italy

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The golden jackal (*Canis aureus*) has recently expanded its range into northeastern Italy, settling in Friuli Venezia Giulia (FVG). Eastern European countries report low prevalence values for cardiopulmonary parasites, but data remain scarce. This study provides the first comprehensive assessment of cardiopulmonary nematodes in golden jackals from northeastern Italy, offering insights into their potential epidemiological role. From February 2009 to March 2025, golden jackals from the FVG region were examined post-mortem, primarily after road accidents deaths. After removal, cardiopulmonary system was opened and inspected macroscopically and microscopically under a stereomicroscope, and lung tissue was washed to collect additional specimens. Nematodes were identified to species level using morphometric keys and confirmed by sequencing mtCO1 gene. Prevalence and mean intensity were calculated for each taxon (Wilson method for 95% confidence intervals). Fifty-two jackals out of 110 were positive, with an overall infection prevalence of 47.3% (95%CI:38.2-56.5). Four nematode species were detected, with *Angiostrongylus vasorum* being the most prevalent (34.5%, 95%CI:26.3- 43.8), followed by *Eucoleus aerophilus* (12.7%, 95%CI:7.7-20.4) and *Crenosoma vulpis* (12.7%, 95%CI:7.7-20.4), and *Dirofilaria immitis* (5.5%, 95%CI:2.5-11.4). *A. vasorum* had the highest mean intensity (7.3), followed by *C. vulpis* (1.2), and *E. aerophilus* and *D. immitis* (0.4). This study highlights the role of golden jackals in the epidemiology of veterinary-relevant cardiopulmonary parasites in FVG. The high prevalence detected for *A. vasorum* suggests a potential role as secondary reservoir, while this species seems to act as a carrier or amplifier for *C. vulpis*, *E. aerophilus* and *D. immitis*. These findings emphasize the need for continued surveillance, considering that this species is strongly expanding its geographical range.

Wednesday 17 September – 13h10 (Ndau & Nari)

064 - Multiplex real-Time PCR for detecting *Theileria bicornis* and *Babesia bicornis* in rhinoceros

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Black (*Diceros bicornis*) and white (*Ceratotherium simum*) rhinoceroses in Southern Africa face significant threats from poaching, habitat loss and translocation-related stress, which have been linked to mortalities associated with *Theileria bicornis* and *Babesia bicornis* infections. *Theileria bicornis* and *Babesia bicornis* have been reported in black and white rhinoceroses in South Africa. Although these parasites have been reported in both species, their epidemiology remains poorly understood. While effective in detecting subclinical infections, current molecular diagnostic assays are not well-suited for routine surveillance or

large-scale screening. To address this gap, we developed and evaluated a multiplex qPCR assay using species-specific TaqMan™ minor groove binder (MGB) probes to simultaneously detect *T. bicornis* and *B. bicornis* in South African rhinos. The assay successfully amplified an 87 bp fragment of the *T. bicornis* and a 51 bp fragment of the *B. bicornis* 18S rRNA gene, achieving high efficiencies of 99.9% and 98.0%, respectively. Probit analysis determined a 95% LOD of $10^{-5.203}$ % and $10^{-5.998}$ % parasitized erythrocytes for *T. bicornis* and *B. bicornis*, respectively. No cross-reactivity was observed with other protozoan parasites, confirming the assay's specificity. Screening of 223 field samples from rhinos in Mpumalanga province found that 25% of black rhinos and 53% of white rhinos tested positive for *T. bicornis*. In contrast, *B. bicornis* was detected in only 1% of black rhinos as a single infection, but co-infection with *T. bicornis* occurred in 16% of black rhinos and 1% of white rhinos. The findings suggest that *T. bicornis* is prevalent in both rhino species in the region, particularly in white rhinos, while *B. bicornis* appears rare and is primarily detected as a co-infection in black rhinos. This multiplex qPCR assay enhances epidemiological surveillance by providing a sensitive and efficient tool for simultaneous detection, enabling more accurate prevalence estimates and a better understanding of co-infection patterns to improve conservation and disease management strategies.

Wednesday 17 September – 08h45 (Ndlopfu)

065 - Parasite infections in wolves: a study on health risks and zoonotic implications

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The grey wolf (*Canis lupus*) population in Italy has expanded due to protective legislation and favourable ecological conditions, yet human-related threats remain significant. Wolf-dog interactions can facilitate disease transmission, impacting wildlife conservation and public health. This study investigated the health status of wolves in the Foreste Casentinesi National Park (FCNP, Italy) using non-invasive methods, focusing on parasitic infestations, particularly echinococcosis. Fecal samples were collected along transects across the FCNP (2019-2020). Samples were stored at -80°C before processing. Genetic analysis was performed on fresh samples. Copromicroscopy (solution of s.g. 1.300) was carried out on all samples available. A duplex real-time PCR for the detection of *E. granulosus* and *E. multilocularis* was conducted on the genotyped and Taeniid-positive samples. Prevalence (C.I. 95%) was computed. A total of 260 wolf samples were analyzed, with 132 samples successfully genotyped, identifying 80 individuals. Copromicroscopy revealed high prevalence of *Eucoleus* spp. (72/80-90.0%;95%CI:81.5–94.8), *Sarcocystis* spp. (34/80-42.5%;95%CI:32.3-53.4), Taeniidae (23/80-28.7%;95%CI:20.0–39.4), Ancylostomatidae (21/80-26.2%;95%CI:17.9– 36.8), while coccidia, *Toxocara canis* and *Trichuris vulpis* had prevalence below 3%. Molecular analysis for *E. granulosus* and *E. multilocularis* on 104 samples returned no positives. Although *E. granulosus* is widely circulating in sheep flocks in Central Italy, our results suggest that wolves in the FCNP do not play any role in the epidemiology of this zoonotic parasite. On the contrary, pathogens shared between wildlife and domestic carnivores (*Eucoleus* spp., Taeniidae and

Ancylostomatidae) were commonly found in our study, highlighting a potential role of carrier and/or spreaders of wolves, especially given the increasing interactions between wild and domestic carnivores.

Wednesday 17 September – 13h25 (Ndau & Nari)

066 - Diversity and distribution of ectoparasites associated with *Rhabdomys* spp. (Muridae) in the Fynbos, Succulent Karoo and Nama-Karoo biomes

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Species in the rodent genus *Rhabdomys* are distributed across southern Africa. Known for their ecological flexibility and opportunistic behaviour, these rodents can adapt to a wide range of habitat types. Despite being morphologically cryptic, they exhibit distinct geographic distributions. In the Western Cape, two species are recognized namely, *R. pumilio* and *R. intermedius*. *Rhabdomys pumilio* is restricted to the Fynbos and Succulent Karoo biomes, while *R. intermedius*, is found in the Nama-Karoo biome. Currently little is known about the ectoparasite diversity associated with both species across the different biomes. To address the paucity in knowledge, the study aimed to record the ectoparasite diversity associated with *Rhabdomys* spp. in the Fynbos, Succulent Karoo and Nama Karoo. A total of 237 *Rhabdomys* individuals were trapped in the three biomes during the Spring/Summer season of 2023 - 2025. More than 10 000 ectoparasite individuals representing five taxa (lice, mesostigmatan mites, trombiculid mites, ticks and fleas) and at least 23 species were recorded. Overall lice were the most prevalent and abundant taxon [86%, 22.9 (± 2.21)], while trombiculid mites (chiggers) were the most diverse, with at least 10 species recorded. Fleas were mostly prevalent and abundant in the Succulent Karoo biome [62%, 2.2 (± 0.22)], while ticks were most prevalent and abundant [42%, 1.2 (± 0.13)] in the Fynbos biome. The study highlights that species in the rodent genus *Rhabdomys* serves as hosts to a wide range of ectoparasite species and some ectoparasite species exhibit a preference for certain biomes.

Tuesday 16 September – 10h30 (Ndau & Nar)

070 – Prevalence of *Anaplasma marginale* and *A. centrale* in African buffalo (*Syncerus caffer*) in the Kruger National Park and characterization of *A. marginale* strains

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Bovine anaplasmosis caused by *Anaplasma marginale* results in loss of productivity and mortality in cattle, while *A. centrale* causes mild infections and is used in an infective bovine blood vaccine. Although *A. marginale* is endemic in South Africa, clinical cases and outbreaks are frequently reported. One potential cause of these outbreaks could be spill-over from African buffalo, which have been reported to carry *A. marginale*. Although little molecular characterization has been done on *A. marginale* from buffalo, one study showed a distinct clade using *msp1β* as the target gene. It is not known what impact potential buffalo-specific *A. marginale* strains have for livestock. This study investigated the prevalence of *A. marginale* and *A. centrale* and the genetic diversity of *A. marginale* in buffalo in the Kruger National Park (KNP), South Africa. DNA from buffalo was screened for the presence of *A. marginale* and *A. centrale* using a duplex real-time PCR assay. Of the 596 samples tested, 60.23% were co-infected, while 4.87% and 17.95% had single *A. centrale* and *A. marginale* infections, respectively. Amplification of *msp1α* from *A. marginale* positive buffalo samples could only be achieved using lower annealing temperatures than when working with cattle samples. Preliminary analysis suggests that the *A. marginale* strains in buffalo differ significantly from cattle strains, possibly indicating limited spillover of *A. marginale* from buffalo to cattle. Another possibility is that *msp1α* was amplified from a closely related novel *Anaplasma* spp. We will conduct microbiome analyses to assess the diversity of *Anaplasma* spp. in these buffalo samples, and design new primers to amplify *A. marginale* strains from buffalo.

Wednesday 17 September – 10h15 (Ndlopfu)

071 - Unravelling the taxonomy of fish haemogregarines, a few species at a time

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Haemogregarines (Apicomplexa: Adeleorina) are obligate parasites of many species of vertebrates, however to date, there is limited understanding of these parasites in the most diverse group of vertebrates, fishes. While many of these parasites from amphibians, reptiles and mammals have been characterised molecularly using the 18S rRNA gene, identification

of haemogregarines infecting fishes has relied solely on morphological identification by microscopy, relying mostly on stages found in the blood of fishes. However, haemogregarines follow a heteroxenous life cycle, which includes stages in both vertebrate and invertebrate hosts, the latter being the definitive host. In fishes, the majority of these parasites belong to the genus *Haemogregarina*, with little knowledge on the definitive host responsible for transmission. Recently, two species of *Haemogregarina*, *Haemogregarina bigemina* and *Haemogregarina daviesensis*, were characterised molecularly using fragments of the 18S rRNA gene and their phylogenetic placement estimated. Whilst the latter species' sequences clustered with other species of *Haemogregarina*, *H. bigemina* clustered with unknown apicomplexan parasites and symbionts of fishes and corals in a clade basal to sequences of members of the coccidia, and as such outside of the *Haemogregarina* clade. While species of *Haemogregarina* are accepted to be leech-transmitted, *H. bigemina* is strongly suggested to be transmitted by gnathiid isopods. This in mind and this species' current phylogenetic placement suggests that not all haemogregarines of fish are leech transmitted and may belong to an entirely new genus. As such this study aimed at identifying further haemogregarines of fishes using a combination of morphology and molecular data.

Tuesday 16 September – 09h00 (Ndlopfu)

072 - Development of a method to extract high molecular weight DNA from a putative novel *Anaplasma* species identified in impala (*Aepyceros melampus*)

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Bovine anaplasmosis, caused by *Anaplasma marginale*, poses a global livestock challenge. Various *Anaplasma* species carry potential zoonotic risk, with over 25 novel species recently identified through next-generation sequencing, including one identified in impala (*Aepyceros melampus*). Characterisation of novel *Anaplasma* species remains difficult due to their obligate intracellular nature and difficulty in culturing them. Whole-genome sequencing (WGS) offers a potential solution but is hindered by difficulties in obtaining host-free *Anaplasma* DNA from low-level infections. Genome sequences of novel *Anaplasma* spp. will aid in understanding the genetic diversity within this genus and assessing pathogenic potential. This study evaluated a method to obtain high molecular weight (HMW) DNA for WGS from the novel impala-associated *Anaplasma*. Blood samples (500 ml in EDTA) were collected from impala culled at the Timbavati Game Reserve, Mpumalanga, South Africa. An *Anaplasma* genus-specific qPCR assay identified positive samples. Blood components were fractionated by centrifugation; qPCR analysis indicated highest levels of *Anaplasma* in red blood cells (RBCs). Whole blood was filtered to isolate RBCs, followed by HMW DNA extraction using two kits. A qPCR assay targeting the mammalian GAPDH gene was used together with the *Anaplasma* genus-specific qPCR assay to determine the relative host and *Anaplasma* DNA concentrations, revealing substantial host DNA depletion (77- to 8773-fold). Overall DNA yields from both kits were extremely low, but whole genome amplification (WGA) should yield sufficient DNA for WGS. Microbiome analysis will be used to assess the bacterial composition;

samples containing single *Anaplasma* infections will undergo WGA and WGS to characterize this novel species.

Wednesday 17 September – 09h00 (Ndlopfu)

073 - Unravelling the evolution of *Amblyomma*: The case of *Amblyomma splendidum*

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Amblyomma splendidum, a west African species, is primarily known to parasitise cattle and African buffalo inhabiting forest niches. This rare species is often morphologically confused for *Amblyomma cohaerens*, with males sharing similar conscutum patterning. Females of *A. splendidum* may be confused with *Amblyomma variegatum* and *Amblyomma eburneum*, as all species have a single enamelled patch on the scutum. There are no molecular studies on *A. splendidum*, and literature on this species is limited. Therefore, this study provides the first molecular comparison between *A. splendidum* and other African *Amblyomma* species. Ten *Amblyomma splendidum* samples were obtained from the Department of Veterinary Tropical Diseases tick reference collection. The 12S rRNA, 16S rRNA and COI mitochondrial markers were targeted for the molecular analysis and Maximum Likelihood analyses were performed using IQ-TREE. The phylogenetic topologies illustrate the clustering of all *A. splendidum* samples with those of *A. variegatum* and *Amblyomma pomposum*. This clade is well supported and removed from the other *Amblyomma* species. The results suggest that, while *A. splendidum* is morphologically distinct, there is insufficient molecular evidence to differentiate it from *A. pomposum* and *A. variegatum*. This underscores the need for a more precise definition and clearer criteria for molecular differentiation at species level.

Wednesday 17 September – 13h40 (Ndlopfu)

074 - Prevalence of trypanosome species in the buffer zone of Maputo National Park, Matutuine District, Mozambique: preliminary results

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Animal African trypanosomosis (AAT), also known as nagana, is a major constraint to livestock development in sub-Saharan Africa. In Mozambique, it was previously estimated that 75% of the country is infested by four species of tsetse flies, the disease vector. In this study, our objective was to determine the occurrence of pathogenic *Trypanosoma* spp. in cattle in the buffer zone of Maputo National Park, an interface of wildlife-domestic animals-humans. In total 728 blood samples were collected from Massuhane, Guengo and Gala villages, Matutuine District, Maputo Province, Mozambique. Detection of trypanosomes was conducted by buffy coat technique and Polymerase Chain Reaction (ITS1). Packed cell volume (PCV) was also

determined to assess occurrence of anaemia. The overall prevalence by buffy coat technique was 14.9% and by PCR was 41.5%. Almost 50% of tested animals were anaemic ($PCV \leq 24$). The prevalence by buffy coat was 9.8%, 12.5% and 22.5% in Gala, Guengo and Massuhane respectively. The most prevalent species detected was *T. congolense* Savannah, accounting for 78.1% of the infections. Other species detected were *T. congolense* Kilifi (4.3%), *T. vivax* (0.7%), *T. simiae* (4.3%) and co-infections (12.6%). Our results highlight the importance of animal trypanosomosis in Mozambique and the need for the development of structured and integrated control measures in endemic areas.

Tuesday 16 September – 14h10 (Nda & Nari)

076 - Perceptions on anthelmintic resistance in goats under communal production systems

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For decades, farmers relied on anthelmintic drug treatments to control gastro-intestinal nematode (GIN) infections which has led to the development of anthelmintic resistance. The objective of the study was to investigate the attitudes and practices of communal goat farmers regarding anthelmintic resistance in communal goat flocks. A structured close-ended questionnaire was used to carry face-to-face interviews with communal goat farmers ($n = 384$) across four local municipalities in uMkhanyakude District. Elderly farmers were 1.4 times more likely to underdose compared to younger farmers ($p < 0.05$). Male farmers and educated farmers were aware of the negative influence on AR development brought by using substandard drugs ($p < 0.01$) and repetitive use of one drug ($p < 0.05$). However, lack of professional veterinary assistance ($p < 0.01$) resulted in many cases of underdosing ($p < 0.05$) and exploitation of expired drugs ($p < 0.05$) among women, illiterate and the old age. Despite varying levels of education, more farmers practiced targeted treatment ($p > 0.05$), this was attributed to poor socio-economic status of the farmers. The elderly farmers are less likely to delay the development and spreading of AR due to their inability to adhere to the recognized principles of responsible and sustainable drug use. Engaging veterinarians, farmers and animal health technicians could achieve sustainable management of GIN infections.

Monday 15 September – 13h35 (Nda & Nari)

078 – Trematode infections in freshwater snails of South Africa: diversity, prevalence, and host interactions

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Freshwater ecosystems in South Africa harbour a considerable diversity of trematodes, yet the intermediate stages of these parasites and their interactions especially with invertebrate hosts remain poorly understood. This study fills critical gaps by assessing the diversity, prevalence and host associations of trematode infections in freshwater snails and linking cercariae and metacercariae stages to elucidate life cycles. A total of 1,332 freshwater snails from six genera (*Radix*, *Pseudosuccinea*, *Bulinus*, *Biomphalaria*, *Physa* and *Tarebia*) were sampled between March 2023 and October 2024 at eight sites stretching from the border of the Kruger National Park in Limpopo to Kareedouw in the Eastern Cape. Trematode infections were detected in 64 snails, with 17 taxa identified. Notable species include *Schistosoma mattheei* and *Fasciola gigantica*, both important pathogens affecting humans, livestock and wildlife. Continued molecular analysis is expected to advance resolution and refine identifications. Cercariae shedding was assessed using a three-day screening protocol, followed by dissection to identify sporocysts and rediae. By integrating snail host data with findings on metacercarial stages in fish hosts from a complementary study, this research elucidates partial life cycles for three trematode genera: *Petasiger*, *Tylodelphys*, and *Uvulifer*. Additional matches are anticipated following the completion of molecular analyses. This is one of the first studies in South Africa connecting trematode life stages across multiple hosts, which offers novel insights into the complexity of trematode-snail interactions and parasitic biodiversity. By shedding light on transmission dynamics, this work represents a significant step toward a comprehensive understanding of African freshwater trematode life cycles.

Wednesday 17 September – 10h45 (Nda & Nari)

079 – The national atlas of tsetse and trypanosomosis in Mozambique: preliminary results

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Mozambique is severely affected by animal trypanosomosis. As yet, no systematic activities to control tsetse and trypanosomosis have been implemented. The success of possible future activities depends on reliable and extensive knowledge of the distribution of tsetse and trypanosomosis in the country. To address the gap in our current knowledge of this distribution, an atlas is being created. Data collected between 2000 and 2022 were gathered, mapped and analysed. A central repository and database were generated. The sources of the data were scientific papers, theses, official reports and surveys. Available data cover the provinces of Maputo, Gaza, Sofala, Manica, Tete, Zambezia and Niassa. They indicate the occurrence of the *Glossina* species *Glossina austeni*, *G. brevipalpis*, *G. morsitans* and *G. pallidipes*, and three *Trypanosoma* species, namely *T. congolense*, *T. vivax* and *T. brucei*. *Trypanosoma congolense* is implicated in 76% of the total trypanosomosis cases. More than 40% of the data are from Maputo province due to the paucity of surveys in other regions of the country. Trypanosomosis were mainly detected using the buffy coat technique (51%), followed by Polymerase Chain Reaction (20%) and blood smears (19%). A regular update of this national database of tsetse and trypanosomosis is fundamental for the development of control strategies for the disease. Despite their usefulness, current results need improvement, particularly in areas where little or no information is available. Therefore, further field surveys on tsetse and trypanosomosis are considered necessary future steps toward the completion of the atlas.

Tuesday 16 September – 13h10 (Ndau & Nari)

081 - Parasitic infections in Golden Jackals: a comparative analysis of diagnostic methods

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Investigations on parasitic infections of golden jackals (*Canis aureus*) relied mostly on necropsies. Copromicroscopy provides a less invasive alternative, but its effectiveness needs further investigation. This study assessed the performance of faecal standard flotation (FT) against scraping, filtration, and counting technique (SFCT) and lung inspection. Seventy-nine road-killed jackals from North-eastern Italy (2009-2025) were examined by SFCT, whereas 75 cardiopulmonary systems were inspected macroscopically and microscopically. Faecal material collected during necropsy was analysed via FT with ZnSO₄ (s.g. 1.350). FT sensitivity and specificity (and Clopper-Pearson 95%CI) were estimated for all parasitic taxa, using both SFCT and lung inspection as gold standard. Necropsy identified 13 intestinal parasitic taxa, of which FT detected six: *Taenia* spp. (prevalence at necropsy: 42%), Ancylostomatidae (29%), *Toxocara canis* (15%), *Mesocostoides* spp. (11%), *Trichuris vulpis* (8%), and

Molineidae (5%). *Eucoleus aerophilus* was found in lungs (16%), and eggs ascribable to *Eucoleus* spp. at FT (31%). Poor sensitivity values were estimated for *T. canis* (0.50%, 0.21-0.80), Molineidae (0.50%, 0.07-0.93), Ancylostomatidae (0.35, 0.16-0.57) and *T. vulpis* (0.33, 0.04-0.77). Sensitivity was even worse for Taeniids (0.18, 0.07-0.35) and *Mesocostoides* spp. (0.11, 0.01-0.48). Specificity ranged from 0.88 to 1. *Eucoleus aerophilus* showed low sensitivity (0.33, 0.10-0.65) and poor specificity (0.67, 0.54-0.78), likely due to the presence of eggs of *E. boehmi*. FT identified approximately half of the parasites found at necropsy, including all the most prevalent. The low sensitivity of FT limits its value in detecting low-prevalence pathogens, although their use can be preserved with a careful sample size planning.

Wednesday 17 September – 13h55 (Nda & Nari)

083 - Mapping intestinal parasites in Golden Jackals in Italy to track health risks

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Intestinal helminths of golden jackals (*Canis aureus*) in the rapidly expanding northeastern Italian population (Friuli-Venezia Giulia, FVG) were comprehensively analysed to elucidate their epidemiological role, given the limited existing data on their parasitic fauna in FVG. From February 2009 to March 2025, mostly road-killed golden jackals from FVG (recorded through InfoFaunaFVG wildlife monitoring network) were examined post-mortem. Intestinal contents were analyzed using scraping, filtration, and counting techniques. Helminths were identified to the species level based on morphometric keys and confirmed by sequencing the mtCO1 gene. Descriptive statistic, including prevalence and intensity (I), were estimated for each helminth species with their 95% confidence intervals. Among 109 examined carcasses, 75.2% (66.4-82.4) were infected with at least one helminth species (range: 1-5), totalling 23 species. The most prevalent nematodes were *Uncinaria stenocephala* (29.4%, 21.6-38.5; I 2.95), *Toxocara canis* (15.6%, 10.0-23.4; I 0.46), *Trichuris vulpis* (8.3%, 4.4-15.0; I 0.23), *Pterygodermatites affinis* (6.4%, 3.2-12.7; I 0.07), and *Molineus legerae* (5.5%, 2.6-11.5; I 0.3). Among cestodes, *Taenia hydatigena* (18.3%, 12.2-26.7; I 1.29), *Mesocostoides* spp. (12.8%, 7.8-20.4; I 3.70), *T. serialis* (7.3%, 3.8-13.8; I 0.45), and *T. krabbei* (5.5%, 2.6-11.5; I 0.07), while *Alaria alata* (6.4%, 3.2-12.7; I 2.95) and *Metagonimus yokogawai* (5.5%, 2.6-11.5; I 20.7) were the most prevalent trematodes. Other species had prevalence values lower than 2%. Despite generally low prevalence and intensity, the rich parasite community of golden jackals includes species shared with domestic dogs (*U. stenocephala*, *T. canis*, *T. vulpis*, *T. hydatigena*) and a zoonotic parasite (*M. yokogawai*). Their prevalence and intensity indicate a potential epidemiological role, underscoring the importance of ongoing veterinary and public health monitoring.

Wednesday 17 September – 13h40 (Nda & Nari)

090 - Harnessing monoterpenoids for mosquito control and malaria transmission

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The development of insecticide resistance in vector populations and drug resistance in the malaria parasites is of major concern. Phyto-insecticides and phyto-medicines have been used traditionally in Africa for centuries and could provide lead molecules for alternative insecticides and antimalarials to decrease the risk of malaria infections and transmission. As such the adulticidal potential of two monoterpenoids, linalool and linalyl acetate, was determined against the malaria vectors present in sub-Saharan Africa, namely *Anopheles funestus* (FANG and FUMOS-R). An adulticidal assay was carried out on adult female mosquitoes (2-5 days old). The monoterpenoids were highly effective adulticidal agents with linalool slightly more active than linalyl acetate against both sensitive and resistant *An. funestus* strains. Linalool proved to be more active than linalyl acetate at 0.002% and 0.02% to knock down FUMOS-R and FANG after 1hr, with FANG less sensitive to the effects of the two monoterpenoids. Linalool knocked down 100% FUMOS-R and FANG at 0.1% compared to 1.0% linalyl acetate. Both monoterpenoids are proposed to be acetylcholinesterase inhibitors, a common target of mosquitocides. To ascertain if the two monoterpenoids possessed *in vitro* antimalarial activity against the chloroquine-resistant FCR-3 *Plasmodium falciparum*, the hypoxanthine incorporation drug sensitivity assay was conducted over 48hrs. Linalyl acetate was found to be 180-fold more active than linalool, with linalyl acetate comparable to quinine's inhibitory activity. As such, these two monoterpenoids possess complementary properties that could be effective in mosquito control and to interrupt malaria transmission.

Wednesday 17 September – 08h45 (Ndau & Nari)

091 - Survey of ticks and their microbiomes spanning national parks in Botswana

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Around 18% of all tick species across the globe are found in Africa. In recent years tick-borne diseases in Africa have increased in prevalence due to anthropogenic and climate-driven impacts. Introduction of ticks to new populations is highest at the wildlife-livestock interface,

as interactions facilitate the dispersal of ticks from free-roaming, wild hosts to domestic animals. Exposure to new environments also influences the tick microbiome. Microbial composition is thought to impact tick-borne pathogen (TBP) transmission, as the presence of specific symbionts may either facilitate or constrain pathogen colonisation and survival. Thus, understanding the drivers of TBP transmission is a fundamental starting point for developing strategies for control of TBDs affecting wildlife and livestock. Through identifying potential relationships between important veterinary pathogens, environmental variables and the tick microbiome, this project aims to provide knowledge and tools for proactive management of ticks and tick-borne pathogens. Between January and March 2024, and January to February 2025, we conducted the first nationwide, spatially randomised survey of ticks from 100 locations across Botswana, to generate unbiased tick distribution data from national parks and locations with high wildlife/livestock interaction. Through metabarcoding with primers targeting the 16S gene for bacteria, and the 18S gene for protozoa, we will characterise the microbiomes of unfed ticks. We will be presenting the sequencing results along with the outcomes of tick distribution surveys to highlight location associated patterns. The findings from these preliminary analyses will be implemented within recently developed modelling frameworks for TBP transmission to enhance our understanding of tick-pathogen-microbiome interactions and their interactions with the environment.

Monday 15 September – 13h35 (Ndlopfu)

093 - Nematode diversity associated with rodents and the extent of parasite sharing between sympatric rodents

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Globally nematodes are common internal parasites of rodents. At present information on the diversity and abundance of parasitic nematodes associated with rodents in South Africa is scant. This study aimed to (1) record the nematode diversity associated with co-occurring rodent species (*Rhabdomys* spp., *Micaelamys namaquensis* and *Otomys unisulcatus*) in the Western Cape Province and (2) describe the nematode species composition in response to rodent identity (life history). In total, 597 rodents were trapped at 12 localities during the summer months of 2023, 2024 and 2025. Overall, 11 nematode genera were recovered across all rodent species. The genus *Syphacia* was the most prevalent and abundant genus within *Rhabdomys* spp. and *M. namaquensis*, while the genus *Nematodirus* was the most abundant and prevalent in *O. unisulcatus*. Nematode abundance was the highest in *Rhabdomys* spp., while nematode species richness was the highest in *M. namaquensis*. Based on preliminary data, at least one undescribed nematode species in the genus *Gastronodius* Singh, 1934, was recorded. The novel data gathered in this study will contribute to a better understanding of nematode diversity in South African rodents and the factors that shape nematode species composition.

Tuesday 16 September – 09h15 (Ndau & Nari)

094 - Evidence of *Plasmodium* parasite sharing between humans and non-human primates in confined Gabonese environments: Implications for zoonotic malaria

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Close interactions between humans and non-human primates in sanctuaries, captivity, and forest-adjacent villages may foster interspecies transmission of *Plasmodium* parasites. The present study was conducted with the objective of evaluating the diversity and potential for cross-transmission of *Plasmodium* species among great apes and humans in Gabon. This was achieved by using molecular and phylogenetic approaches. A total of 349 blood samples (165 from chimpanzees, 77 from gorillas, and 107 from humans) and 88 faecal samples from wild apes were collected across 13 sites. The overall infection rate was 36.4%, with the highest rate observed in chimpanzees (43.6%), followed by gorillas (31.2%) and humans (29%). Molecular and phylogenetic analyses revealed a high diversity of *Plasmodium* species, including human parasites (*P. falciparum*, *P. malariae*, *P. ovale-curtisi*, *P. ovale-wallikeri*) in apes, and one ape parasite (*P. malariae*-like) in a human. Of particular note is the observation that the majority of human-associated infections in apes were detected in individuals residing in or in close proximity to human settlements. These findings suggest that apes in anthropized environments may act as reservoirs for human *Plasmodium*, thus complicating control and elimination strategies. The spatial clustering of infections in forest-edge communities further highlights the risk of zoonotic spillover and the potential for reverse transmission. The findings emphasise the necessity for a One Health surveillance framework to be implemented in order to monitor malaria transmission across species and mitigate emerging public health threats.

Monday 15 September – 10h45 (Ndlopfu)

099 - An innovative imaging tool and the impact of invasive snails on amphistomes of large African herbivores

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Humans impose significant pressure on large herbivore populations through hunting, poaching, and habitat destruction. Anthropogenic pressures can also occur indirectly, such as the human-facilitated introduction of invasive species, leading to drastic changes in parasite diversity and transmission. Amphistomes, or stomach flukes, cause amphistomiasis or stomach fluke disease, which is highly prevalent in (pseudo)ruminants across many parts of the world and can be especially lethal to young animals. Despite a serious burden, significant gaps in our understanding of amphistome biology persist, extending from host range, lifecycle information and geographic distribution, to molecular characteristics. In this study, we evaluated micro-computed tomography (μ CT) imaging as a non-destructive alternative for identifying amphistome species, aiming to unlock historical collections and unique specimens for contemporary research. We generated reference sequences for four amphistome species of large herbivores: three from the common hippopotamus and one from the Cape buffalo. By comparing μ CT imaging with traditional sectioning and incorporating molecular barcoding, we revealed the need for a taxonomic revision of the genus *Carmyerius*, focussed on identifying new diagnostic characters to better reflect species boundaries. Our findings also indicate that non-endemic snails affect the transmission of amphistomes, which infect large African herbivores. This has important implications, as existing research links trematode parasite infections combined with other stressors to declining wild herbivore populations. Therefore, we argue that monitoring the anthropogenic impact on parasite transmission should become an integral part of wildlife conservation efforts.

Tuesday 16 September – 13h25 (Ndlopfu)

101 - Purposeful design causes microhabitat restriction and enables reproductive success

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Clarias gariepinus (Burchell, 1822) is a preferred aquaculture species in Africa. They are omnivorous fish and therefore host a large variety of parasites. In South Africa, these include three nematode species in the digestive system. Pathology was compared to the wound-inflicting structures of the parasites. Fish were collected from natural waters and screened for parasites. Three nematode species were identified: *Spinitectus petterae* Boomker, 1993, *Procamallanus* (*Procamallanus*) *pseudolaeviconchus* (Wedl, 1861), and *Paracamallanus cyathopharynx* (Baylis, 1923), from the posterior cardiac stomach, intestine and rectum, respectively. Host and parasite tissue were prepared for light and scanning electron microscopy and histology. The stomach features deep folds, and *S. petterae* bears robust annular rings with cuticular outgrowths around the head region, a tiny rigid buccal capsule and a muscular oesophagus. Observations of live specimens confirmed that they move in a rotor-wise manner between stomach folds, causing deep pits and sloughed tissue. Leucocyte infiltrations, acute ulcerations, destruction of the lamina propria and the gastric gland layer and granuloma formation were observed. The parasites became deeply embedded and the cuticular outgrowths act in a harpoon-like manner to maintain its position. Eggs become trapped in the granulomas. Sloughed host tissue is ingested. In camallanids, the outer cuticle is smooth, and the buccal capsules are large, cup-shaped cuticle-lined structures, which is subdivided in *P. pseudolaeviconchus* into an anterior and posterior section. Parasites retain their position with vacuum created by the rim of the buccal capsule on the intestinal epithelium and enlargement of oesophagus which sucks epithelium and connective tissue into the buccal capsule. Ingestion follows when cells are sloughed off into the buccal capsule and intestine. In *P. cyathopharynx*, two tridents occur external and lateral to the slit-like buccal capsule that can be closed. Internally, long ridges occur on the dorsal and ventral surface. Parasites attach to secondary folds by closing the buccal capsule and leaving an impression on host epithelium. No immunological response was noticed. The morphology of the buccal capsule nematodes restricts their microhabitat, cause aggregation of species, reducing competition, and thereby favouring species reproductive success.

Monday 15 September – 09h15 (Ndau & Nari)

102 - Global variations and implications of microbiome communities in ixodid ticks (Arachnida: Ixodidae): A systematic review

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Ticks are blood-feeding arthropods that infest terrestrial vertebrates and transmit a wide range of human and animal pathogens. Primary pathogens have received great attention, but the overall microbial communities harboured by ticks remain understudied. The aim of this systematic review was to summarise the current literature on bacterial communities in ixodid tick species (Arachnida: Ixodidae) globally, focusing on studies that utilised NGS Illumina

sequencing of the 16s rRNA V3 – V4 hypervariable region. The tick genera that were analysed in the reviewed studies were *Amblyomma* (13/58), *Dermacentor* (13/58), *Haemaphysalis* (19/58), *Hyalomma* (7/58), *Ixodes* (22/58) and *Rhipicephalus* (10/58). Results showed that ixodid tick microbiomes have been documented in 58 countries: Asia (24), North America (16), Europe (8), Africa (5), South America (3) and Australia (2). Overall, Ixodidae ticks revealed a limited core microbiota dominated by Proteobacteria, Bacteroidetes, Firmicutes and Actinobacteria regardless of tick species, sex, host, geographic region and tick tissue analysed. Taxonomic composition varied across studies, with *Coxiella*, *Francisella* and *Rickettsia* as the most consistently reported endosymbionts. Alpha and beta diversity of microbial taxa differed according to tick species, sex, developmental stage, feeding status and tick organ, with the Malpighian tubule, midgut and reproductive tissues as the primary tissues in which bacterial communities resided. Location and pathogen infection status appeared less important in determining tick microbiome composition. A definitive interpretation of temporal changes on the microbiome is limited by paucity of published studies. We herein integrated findings of microbial composition of ixodid tick species globally, and the different factors affecting richness and diversity.

Monday 15 September – 13h50 (Ndlopfu)

103 - Rodent malaria parasites detected in the invasive *Rattus rattus* in Gabon

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Invasive species are increasingly recognized for their role in reshaping host–parasite interactions. Here, we report the first molecular detection of *Plasmodium yoelii* in the invasive black rat (*Rattus rattus*) in Gabon, based on a systematic screening of 527 rodents captured in rural villages between 2021 and 2022. Two *R. rattus* individuals tested positive for *P. yoelii*, with phylogenetic analyses confirming their identity with strains previously found in native rodent hosts from the region. Previous studies in the region have identified *Mastomys natalensis*, *Praomys misonnei*, and other native murids as hosts of *Plasmodium yoelii*, highlighting that susceptibility is not restricted to invasive rats but includes a diversity of native rodent taxa. These findings challenge the traditional view that rodent malaria parasites are confined to native species and identify *R. rattus* as a potential—though likely incidental—host within local *Plasmodium* transmission networks. Despite the low prevalence (0.38%), this result raises important questions about the ability of invasive rodents to integrate into local parasite cycles and influence disease dynamics.

Monday 15 September – 09h15 (Ndlopfu)

104 - From stigma to strategy: advancing the conservation and perception of metazoan parasites

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Parasites play essential roles in ecosystems by facilitating biomass transfer, maintaining food web complexity, regulating host populations, and driving evolutionary processes in other species. Yet, they remain among the least protected by wildlife and ecosystem conservation initiatives with Red Listing of parasites being in its infancy. During a workshop on conservation and Red Listing of parasites organised in 2024 (in Belgium), experts undertook a collaborative effort to establish priorities enabling assessment of metazoan parasites of animals. Applying an adapted version of the Nominal Group Technique, we addressed five themes, including ethics and perceptions. Indeed, recent research provides empirical evidence that emotional responses to different species are key factors influencing people's willingness to support conservation efforts, which makes the human perception of parasites a similarly important aspect. The World Archives of Species Perception (WASP) project represents the most extensive and inclusive scientific effort to date to address the knowledge gap surrounding public perceptions of biodiversity. Building upon the general WASP project methodology and inspired by the above-mentioned workshop, we developed a spin-off for human perception of parasites (WASP-P) to understand how different traits of individual species across metazoan parasite taxa are perceived by the public and how this can help facilitate more effective conservation. Preliminary results suggest rich patterns in public perception of different parasite species that warrant deeper investigation. The ongoing efforts will provide valuable insights for the IUCN SSC Parasite Specialist Group and contribute to the development of more effective, targeted strategies for parasite conservation and policy engagement globally.

Monday 15 September – 14h05 (Ndaou & Nari)

107 - Reassessing the genus *Haemocystidium* (Apicomplexa: Haemoproteidae): insights from mitochondrial DNA genomes and morphological data

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Haemocystidium Castellani & Willey, 1904 is a genus of apicomplexan blood parasites infecting reptiles, including lizards, snakes, and chelonians. Despite being described over a century ago, the genus remains poorly defined, with ongoing debates about its validity as a distinct lineage within the Haemosporida. This uncertainty is largely due to limited life cycle data, overlapping morphological traits with *Plasmodium* and *Haemoproteus*, and the incomplete understanding of its biology. In this study, we integrate mitochondrial DNA (mtDNA) genomes and morphological data from species infecting a wide range of hosts, including African lizards, snakes, and tortoises, as well as North and South American turtles and lizards. This dataset covers all major host groups associated with the genus, providing a robust foundation for systematic revision. Phylogenetic analyses of complete mtDNA strongly support the monophyly of *Haemocystidium*, placing it as a distinct, evolutionarily divergent lineage within the Haemosporida, separate from *Plasmodium* and avian *Haemoproteus*. Morphological comparisons show key diagnostic features, including the absence of merogony in peripheral blood, the presence of hemozoin pigment, and gametocyte development within erythrocytes. However, vector identities remain largely unknown, highlighting a critical gap in our understanding of this genus's transmission dynamics. Our findings support the retention of *Haemocystidium* as a distinct genus, resolving long-standing taxonomic uncertainties and laying the foundation for future studies on this group.

Monday 15 September – 11h15 (Ndlopfu)

111 - Molecular data reveal a complex of cryptic species within *Corynosoma australe* Johnston, 1937 (Acanthocephala: Polymorphidae), a parasite of pinnipeds from both the Northern and Southern Hemispheres

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Corynosoma australe is a widely distributed acanthocephalan specific to pinnipeds. Originally described from South Australia, *C. australe* has since been reported in Antarctic/subantarctic and temperate regions of the Southern Hemisphere, as well as along the coasts of the Californias. Juveniles of this species have also been recorded in elasmobranchs, fishes and cetaceans. Despite the broad spectrum of hosts and wide geographical distribution of *C. australe*, genomic data are currently only available for populations from the Americas. Here, we perform a molecular screening of juvenile and adult specimens of *C. australe* collected from elasmobranchs, teleost fishes, cetaceans, and pinnipeds from coastal waters of Argentina, Australia, southern Africa, and the United States. Almost complete sequences for 18S, 28S and cox1 were generated and compared with all sequence data available in GenBank for this species. Genetic divergence, in combination with phylogenetic analyses, suggests that *C. australe* represents a complex of cryptic species composed of at least two morphologically indistinguishable lineages. The first lineage corresponds to isolates of *C. australe* s.s. from fish and seals from South Australia and the west coast of southern Africa. Lineage two is distributed in temperate waters along the Southwest Atlantic and the Pacific coasts of North and South America. Our study suggests that Lineage 2 may correspond to *Corynosoma obtusens*, which was described from sea lions in California and has recently been synonymised with *C. australe*. Our molecular data opens new opportunities for future ecological studies on the distribution, host ranges, and genetic structure of marine mammal acanthocephalans.

Wednesday 17 September – 14h10 (Ndlopfu)

114 – Monorchiid trematodes in Indo-Pacific butterflyfishes: enabling a biogeographical paradigm for fish parasites of the region?

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The tropical Indo-Pacific, stretching from Hawaii and French Polynesia in the east to the east coast of Africa in the west, has a distinctive fauna of free-living marine animals, including many that span the entire region. How the parasites of these free-living animals are distributed is not well understood. Two issues are significant. First, differences between the life cycles of free-living and parasitic organisms mean that their biogeographical patterns are not necessarily the same. Second, knowledge of the distribution of parasites lags far behind that of their hosts so that the patterns are not necessarily yet evident. Here we review biogeographical knowledge for 20 species of the monorchiid trematode genus *Hurleytrematoides* based on combined morphological and molecular data. Although the data are still imperfect, at least two species are distributed across almost the entire region. In contrast, several species can be inferred to have highly localised distributions based on convincing evidence of absence elsewhere. Wide distributions are almost always associated with distinct cox1 populations, sometimes with blurring of the distinction between populations

and species. Given so much variation in the distribution of species of a single trematode genus in a single fish family, we infer that an overall distributional paradigm for fish trematodes in this region is not yet possible, but that we have a framework of the possibilities.

Tuesday 16 September – 10h45 (Ndlopfu)

118 - Beyond restoration: Environmental drivers of trematode dynamics in recovering streams

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Freshwater ecosystems are among the most threatened habitats worldwide, facing severe biodiversity loss driven by a combination of natural and anthropogenic stressors. Urban streams are particularly impacted, often undergoing long-term degradation, yet the ecological processes shaping parasite-host interactions remain poorly understood. Digenean trematodes are a diverse group of parasites with complex life cycles involving multiple hosts. Their occurrence and abundance in ecosystems are therefore influenced by a range of biotic and abiotic factors, making them sensitive indicators of ecosystem functioning and environmental changes. In this study, we investigated trematode communities in their first intermediate host following restoration in a Central European urban stream that faced a century of degradation as an open sewer system. Over two consecutive years of monthly sampling, we examined 5,479 snails to assess host and trematode species richness, prevalence, and life cycle characteristics. We recorded a total of 25 trematode taxa, with an overall prevalence of 26% and distinct seasonal transmission dynamics. The generalist snail *Ampullaceana balthica* was identified as a key host species, being the most abundant snail as well as host to the greatest trematode diversity and prevalence. To identify the primary drivers of trematode dynamics in the recovering system, we conducted comprehensive statistical analyses incorporating water quality and environmental parameters, which point to land use as the dominant factor influencing trematode species richness and prevalence. Our findings demonstrate how trematode communities can reflect underlying ecological processes and emphasize the role of complex parasite-host interactions in advancing our understanding of biodiversity and ecosystem functioning.

Monday 15 September – 11h30 (Ndau & Nari)

120 - A large-scale study on gastrointestinal helminth community of loggerhead sea turtles *Caretta caretta*: ecological drivers of diversity and insights into environmental changes

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Heteroxenous, trophically transmitted helminths constitute an important part of the marine food webs. As such, they are sentinels of the integrity of the trophic chain, indirectly reflecting variations of abiotic components of the ecosystem. The opportunistic diet of loggerhead sea

turtles, *Caretta caretta*, their long life-span and migratory behaviour contribute to shaping the wide diversity of its parasitic community. With the aim of exploring drivers of diversity and variations in time of the gastrointestinal helminth community, parasites were collected from the digestive tracts of 157 loggerhead sea turtles that stranded and died along the NW Adriatic Sea between 2009 and 2023 and were morphologically identified. Prevalence, intensity, abundance, relative abundance and importance index were calculated for each taxon. Ontogenic stages (epipelagic/transitional and benthic feeders) and sex of the hosts, seasons and observation periods (2009–2014 vs 2015–2023) were compared to unveil any difference in parasite community structure, richness and diversity. Overall, seven digenean and two nematode species were recovered, with dominant taxa typically isolated in other neritic grounds in the Mediterranean Sea, confirming the role of the ecosystem in shaping community diversity. The ubiquitous digeneans *Enodiotrema megachondrus* and *Calycodes anthos* had higher importance in small juveniles, likely feeding on epipelagic prey. Prevalence, intensity and abundance of helminths were significantly higher during the colder months. Increase in prevalence and intensity of helminthic infections and variations of community structure in the second period of observation suggest potential alterations in biotic and/or abiotic components of the Adriatic ecosystem, potentially associated with the underlying climate change.

Tuesday 16 September – 10h15 (Ndlopfu)

121 - Phylogeography of *Galba truncatula* and implications for the spread of fluke diseases of domestic animals and wildlife

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The lymnaeid mud snail, *Galba truncatula*, is the key intermediate host to a multitude of trematodes, in particular liver and rumen flukes of livestock and wildlife. The snail is a key host to the zoonotic liver flukes within the genus *Fasciola* but has also been implicated in the establishment of the invasive parasite *Fascioloides magna* within deer populations across Europe. The occurrence, range and movement of *G. truncatula* is the single most important factor influencing the transmission of such fluke species, yet the understanding of the evolutionary history of the global diversity and range expansion of this snail remains unknown. Using both mitochondrial and nuclear markers and employing a phylogenetic approach, evidence of a rapid global population expansion event and cryptic invasions, especially into the UK, was identified. Similarly, despite indications of mito-nuclear discordance within *G. truncatula* populations, we identified evidence of translocations of snail populations from Europe to South America and Africa. These results indicate an increase in the snail's range as both a native and an invasive species, suggesting a wider environmental range for fluke transmission to establish. Data generated here suggests anthropogenic influence in the movement of *G. truncatula* and highlights a potential role for migratory waterfowl in the distribution of the snail, and ultimately the parasites they transmit.

Tuesday 16 September – 13h40 (Ndlopfu)

123 - Speciation in brachycladiid liver flukes, cryptic parasites of marine mammals, with applications for cetacean conservation

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Little is known about the speciation and divergence events that underpin variation within the trematode family Brachycladiidae, with issues surrounding accurate taxonomy and the extent to which specific parasite species can utilise multiple hosts. This is particularly true for the globally distributed yet phylogenetically cryptic fluke *Campula oblonga*. We hypothesised that *C. oblonga* represents multiple species, and that the divergence is ultimately linked to the specific evolutionary histories and ecological traits of the specific cetacean host species. A molecular phylogenetic and phylogeographic analysis was applied to *C. oblonga* populations parasitising harbour porpoises (*Phocoena phocoena*), Dall's porpoises (*Phocoenoides dalli*), and narrow-ridged finless porpoises (*Neophocaena asiaeorientalis*). Phylogenetic analyses of *C. oblonga* illustrated divergence events coincided with host divergence, but also that *C. oblonga* fell into at least three distinct molecular taxonomic units, considered to be distinct species. Variation in *C. oblonga* sequences from European harbour porpoises and Japanese Dall's porpoises was low enough to consider them the same parasite species. However, the variation between the clades containing *C. oblonga* sequences from Japanese harbour porpoises and South Korean narrow-ridged finless porpoises was sufficiently different for these to be considered discrete species from one another, and different from the species infecting European harbour porpoises and Japanese Dall's porpoises. These findings indicated that parasite speciation occurs across spatial and host species scales, illustrating the importance of not only geographical isolation but also host specialisation, with potential applications for cetacean conservation, utilising parasite genotype as an indicator of stranded or bycaught cetacean source populations.

Tuesday 16 September – 09h15 (Ndlopfu)

124 - Investigating vector-borne protozoa in wild carnivores from northeastern Italy

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Vector-borne protozoa (VBP) infect mammals globally, often causing severe disease in domestic ones. Wild canids (e.g., golden jackals, grey wolves, red foxes) and felids (i.e. wildcats, lynxes) may act as reservoirs, influencing pathogen epidemiology. In north-eastern (NE) Italy, the VBP occurrence remains poorly investigated, despite ongoing changes in their presence and distribution patterns. This study provides preliminary data on *Cytauxzoon* spp., *Hepatozoon* spp., and *Babesia* spp. in two wild species from NE Italy, characterised by a recent demographic increase. Forty-nine golden jackals (*Canis aureus*) and 40 European

wildcats (*Felis silvestris silvestris*) found dead were collected and submitted for necropsy. Bone marrow, spleen, lymph nodes, lung, liver, heart and blood clots were collected from both species and analysed by conventional PCR (18S-rRNA) for all investigated genera and species. A nested PCR (cytochrome b gene) was used for *Cytauxzoon* species identification. Prevalence values and 95% confidence intervals (CI) were calculated. *Hepatozoon canis* was detected in 31/49 (63.3%; 95% CI: 49.3-75.3) jackals, mainly in bone marrow. *Cytauxzoon europaeus* was identified in 7/40 (17.5%; 95% CI: 8.8-32.0) wildcats, all from spleens and blood clots. *Hepatozoon* DNA was detected in 22/40 (55.0%; 95% CI: 39.9-69.3) wildcats: four animals were positive for *Hepatozoon silvestris* (mainly cardiac muscle) and 18 for *Hepatozoon felis*. No samples tested positive for *Babesia* spp., and no co-infections were detected. These preliminary results suggest that golden jackals and wildcats are involved in the circulation of *Hepatozoon* and *Cytauxzoon* species, possibly playing an important epidemiological role, while *Babesia* species do not seem to circulate in these wild hosts. However, further analysis will help to improve the identification of their epidemiological relevance for VBP.

Wednesday 17 September – 11h00 (Ndlopfu)

127 - Geographical distribution, ecology and infection status of hosts of *Fasciola* species from selected localities in South Africa

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The study aimed to assess the distribution, ecology and infection status of lymnaeid snails, the main intermediate hosts of *Fasciola* spp., from selected localities in five provinces of South Africa. To achieve this, a freshwater snail survey was conducted in five South African provinces between 2021 and 2022, targeting water habitats where human and/or animal activities were occurring. Snails were collected using a scoop and/or by hand picking, and information on the localities was recorded using pre-designed forms. A total of 3417 freshwater snails across 26 habitats were collected during this period, of which 1059 were lymnaeids. *Pseudosuccinea columella* and *Radix natalensis* were the only lymnaeid snails identified, and *P. columella* was the most distributed lymnaeid snail, recorded in five surveyed provinces, while *R. natalensis* was the most abundant lymnaeid species (649/1059) despite only being collected from two provinces. Differences in abundance when compared to *P. columella* were not statistically significant ($p > 0.05$). The Limpopo province, where both species occurred, recorded the highest number of lymnaeid specimens (746/1059). Results showed that lymnaeid snails favoured perennial water bodies (dams and rivers) with muddy substrate and abundant aquatic grass, but the differences in abundance between different habitat types (perennial and seasonal sites) and activities occurring on site (human and animal vs animal only) were not statistically significant ($p > 0.05$). The two lymnaeid species mostly cohabitated together, or with other snail species such as *Bulinus globosus*, *B. tropicus*, *B. forskalii*, *Biomphalaria pfeifferi*, *Gyraulus conollyi*, *Physella acuta*, and *Tarebia granifera*. The province, site type, substrate, activity, and pH were important indicators of *P. columella* abundance, while substrate and activity were the important indicators of the abundance of *R. natalensis*. A total of 134 snails were screened for trematode infection using the 28S marker, and 28 snails were screened using the ITS-1 marker. None of the successful sequences matched

Fasciola spp. Results highlight the need to design specific PCR primers sensitive to *Fasciola* spp. detection in vector snails. We further recommend expanding the survey of lymnaeids to include the other regions of South Africa to understand the distribution and regional biodiversity of lymnaeids, and potential risk in the spread of *Fasciola* spp.

Tuesday 16 September – 13h55 (Ndlopfu)

128 - Plastic, fantastic: avian malaria plasticity in response to mosquito bites and co-infections

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Phenotypic plasticity enables parasites to adjust key life-history traits in response to environmental variation. For vector-borne pathogens, plastic responses to cues associated with vector presence or within-host competition could enhance transmission success, but empirical evidence remains limited. In this study, we investigate whether *Plasmodium relictum*, a widespread avian malaria parasite, exhibits adaptive plasticity in response to mosquito bites and co-infection with a conspecific lineage. We also explore the physiological mechanisms that may enable *P. relictum* to detect and respond to vector and competitor cues, including changes in host immune markers and production of extra-cellular vesicles. Our findings highlight the capacity of *P. relictum* to fine-tune its within-host dynamics in response to both external (vector) and internal (competitor) cues. This plasticity may play a crucial role in the ecological success and epidemiological impact of avian malaria, with broader implications for understanding parasite evolution under fluctuating transmission environments.

Monday 15 September – 09h30 (Ndlopfu)

129 - Prevalence and diversity of *Mycoplasma*, *Anaplasma* and *Bartonella* in captive and free-ranging black-footed cats (*Felis nigripes*) from South Africa

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The black-footed cat *Felis nigripes*, is a small wild felid of conservation concern, yet data on its haemoparasite prevalence and diversity remain limited. In this study, we confirmed haemoparasite presence using a PCR multi-gene screening approach to detect *Mycoplasma*, *Anaplasma*, and *Bartonella* in 15 free-ranging cats sampled from two locations in the Northern Cape Province, and six captive black-footed cats sampled from Mpumalanga Province, South Africa. PCR screening of DNA extracted from EDTA blood samples confirmed that none of the captive animals were positive for the three haemoparasite genera evaluated in this study. A single free-ranging animal was positive for a species of *Mycoplasma* previously found in cheetah from Namibia; the species is closely related to *Mycoplasma haemocanis* and *M. haemofelis*, but distinct from both across the 16S rRNA gene region. In contrast, the RnaseP gene phylogeny revealed a closer relationship to *Mycoplasma haemocanis*. Four free-ranging animals were PCR-positive for *Anaplasma*, and two distinct strains (A and B) were identified.

The 16S rRNA and *groEL* gene phylogenies confirmed that strain A is closely related to *Anaplasma bovis* and strain B groups with uncultured *Anaplasma* strains from Zambia and South Africa. However, both *Anaplasma* strains are distinct from each of their closest conspecifics. *Bartonella* was not detected in any of the cats. This study reports the first detection and characterisation of *Mycoplasma* in free-ranging BFCs and confirms the presence of two novel *Anaplasma* species.

Wednesday 17 September – 09h30 (Ndlopfu)

131 - From park to periphery: haemoparasite infections in indigenous rodents at the wildlife-livestock-human interface in Greater Kruger

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The western boundary of the Kruger National Park (KNP) borders the densely populated Bushbuckridge Municipality, enabling pathogen exchange between wildlife, livestock, and humans. Rodents are abundant across both the protected and surrounding peri-urban areas, aided by porous fencing and inadequate infrastructure. Although globally recognised as reservoirs of vector-borne haemoparasites, the role of rodents in zoonotic transmission in South Africa remains poorly understood. This study investigated the prevalence and genetic diversity of three bacterial genera of medical and economic importance in rodents sampled across a land-use gradient. DNA extracted from bloodspots of 160 indigenous murid rodents, sampled across this gradient were screened for the presence of *Anaplasma*, *Bartonella*, and haemotropic *Mycoplasma* (haemoplasma). Infection status was confirmed by multi-locus sequence analysis (MLSA), and cryptic host species were identified using species-specific multiplex PCR and/or cytochrome *b* gene sequencing. *Bartonella* was detected in 60.62%, *Anaplasma* in 26.88%, and haemoplasma in 20.00% of rodents, with 17.50% co-infected with two or more species. Co-infections were low in solitary *Lemniscomys rosalia*, and highest in two gregarious species, *Aethomys ineptus* and *Gerbilliscus leucogaster*, potentially broadening pathogen burden and symptom severity. *Bartonella* prevalence was significantly higher in anthropogenic areas (26.56%) than in protected zones (3.13%). Phylogenetic analysis identified seven *Bartonella* lineages, including those closely related to known zoonotic species. Two distinct *Anaplasma* lineages were identified, sister to the livestock pathogen *A. bovis*. *Mycoplasma* prevalence, diversity and host specificity were low. These findings highlight the utility of minimally invasive sampling in monitoring haemoparasite dynamics at wildlife-livestock-human interfaces in southern Africa.

Tuesday 16 September – 10h45 (Ndau & Nari)

132 - Haemoproteoza of wildlife: the dilemma of “dead” names

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Before the advent of molecular characterisation, species were distinguished solely on morphological features (sometimes including chromosomes), which required designation of type specimens. This is problematical in haemoproteoza, since many species are indistinguishable morphologically. Descriptions accompanying creation of new species names were often inadequate or lacking entirely. Naming or identification of species was usually based on two conflicting assumptions: (a) haemoproteoza are strictly host-specific, or (b) haemoproteoza are shared between members of the same taxon (which was arbitrarily selected, mainly genus or family). This has led to much confusion in the literature. One specific dilemma is that it is often impossible to determine to which haemoproteozoan (characterised molecularly) a previously published name applies. While diligent researchers refrain from referring to old names, others quite happily use them haphazardly, leading to more confusion. Instead of not using older names at all, which would render them “dead”, my proposal is that specific gene sequences entered into GenBank, where appropriate, should be designated as definitive for these “dead” names. This information, plus justification, should be published in a readily available journal. Some pragmatism may be required, but common sense should prevail. An example of pragmatism was designating a specific gene sequence for the pathogenic *Babesia felis* sensu stricto [1], even though the paper in which this species was named stated clearly that it was non-pathogenic in domestic cats [2].

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Monday 15 September – 11h00 (Ndlopfu)

136 - Evaluation of the vectorial competence of *Glossina brevipalpis* in the transmission of *Trypanosoma congolense*-savanna type, in the Matutuine District, Maputo Province, Mozambique

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African Animal Trypanosomosis (AAT) is a parasitic disease caused by trypanosome species, posing a major challenge to animal health and production in Africa. In the Matutuine District, southern Mozambique, where *Glossina brevipalpis* is prevalent, AAT has persisted for over a century. Previous research conducted in South Africa suggested that *G. brevipalpis* plays a marginal role, in the transmission of *Trypanosoma congolense*. However, due to the widespread presence of *G. brevipalpis* in South-east Africa and the epidemiological significance of these findings, this study aimed to re-evaluate its vectorial competence. The research involved 915 *G. brevipalpis* flies, fed six times on cattle infected with *T. congolense*. The flies were later fed on clean animals, followed by extended feeding on four susceptible cattle for 30 days. Monitoring of these animals over 60 days included body temperature, packed cell volume (PCV), buffy coat technique (BCT), and polymerase chain reaction (PCR) analyses. Weekly fly dissections examined the development of trypanosomes in the midgut and proboscis. Results showed that the four susceptible cattle became infected with *T. congolense*, while the animal used for proboscis cleaning remained uninfected. Dissections revealed that 89% of flies were positive for trypanosome through microscopy and 100% through PCR. These findings confirm that *G. brevipalpis* is a competent biological vector for transmitting *T. congolense*, challenging earlier assumptions and emphasizing its role in AAT dynamics.

Tuesday 16 September – 13h55 (Ndaou & Nari)

139 - The epidemiology and growth impact of microsporidia infections on children from low resources settings in the MalEd cohort

Amidou Samie and the MAL-ED Network Investigators

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Microsporidia are fungal pathogens though originally known as protozoan parasites. They are responsible for chronic diarrhea among HIV as well as non-HIV patients. However, there is a dearth of information on their occurrence and impact on child growth in community settings. In the present study we used qPCR assays to detect *E. bieneusi* and *E. intestinalis* from 41,327 monthly asymptomatic stools as well as stool collected during diarrheal episodes from 1715 children in the MalEd cohort. Anthropometric data were collected on a monthly basis for up to two years. Descriptive analysis of the data provided the overall distribution of microsporidia. We estimated the effects of microsporidia carriage on linear growth at 2 years of age. We also looked at the impact of other socioeconomic factors on the occurrence and distribution of microsporidia in the study population. The overall prevalence of *E. bieneusi* was 5.9% varying from 0.7% in Brazil to 13% in Tanzania while that of *E. intestinalis* was 0.4% with the highest in India (1%) and lowest in Brazil (0%). *E. bieneusi* was significantly high in Tanzania, Pakistan and Bangladesh ($p < 0.001$) while it was less prevalent in Brazil, India and South Africa. Overall, there was a significant difference between the prevalence of *E. bieneusi* in male (5.5%) and females (6.3%) ($p < 0.001$). Children who have taken rotavirus vaccine tended to be protected against *E. bieneusi* (OR=0.694; 95%CI: 0.564 – 0.854). *E. bieneusi* was not associated with diarrhea, dehydration, fever, loss of appetite and vomiting. However, *E. bieneusi* infections

were significantly associated with stunting (7.3% vs 4.9%) ($p < 0.0001$; OR=1.524, 95%CI: 1.405 – 1.652), underweight (7.5% vs 5.1%) ($p < 0.0001$; OR=1.429; 95%CI: 1.303 – 1.566) and wasting (6.9% vs 5.8%) ($p = 0.012$; OR=1.209; 95%CI: 1.043 – 1.401). Risk factors for *E. bieneusi* included lower income, poor sanitation, low maternal education, poor floor quality, keeping cattle and chicken in the household and poor quality of drinking water source. *E. bieneusi* infection was associated with faltering growth and low socio-economic factors encouraged the spread of infections among the children.

Wednesday 17 September – 09h00 (Ndau & Nari)

140 - Genetic diversity of *Entamoeba* species, and their impact on diarrhoea occurrence among under five-year-old children in Vhembe, South Africa

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Amebiasis is a common parasitic infection that contributes to the burden of diarrhoea in areas with poor sanitation and an inadequate water supply worldwide. However, the genetic diversity of these organisms remains poorly understood. In the present study, we investigated the genetic diversity of *Entamoeba* species, and the impact of these organisms on the occurrence of diarrhoea among children in Vhembe, South Africa. A total of 534 stool samples from children aged 5 years and below were used. All samples were processed by direct wet mount and were microscopically. Genomic DNA was extracted from all the stool samples and subjected to conventional PCR. Positive amplicons were sequenced by the Sanger method and 15 were selected for Next-generation sequencing in the MiSeq platform based on the *Entamoeba* 18S rRNA gene, using a MiSeq v3 (600 cycles) kit. The BLAST-based data analysis was performed using an Inqaba in-house developed data analysis pipeline. The phylogenetic tree was constructed to determine the species relatedness in the study population. Of the 534 samples, (24.3%) were microscopically positive for *Entamoeba* cysts. Forty-three (8%) of the total samples were positive for *Entamoeba* genus by PCR. Twenty positive amplicons were sequenced by Sanger sequencing technologies. Of these, 11/20 (55%) were *E. polecki* 8/20 (40%) followed by *E. coli* 2/20 (10%) and *E. muris* 1/20 (5%). In some cases, *E. polecki* and *E. moshkoviskii* were isolated from participants who experienced intermittent episodes of diarrhea, nausea, and malaise associated with large numbers of *E. polecki* and *E. moshkoviskii* in the stool. NGS showed that *E. coli* 9/15 (60%), *E. polecki* 3/15 (20%) and *E. moshkoviskii* 2/15 (13%) were the most common. The phylogenetic tree showed the close relationship between isolated species and the ones in the GenBank. The present study demonstrated a shift on the distribution of *Entamoeba* species in these communities with traditionally considered non-pathogenic species becoming more common. Further studies need to define the role of these species on the occurrence of diarrhoea in the region.

Wednesday 17 September – 09h30 (Ndau & Nari)

141 - Immune modulation and hidden costs of asymptomatic malaria in wild chimpanzees

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While *Plasmodium* infections are well-known for their clinical impact in humans, the health consequences for wild African great apes remain unresolved, especially when infections appear asymptomatic. Understanding these effects is critical for conservation and offers unique insight into the evolution of malaria tolerance in primates. In the present study, we analyzed blood samples from 27 wild-born chimpanzees (*Pan troglodytes troglodytes*) in Gabon, combining next-generation sequencing and targeted PCR to assess *Plasmodium* infection status and species composition. Twenty-three hematological, renal, hepatic, and immunological parameters—including plasma cytokine/chemokine profiles and stimulated PBMC responses—were quantified and compared between infected and non-infected individuals. *Plasmodium* infections were highly prevalent (48.2%) and especially common in younger chimpanzees, who also exhibited higher parasitemia. Infected individuals showed altered blood profiles, with elevated white blood cell and neutrophil counts, increased urea, reduced creatinine, and significant shifts in immune parameters. Notably, infected chimpanzees demonstrated robust upregulation of both pro-inflammatory (TNF, IFN- γ , CCL3, IL-1 β) and anti-inflammatory (IL-10) cytokines—mirroring immune regulation in asymptomatic human malaria. Upon ex vivo stimulation, PBMCs from infected chimpanzees produced more IL-10 but lacked a parallel increase in pro-inflammatory cytokines, indicating potential long-term immunosuppression. These findings suggest that even “silent” malaria infections can impose physiological costs, potentially increasing susceptibility to other pathogens. Our results reveal that asymptomatic malaria in wild chimpanzees is probably not immunologically silent. Chronic *Plasmodium* infection is associated with distinct immune modulation, early

signs of renal stress, and likely hidden impacts on health and resilience. These findings have critical implications for conservation, emphasizing the importance of integrated health monitoring in great ape populations, and provides an evolutionary perspective on malaria tolerance mechanisms shared across primates.

Monday 15 September – 10h30 (Ndlopfu)

143 - Highlighting malaria in Uganda with an assessment of an associated risk of infection within semi-captive chimpanzees

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In this presentation, I first review our team's past work on public health mapping initiatives in Uganda to monitor malaria and intestinal schistosomiasis amongst preschool-aged children and their mothers. Drawing upon general observations along the shoreline of Lake Victoria as well as seminal infection dynamic studies that detected treatment failure(s) against *Plasmodium falciparum*, *Plasmodium ovale* and *Plasmodium malariae*, I place attention on the unusual setting of the Ngamba Island Chimpanzee Sanctuary (NCIS). Here, within this semi-captive setting, just under 40 rescued chimpanzees are held. Like humans nearby, these animals are vulnerable to malaria and intestinal schistosomiasis. Indeed, over the last two decades, regular monitoring of these animals' health has been undertaken; most recently this year, an analysis of *Plasmodium* spp. within faeces and blood took advantage of real-time PCR assays. Analysis of preliminary results points towards cryptic infections in certain animals, with the pro and con of faecal detection assays discussed. Our appraisal is then set within the newly recognised deeper evolutionary origins of malaria within non-human primates, alongside today's interplay between animal conservation and anthroponozoonosis.

Monday 15 September – 09h45 (Ndlopfu)

144 - Host and parasite contribute to ectoparasite species assemblages on sympatric rodents

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Fleas, lice, ticks and mites are frequently associated with rodents though not uniformly distributed among rodent species. Host-associated factors such as nesting behaviour, sociality and habitat preference can facilitate life-history specific parasite profiles. Although historic monographs provide ectoparasite-host lists for most rodent species little is known regarding the relationship between host identity and parasite assemblages in sympatric rodent species. The study aimed to address this gap by 1) providing updated and novel species lists and abundance data for ectoparasites associated with four rodent species (*Gerbillus*

leucogaster, *Mastomys coucha*, *Mastomys natalensis* and *Saccostomus campestris*) and 2) assess the role of host identity in shaping the ectoparasite assemblages on sympatric rodent species. Rodents were live trapped during spring/summer in 2019 and 2020 in Mpumalanga and all ectoparasites removed. In total 13 289 ectoparasite individuals representing 39 species (6 fleas, 3 lice, 6 ticks and 24 mesostigmatic mites) were recorded. *Gerbilliscus leucogaster* harboured 19 species, *M. coucha* 21 species, *M. natalensis* 30 species and *S. campestris* 15 species. Seven parasite species were shared. The overall mean dissimilarity among the ectoparasite species for the rodent species were 0.78 ($p < 0.001$). The average pairwise dissimilarity was 0.39 between *M. coucha* and *M. natalensis*, 0.73 between *G. leucogaster* and *S. campestris* and > 0.95 for all other pairwise species comparisons. Several mite species, in addition to fleas and lice contributed mostly to the dissimilarity between rodent species. It is evident that host and parasite life-histories are important contributing factors for ectoparasite species assemblages.

Tuesday 16 September – 11h15 (Ndau & Nari)

END ORAL PRESENTATIONS

Poster Presentations

005 - Acaricide resistance of *Rhipicephalus decoloratus* ticks collected from communal grazing cattle in South Africa

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Rhipicephalus decoloratus is widespread throughout the rest of South Africa and it affects both domestic and wild animals. This study aimed to determine acaricide resistance in *Rhipicephalus decoloratus* ticks collected from grazing in Elundini, Senqu, and Walter Sisulu Local Municipalities of the Eastern Cape Province. A sample of 20–30 adult engorged female *R. decoloratus* ticks were collected from at least 10 randomly selected cattle (highly tick-infested) at each dip tank and placed into the labelled plastic collection bottles containing absorbent paper and with a perforated lid at a constant room temperature of $\pm 28^{\circ}\text{C}$ and $> 70\%$ relative humidity until resistance testing commenced. The Shaw larval immersion test method was used to determine *R. decoloratus* larvae resistance to various acaricide concentration levels [amidines, organophosphate (OP), and synthetic pyrethroids (SPs)]. This study found that most ticks were susceptible to exposure to different acaricide field concentrations of amidines (49% at 250 ppm), OPs (33% and 47% at 300 ppm and 500 ppm, respectively), and SPs (44% and 23% at 150 ppm and 300 ppm, respectively). The resistance testing results showed no resistance to amidines at any localities and no resistance to OP in the Senqu region. The larvae's resistance is a cause for worry. Hence, the continuous monitoring of tick resistance to commonly used acaricides will help mitigate widespread acaricidal resistance and sustain livestock productivity.

008 - Changes in nest microclimate affect concentration of gases and ectoparasite abundance in nests of eurasian blue tits (*Cyanistes caeruleus*)

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The presence of nestlings influences the microclimate inside avian nesting cavities. These changes can be used by parasites to locate their host but can also affect the development of parasites inside nest cavities. We explored the relationship between temperature and relative humidity and the abundance of ectoparasites and gas concentrations in blue tit nest boxes (n = 84) during the nestling period by comparing two years with differing climatic conditions. The average temperature at night in nest boxes was colder during 2016 (12.6 °C) than 2017 (14.4 °C), and in the latter, even warmer conditions were attained due to the experimental manipulation of temperature (16.9 °C). CO₂ concentration was higher in nest boxes in the warmer year and CH₄ concentration was lower than that in forest air, particularly in the wettest and coldest year. Different relationships were found between the abundance of different ectoparasites and the temperature, relative humidity, and gas concentration measured at different days of nestling age. For example, a positive association was observed between flea larval abundance and temperature at nestling age of 8 days, but a negative one was observed for mites under the same microclimate conditions. Moreover, a negative relationship was observed between the abundance of mites, midges, and blackflies and CH₄ concentration at different nestling ages. Changes in climatic conditions can also affect the concentrations of CH₄ and CO₂ inside and outside nest boxes, which in turn differentially affect ectoparasite abundance.

009 - Molecular detection of *Trypanosoma congolense* savanna infecting cattle in north-eastern KwaZulu-Natal Province, South Africa

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Trypanosoma congolense savanna (S) is a widely distributed species that infects cattle in northeastern KwaZulu-Natal (KZN), South Africa. It is a significant parasite for livestock in South Africa due to its pathogenicity and the possibility of mixed infections with other genotypes. In an effort to regularly monitor the prevalence of *T. congolense* (S) infections, this study used species-specific PCR assay targeting the 316 base pairs (bp) mini-chromosome satellite DNA repeat region for detecting *T. congolense* (S) infecting cattle in the north-eastern KZN. Preliminary data on 412 cattle blood samples from four municipalities namely uMhlababuyalingana (n=59), Mtubatuba (n=58), Jozini (n=115), and the big five Hlabisa (n=180) within Umkhanyakude district in the northeastern KZN were conducted. The overall *Trypanosoma congolense* (S) infections across all the municipalities were 212/412 (51.46%)

based on the *T. congolense* (S) PCR assay. The current results are consistent with the previous studies that reported TCS as the predominant species responsible for African animal trypanosomiasis in cattle in northeastern KZN. The *T. congolense* (S) infections are an ongoing concern for animal health in South Africa they cause mortality in livestock and increase significant economic challenges, especially for farmers near game reserves where infections are more prevalent.

015 - Mitochondrial DNA phylogeography of a species-specific sucking louse, *Johnsonphthirus heliosciuri*, acts as a proxy to provide insights into the population connectivity of its host, Smith's bush squirrels, *Paraxerus cepapi*

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Permanent species-specific lice and their hosts often show congruent phylogenetic or phylogeographic structures due to co-speciation. Due to the smaller effective population sizes of parasites, their phylogeographic structures are often more pronounced than that of their host. Phylogeographic structure present in a permanent species-specific louse can thus act as a more sensitive tool to show host dispersal. This study investigates the phylogeographic structure of a squirrel, *Paraxerus cepapi*, and one of its louse species, *Johnsonphthirus heliosciuri* sampled from eight localities in South Africa. Statistical haplotype networks derived from 51 host mitochondrial DNA control region sequences indicated a lack of geographic genetic structure among sampling localities with most of the genetic variation contained within populations (Φ_{st} 0.304, $P < 0.05$). In sharp contrast, sequence analyses of 43 louse mitochondrial DNA COI sequences showed a clear pattern of geographic genetic structure and most of the variation was confined to between populations (Φ_{st} 0.797, $P < 0.05$). Nuclear Eukaryotic Elongation Factor 1 data showed an absence of any geographic structure for both species. The lack of phylogeographic congruence between the host and louse, and between the two molecular markers used in this study, can most likely be attributed to stochastic differences in the evolutionary rates of parasite and host DNA. In this study, the species-specific permanent parasite acted as a proxy, or a biological 'magnifying glass', for host phylogeography and the mtDNA data suggest that recent anthropogenic habitat fragmentation indeed may limit squirrel movement across the landscape.

017 – Going into details: first molecular data and SEM observations of *Capillaria pterophylli* (Nematoda) from ornamental fish of the Cichlidae family

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Capillaria pterophylli is one of four species of *Capillaria* known to infect neotropical fish of Cichlidae. A total of 248 specimens, representing seven species of neotropical ornamental cichlids, were received from Indonesia (IND), Sri Lanka (SL), and Thailand (TH) through an established import company. Internal organs were examined for the presence of nematodes. Collected nematodes were studied morphologically using scanning electron microscopy (SEM), and the 18S rDNA region was sequenced. Parasitological examination revealed that three fish species were infected with *C. pterophylli*, i.e., *Andinoacara pulcher* (SL), *Uaru amphiacanthoides* (IND), and *Pterophyllum scalare* (IND and SL). The highest infection rate was observed in *P. scalare* from Indonesia, with a prevalence (P) of 52.9% and an intensity of infection ranging from 1 to 32. Very low infection levels were observed in *U. amphiacanthoides* (P = 6.67%) and *P. scalare* from Sri Lanka (P = 5%). The newly generated sequence was unique within the database. Phylogenetic analysis placed *C. pterophylli* as a sister taxon to a cluster of avian *Capillaria* spp. The uncorrected *p*-distance between *C. pterophylli* and avian species ranged from 10.9–12.9%. These findings suggest a need to re-evaluate the taxonomy of *Capillaria* spp., as the genetic distances between genera included in the analysis were lower than those between different *Capillaria* species. SEM observations provided detailed imagery of the surface of the parasite's eggs and confirmed the presence of numerous papillae on the posterior part of the parasite's body.

027 - Is that a bedbug? First record of *Cimex lectularius* L. inside Eurasian Blue Tit (*Cyanistes caeruleus* L.) nests

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Nest-dwelling ectoparasites are frequently found affecting avian host species. Eurasian Blue Tit (*Cyanistes caeruleus* (Linnaeus, 1758)) nests are commonly infested by blowfly larvae *Protocalliphora azurea* (Fallén, 1817), mites of the genus *Dermanyssus* Dugès, 1834 and fleas *Ceratophyllus gallinae* (Schrank, 1803). However, we have recently detected several individuals of Cimicidae bugs in nests of this bird species. In this study we analysed the bug specimens found in four different nests over three years in a deciduous Pyrenean oak forest located in Valsaín, central Spain. Morphological characteristics of 15 males, 19 females and 45 nymphs were measured, and results showed a great similarity with characteristics of the species *Cimex lectularius* (Linnaeus, 1758). However, we found a slight difference on head width to third antennal segment ratio (1.51, SD 0.121) with respect to the value reported for *C. lectularius* (1.45, SD 0.096). In addition, fragments of the cytochrome oxidase subunit I (COI) and the 16S rRNA (16S) genes of 10 specimens (4 male, 3 female and 3 nymph) have been successfully sequenced. The analysis of this partial sequences showed a 99.83% similarity on BLAST to *C. lectularius* sequences from Hungary, China and USA. These findings highlight the cosmopolitan nature of *C. lectularius*, demonstrating its ability not only infecting humans, but birds, such as the Eurasian Blue Tit, as well.

031 - Trypanosome infection prevalence in *Glossina brevipalpis* collected from the communal areas of north-eastern KwaZulu-Natal, South Africa

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Animal African Trypanosomiasis (AAT) is a protozoan disease caused by salivarian trypanosomes parasites. These parasites are cyclically transmitted by different *Glossina* spp. during blood meal feeding. For many years, the Sub-Saharan African countries have suffered massive economical loss due to the presence of these flies and their parasites. The aim of this study was to analyse the infection prevalence of trypanosome parasites in *Glossina brevipalpis* collected in 5 different communal areas of north-eastern KwaZulu-Natal Province (KZN). DNA was extracted from 241 (110 males and 131 females) flies using Qiagen blood and tissue DNA extraction kit. Polymerase Chain Reaction (PCR) amplification using Internal Transcriber Spacer (ITS) and other species-specific primers showed that 66.8% (n = 161) samples tested positive for trypanosome infections. These infections were from *Trypanosoma congolense* Savannah, *T. congolense* Kilifi and other *Trypanozoon* species. Trypanosome co-infections were recorded in 18% (n = 44) samples consisting of 21 males and 23 females. The results showed that the two *T. congolense* strains (*T. congolense* Savannah and *T. congolense* Kilifi) responsible for AAT are circulating the communal areas of KwaZulu-Natal Province. In addition, most rural farmers in the area live in proximity with wildlife and their livestock is at risk of trypanosome infections. Therefore, the intervention of socioeconomic studies is required to assist farmers especially in rural areas on how to manage such infections in livestock.

036 - Gastrointestinal nematodes and *Enterobacteriaceae* bacteria infecting horses in Potchefstroom town of North-West Province, South Africa

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This study investigated the seasonal prevalence of nematodes and antibiotic resistance profiles of *Enterobacteriaceae* bacteria infecting horses in Potchefstroom. Nematode prevalence was assessed across six stables, revealing a significantly higher burden during the summer months in four stables. The study identified *Strongyloidea* spp. as the most prevalent nematode, along with *Oxyuris equi* and *Strongyloides westeri*, detected through morphological analysis. Nematode prevalence was significantly higher in summer (~68%) due to warm and humid conditions, with ROS'Amo Perdryskool, SAPS Mounted Academy, Potch Polocrosse Club, and Potchefstroom Ruiter Klub showing infection rates above 70%. In contrast, the winter prevalence was lower (~45%), except for Cammelot Equestrian Center and Adelprag Friesian Stud. These findings emphasize the seasonal dynamics of nematode

infections and the role of strategic deworming in parasite control. The study also identified six Enterobacteriaceae species from randomly selected horse faecal samples, with *Escherichia coli* (40%) being the most prevalent, followed by *Siccibacter turicensis* (25%) and *Atlantibacter hermannii* (15%). Antibiotic resistance testing indicated a high level of resistance to Amoxicillin and Trimethoprim across most bacterial samples, raising concerns about the efficacy of standard antibiotics in treating equine bacterial infections.

038 - Hiding in the protected area: New species of *Paradiplozoon* Akmerov, 1974 (Polyopisthocotyla) from two endemic cyprinids hosts in South Africa's Cape Fold freshwater ecoregion

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The South African Cape Fold ecoregion (CFE) is home to a magnificent species diversity with a high level of endemism; however, limited information exists on the diversity of fish parasites. Species of *Paradiplozoon* Akmerov, 1974 mainly infect cyprinid hosts and are predominantly found in Europe and Asia. Six valid species are recognised from African fish, with three species described and reported from *Labeo* and *Labeobarbus* spp. in South Africa. During a study focused on exploring fish parasite diversity of endangered fishes of the CFE, 15 individuals of the near-threatened Clanwilliam sawfin, *Cheilobarbus serra*, and Clanwilliam redbin, *Sedercypris calidus* were collected from the Matjies and Rondegat rivers, Cederberg Wilderness Area, Western Cape Province. *Paradiplozoon* specimens were found on the gills of 15 *C. serra* (P = 66.6%, IF = 1–6) and 15 *S. calidus* (P = 60%, IF = 1–6). Molecular and morphometric analysis of the collected specimens confirms that they differ from any known species of *Paradiplozoon*. A BLAST Search identified *P. ichthyoxanthos* as the closest species to the newly generated ITS2 rDNA sequence differing in 11 sites (1.8%). Based on the uncorrected *p*-distances, three African species of *Paradiplozoon* (*P. vaalense*, *P. krugerense*, and *P. morrocoensis*) are far related to the new *Paradiplozoon* sp., with interspecific variability of 13%, 31%, and 29.3%, respectively. The identification of the new species of *Paradiplozoon*, the fourth species from South Africa, indicates that the diversity of these parasites is severely understudied on the African continent.

040 - Molecular characterisation and phylogeny of three South African marine fish haemogregarines (Adeleorina: Haemogregarinidae)

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Currently, little is known about the biology of fish haemogregarines despite their high prevalence in fish populations, their taxonomic classification primarily reliant on developmental morphology in vertebrate hosts. However, haemogregarines follow a heteroxenous life cycle,

requiring both vertebrate and invertebrate hosts, with life cycle and vector knowledge remaining limited. Fish haemogregarines include several genera, with *Haemogregarina* being the most prevalent, a genus strictly vectored by leech hosts. Recently, phylogenetic analyses have proved useful in the identification of haemogregarine genera and the potential vector, particularly for those of herpetofaunal haemogregarines. To date, only two species of fish haemogregarines, *Haemogregarina bigemina* and *Haemogregarina daviesensis*, have been molecularly characterised. Notably, *H. bigemina* clustered outside the *Haemogregarina* and adeleorine clade, raising questions about its taxonomy and vector associations, along with that of other fish haemogregarines. Species of *Haemogregarina* are notably diagnosed by peripheral blood merogony or division. However, this is not evident in all fish haemogregarines. Morphologically, this led to a taxonomic revision and establishment of the genus *Desseria* by Siddall (1995), accommodating fish haemogregarines that lack erythrocytic merogony. The aim of this study is, therefore, to contribute to the phylogenetic resolution and taxonomy of this group of fish blood parasites by molecularly characterising a *Desseria*-like haemogregarine infecting the mullet (*Chelon richardsonii*) from Tsitsikamma National Park, using the 18S rRNA gene. Blood samples were examined morphologically and molecularly, with parasite stages micro-graphed and measured, comparing these to previous descriptions. Phylogenetic analyses are expected to cluster sequences according to clade group, genus and potential vector.

041 - The role of the Medical Entomology Museum in advancing vector-borne disease research and parasite surveillance

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The Medical Entomology Museum (MEM) at the National Institute for Communicable Diseases (NICD) plays a pivotal role in the study of vector-borne parasites, serving as a vital resource for entomological research and disease surveillance. Established in 1926 by Dr. Alexander Ingram in response to malaria outbreaks in South Africa, it has since evolved into one of Africa's most comprehensive repositories of medically significant insect specimens. MEM houses over 60,000 specimens, including more than 600 type specimens essential for studying vectors of malaria, lymphatic filariasis, and arboviruses¹. Historical collections, initiated by pioneers like Dr. Botha de Meillon, have provided foundational insights into vector ecology, species distribution, and parasite transmission (South African Department of Health, 2024). Today, these collections continue to support molecular and morphological research, aiding in species identification and insecticide resistance monitoring. Beyond research, MEM contributes to vector surveillance, preserving specimens for epidemiological studies, tracking population shifts, and documenting emerging threats. Modernization efforts, including digitization and high-resolution imaging, enhance accessibility for global collaborations. Additionally, the museum serves as a training hub, equipping entomologists with expertise in vector identification and diagnostic techniques crucial for parasite control. As global efforts to combat vector-borne diseases intensify, MEM remains an indispensable scientific asset, bridging historical data with contemporary research. By preserving vector biodiversity records

and fostering interdisciplinary collaborations, it continues to shape the future of vector-borne parasitic disease research, surveillance, and control strategies.

044 - The first characterisation of the secretome in the acanthocephalan *Pomphorhynchus laevis* from *Barbus barbus*

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The secretomes (ESPs) produced by parasites play a key role in modulating the host's immune responses. While these interactions have been studied in the most important groups of helminths such as various flatworms and nematodes, there are no data for syndermata such as rotifers or spiny-headed worms (Acanthocephala). The present study aims to fill this gap by characterising the secretome of *Pomphorhynchus laevis*, an endoparasite of the common barbel *Barbus barbus* (Cyprinidae), and providing an evolutionary perspective on the ESPs produced by parasites. For the first time, we use proteomic analyses to characterise the secretome of *P. laevis* and identify key proteins involved in host manipulation, immune modulation and parasite survival. These results may reveal potential biomarkers for parasite detection or new therapeutic targets for the treatment of acanthocephalan infections.

052 – Detection of *Trypanosoma equiperdum* antibodies from South African horses and donkeys using complement fixation test

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Dourine is a significant chronic venereal disease of equines caused by *Trypanosoma equiperdum* which is transmitted sexually from animal to animal. A total 771 clinical cases of dourine infections in horses have been reported across all provinces in South Africa by state veterinarians from Department of Agriculture, Land Reform and Rural Development (DALRRD) between 1993 – 2016. There is no approved treatment regimen for dourine in South Africa. The World Organization for Animal Health (WOAH) recommends the complement fixation test (CFT) as the standard serological test for diagnosing dourine due to its high specificity and sensitivity in the detection of *T. equiperdum* antibodies. Control of infections in complement fixation test confirmed cases is by slaughtering of infected horses. This study used USDA antigen CFT assay to examine seropositivity rates from serum samples collected from 141 horses and 29 donkeys from different provinces in South Africa. The seropositivity rates for horses were 1 (5.26%) Northern Cape, 4 (5.13%) Mpumalanga and 3 (6.82%) North-West provinces. For donkeys, only 2 (11%) samples from North-West province were seropositive whilst no positives were detected from Northern Cape and Mpumalanga provinces. These are preliminary results and more samples from other provinces will be screened to determine overall prevalence of dourine in South Africa.

053 - Diving into discovery: Uncovering new marine fish leech species in South Africa

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Hirudinea, or leeches, are a subclass of segmented worms (phylum Annelida) characterised by suckers at both ends of their bodies and a lack of bristles, with many species being ectoparasitic bloodsuckers or predators. Marine fish leech fauna is highly diverse, with new species being discovered annually. However, some regions remain poorly explored, with only two species of piscicolid leeches described from the coastal waters of South Africa. Globally, approximately 20 marine fish leech species are known, and given South Africa's status as one of the world's most biodiverse countries, the potential for discovering new species is high. These blood-feeding invertebrates are known to transmit pathogens by feeding on infected vertebrates, highlighting the importance of understanding these species. This study aimed to enhance our knowledge of marine fish leech diversity through morphological characterization, histological identification, and molecular analysis. Leeches were collected from various marine teleost fish host species, namely: Cape stumpnose (*Rhabdosargus holubi*), Cape white seabream (*Diplodus capensis*), flathead grey mullet (*Mugil cephalus*), grooved mullet (*Chelon dumerili*), klipfish (*Clinus superciliosus*), South African mullet (*Chelon richardsonii*), striped mullet (*Chelon tricuspidens*) and white steenbras (*Lithognathus lithognathus*) at five different locations on South Africa's south coast. Morphological characterisation and histological identification were performed to the lowest taxonomic level possible. Molecular analyses, using multiple genetic markers, were conducted on leech specimens. Using complementary morphological and molecular data, three species were identified, with two of these likely new to science. This represents a significant contribution to understanding marine parasite biodiversity in South Africa.

054 - Physiological costs of sub-clinical haemoparasite co-infections in Namibian cheetahs (*Acinonyx jubatus*)

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Co-infection by parasites is ubiquitous in wild animal populations. Pathogen (co-)infections can affect individual health and fitness and have the potential to influence population dynamics. However, these infections often remain sub-clinical, and their effects are therefore

unknown or overlooked. To better understand the potential underlying costs and effects associated with long-term co-infections, we characterized inflammatory and biochemical parameters in free-ranging Namibian cheetahs (*Acinonyx jubatus*) in a long-term study (n = 194). This cheetah population is known to harbour a consistent pool of co-infecting vector-borne pathogens, including bacteria (*Rickettsia* spp., Anaplasmataceae) and protozoans (*Babesia* spp., *Hepatozoon* spp.). The inflammatory response was characterized by the levels of pro-inflammatory cytokines (IL-1 β and TNF- α), an acute phase protein (SAA), as well as markers of macrophage activity (neopterin) and oxidative stress (reactive oxidative metabolites and antioxidant capacity) in serum and plasma. Serum biochemical markers were chosen to cover liver and kidney function and muscle health (AP, ALT, GLDH, GGT, total bilirubin, bile acids, AST, CK, LDH, total protein, urea, creatinine). We investigated the relationships between the previously identified co-infecting pathogens and the inflammatory and biochemical profiles, life-history parameters and environmental factors. Our results suggest that life-history parameters, such as age and sex are more important determinants of the described immunological and physiological measures than the haemoparasite community in the animals. We discuss the importance of the measured parameters in wildlife health monitoring and what long-term effects the vector-borne pathogens infections can have on the genetically constrained cheetah population.

055 - Movement costs of sub-clinical babesiosis in free-ranging Namibian cheetahs (*Acinonyx jubatus*)

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Wild animals are exposed to and infected by a number of parasites, however most of them do not present overt clinical signs. The costs associated with such sub-clinical parasite infections are therefore often overlooked. The tick-borne protozoan *Babesia* is a prevalent parasite of African carnivores. The infection causes acute haemolytic anaemia particularly in canids and can consequently lead to anorexia and lethargy. On the other hand, feline babesiosis is often chronic, with no clinical symptoms, but still might bear costs. Here we investigate the potential effects of *Babesia lengau*-like parasite infections on movement behavior in a free-ranging population of cheetahs in central Namibia. We described movement patterns and behavior based on GPS and accelerometry data, using supervised machine learning algorithms to identify individual characteristics (home range size, daily walking distance, walking speed and resting budget). Infection with *Babesia lengau* was determined by PCR. We hypothesized that the costs associated with sub-clinical *B. lengau*-infection can manifest in constrained movements, limiting or enhancing certain aspects (e.g. walking speed or resting time) of movement behavior. Our results suggest that infection with *B. lengau* might be more costly for female than for male cheetahs, and that males with different spatial tactics (territory holder vs. floater) are differentially affected by the infection. The diverse relationships between infection status and movement behavior highlight the complexity of interactions between the immunological, physiological and energetic constraints of the host and important, hidden fitness costs of subclinical infections.

060 - Estimating *Toxoplasma gondii* exposure in Swedish wolverines (*Gulo gulo*) – a retrospective study

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The wolverine (*Gulo gulo*), the largest member of family Mustelidae, is a top predator and scavenger found in circumpolar regions throughout North America and Eurasia. Due to its trophic position and large home range sizes, the species could serve as sentinels for ecosystem health of northern Arctic tundra, taiga, mountain, and boreal forest ecosystems. The species is listed as Vulnerable by the IUCN, and still limited information exists on the potential importance of diseases in regulating and/or threatening wolverine populations, especially in the recovering Scandinavian population. *Toxoplasma gondii* is a zoonotic food borne parasite which has been reported in mortality events of various Mustelid species. Exposure to the parasite has been found in Canadian wolverines, but there is no information from Scandinavia, where felids, the final host of the parasite, are less common compared to North America. Using a commercially available multi-species ELISA kit, we tested archived samples (n=108) collected between 1994 and 2003 from Swedish wolverines for the presence of antibodies to *T. gondii*. A seroprevalence of 24% was found, which is lower than previously reported from Northwest Territories (62%) or Nunavut (41%), Canada (but see British Columbia (0%)). Surprisingly, there was no significant difference in exposure between sex (18% in males vs. 28% in females) and age (33% in adults vs. 19% in juveniles) groups. With climate change, a northern expansion of parasites is expected, thus monitoring the population health of Swedish wolverine populations is relevant for both One Health and conservation biology.

067 - Potential applications of *Toxorhynchites* mosquitoes in integrated pest management (IPM) strategies

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The role of *Toxorhynchites* mosquitoes in biological control is gaining increasing attention in vector-borne disease management. This genus, comprising approximately 90 recognized species, is curated at the Medical Entomology Museum of the National Institute for Communicable Diseases Museum, housed within the Vector Control Reference Laboratory. Often referred to as "elephant mosquitoes" or "mosquito eaters," *Toxorhynchites* are unique in the Culicidae family due to their non-hematophagous adult diet and predatory larval stage. Unlike disease-transmitting mosquitoes, adult *Toxorhynchites* sustain themselves on nectar and plant juices, while their larvae are aggressive predators of other mosquito larvae,

particularly *Aedes*, *Anopheles*, and *Culex*, vectors of diseases like malaria, dengue, Zika, and West Nile virus. Given concerns over insecticide resistance, integrating *Toxorhynchites* into biological control programs offers a sustainable alternative to chemical insecticides. These mosquitoes are visually distinctive with large size and iridescent metallic coloration. Found in tropical and subtropical regions, they align with areas where mosquito-borne diseases remain endemic. The MEM collections provide crucial data to support vector surveillance and control strategies. By fostering interdisciplinary collaborations in medical entomology, these natural predators could help combat parasitic diseases, reinforcing integrated vector management (IVM) and reducing reliance on chemical insecticides.

068 - Ectoparasite diversity and distribution in *Rattus rattus* and *Rattus tanezumi* from rural communities in the Savanna biome, South Africa

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The genus *Rattus* is a known reservoir for disease-causing bacteria, including *Yersinia pestis* (plague), *Bartonella* spp. (cat scratch fever), and several rickettsial infections. In many African rural communities, poor housing infrastructure facilitates the presence of commensal rodents like *Rattus* species. This study provides the first comprehensive assessment of ectoparasites associated with *Rattus rattus* and *Rattus tanezumi* in rural communities of the Savanna biome, South Africa. The study aimed to identify key ectoparasite species of veterinary and medical importance and examined the influence of habitat, locality, and host traits on ectoparasite loads. Over six years, 47 *R. rattus* and 43 *R. tanezumi* individuals were examined, revealing three ticks, six mites, five fleas, and three lice species. The dominant ectoparasite species were *Polyplax spinulosa* (louse, n=421), *Echidnophaga gallinacea* (flea, n=252), and *Ornithonyssus bacoti* (mite, n=147). Notably, *Xenopsylla brasiliensis*, a known *Y. pestis* vector, and *E. gallinacea*, a flea with a broad host range capable of transmitting rickettsial infections, were present. Locality and host traits significantly influenced the abundance of lice, mites, and fleas. Despite the widespread distribution of *Rattus* species, studies on their parasitic fauna remain scarce, raising concerns about their role as reservoirs for zoonotic diseases. Further research is urgently needed to assess the ectoparasitic community of *Rattus* spp. across their range and clarify their role in zoonotic disease transmission in southern Africa.

075 - Diversity of *Sarcocystis* in wildlife from the Greater Kruger, South Africa

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Sarcocystosis, caused by *Sarcocystis*, is a disease affecting a large number of animals. *Sarcocystis* has a two-host life cycle; with carnivores as definitive and herbivores as intermediate hosts. The epidemiology involves determining spatial distribution, transmission cycles and the impact the parasite has on animals and humans. Infected hosts manifest clinical signs or symptoms such as fever, inappetence and myositis. *Sarcocystis* species have been identified in South Africa, but their diversity and ecosystems remain unexplored. This study investigates the occurrence of *Sarcocystis* species in wildlife from the Greater Kruger. Tissues collected from klipspringers and hyenas were confirmed to be *Sarcocystis*-positive by histopathology. The 18S rRNA was used to screen and confirm the presence of *Sarcocystis* DNA using PCR. Positive amplicons were sent for Sanger sequencing. The sequences were blasted on NCBI, and the top two matches were selected, including *Toxoplasma gondii* as an outgroup. After sequence analysis a Maximum likelihood phylogenetic tree was constructed. The *Sarcocystis* species DNA isolated from the klipspringer formed a clade with *Sarcocystis hircicanis* and *S. arieticanis* (94% bootstrap), but a weak 60% bootstrap with *S. arieticanis*. The hyena sequences formed a clade with *S. caninum* and *S. artica* (92% bootstrap). No published data has identified these species in South Africa. Further parasitological and molecular investigation is required to elucidate if they represent new species and which prey-predator relationship they represent. The results provide interesting insights on possible new species circulating in South African wildlife and the need for further research on this topic.

077 - Occurrence of *Anaplasma marginale* in cattle from villages in the Mnisi Community, Mpumalanga province, South Africa

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Bovine anaplasmosis is a tick-borne disease caused by the obligate intracellular rickettsia, *Anaplasma marginale*, and to a lesser extent, *Anaplasma centrale*. Fulminant anaplasmosis

cases are frequently reported at the Hluvukani Animal Health Clinic in the Mnisi community, Mpumalanga Province, South Africa. A previous study identified calves from wildlife-interfacing areas that were not infected with *A. marginale* in their first year, while those in peri-urban areas were all infected early. Anecdotal reports indicated that there were more cases of clinical anaplasmosis in the wildlife interfacing areas. This study aimed to analyse the dynamics and distribution of *A. marginale* and *A. centrale*-positive cattle and clinical anaplasmosis. A total of 514 cattle samples were screened for *A. marginale* and *A. centrale* using a duplex qPCR assay. *Anaplasma* spp. were detected in 282 cattle (54.9%), comprising single *A. marginale* infections in 263 cattle (93.3%), single *A. centrale* infections in 6 cattle (2.1%), and co-infections in 13 cattle (4.6%). While *A. marginale* was detected in cattle from all villages, significant differences were found between both *A. marginale* and *A. centrale* infections between villages. A Spearman's correlation test indicated that villages with more *Anaplasma* infections tended to report fewer clinical cases, although this was not significant. These results suggest that a localized lack of endemic stability at the wildlife interface could result in clinical cases caused by *A. marginale* infection occurring at a later point in life. The *A. marginale* genotypes will be analysed to assess differences between villages cross correlating with cases of anaplasmosis.

080 - Assessment of quantitative real-time PCR assays to detect a novel *Anaplasma* species in dogs

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The rapid advancement of next-generation sequencing technologies has led to the discovery of novel *Anaplasma* species, highlighting the growing complexity within the *Anaplasma* genus. One such novel species, *Anaplasma* sp. SA Dog, closely related to *Anaplasma phagocytophilum*, has been identified in canids in southern Africa. Accurate detection of these closely related species is essential, particularly given the zoonotic significance of *A. phagocytophilum*. A quantitative real-time PCR (qPCR) assay targeting the *A. phagocytophilum* *msp2/p44* gene, thought to cross-react with *Anaplasma* sp. SA Dog, and an *Anaplasma/Ehrlichia* group-specific qPCR assay targeting the 16S rRNA gene, were used to screen 553 DNA samples extracted from dog blood collected in the Mnisi community, Mpumalanga. Of these, 73 samples tested positive with high Ct values using the *A. phagocytophilum* qPCR (13%), while the *Anaplasma/Ehrlichia* qPCR yielded 187 positives (36%); 24 samples (5%) tested positive by both assays. A subset of positive samples was subjected to full-length 16S rRNA gene PacBio sequencing. No *A. phagocytophilum* 16S sequences were detected in the microbiome data from samples that tested positive for *A. phagocytophilum*. *Anaplasma* sp. SA Dog, *A. platys*, and *Ehrlichia canis* 16S sequences were identified in *Anaplasma/Ehrlichia* qPCR positive samples. Shotgun Illumina sequencing of an *Anaplasma* sp. SA dog sample yielded two *Anaplasma* sp. SA dog *msp2/p44* sequences. Cloning and sequencing of the qPCR amplicons generated by the *A. phagocytophilum* assay revealed that the sequences matched several *A. phagocytophilum* *msp2/p44* gene with 100% identity, but multiple mismatches with the two *Anaplasma* sp. SA Dog *msp2/p44* sequences were observed. The data suggests that the *A. phagocytophilum* qPCR does not cross-react

with *Anaplasma* sp. SA Dog. There are up to 113 copies of the *msp2/p44* gene in the *A. phagocytophilum* genome, which might explain the ability of the *A. phagocytophilum* qPCR to detect extremely low-level infections that are not detectable in microbiome data. A species-specific assay for *Anaplasma* sp. SA Dog is needed to clarify its epidemiology and clinical significance in domestic dogs and other hosts.

082 - Snail mail: delivering parasites to aquatic hosts

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The family Liolopidae Dollfus, 1934 comprises trematodes that parasitise the stomach and intestines of ectothermic tetrapods. Records of species are scarce, with 14 species across five genera being described, including the recently established *Paraharmotrema* (from terrapins). While adult parasitic forms are well-characterised morphologically, molecular data remain incomplete, and little is known about their life cycles and transmission pathways. This study aimed to identify potential intermediate hosts for *Paraharmotrema karinganiense*, recently described from the serrated hinged terrapin (*Pelosios sinuatus*) in Mozambique. African apple snails (*Lanistes ovum*, n = 10) and turquoise killifish (*Nothobranchius furzeri*, n = 59) were collected from temporary pans in Karingani Game Reserve, Mozambique. Encapsulated and encysted metacercariae were recovered from killifish, excysted, heat-fixed, and preserved for morphological and molecular analyses. Individuals of *L. ovum* were maintained in containers with 250mL artificial water. An initial screening regime over three consecutive days was followed by four-day intervals to monitor cercarial shedding. Shed cercariae were examined using light and scanning electron microscopy and preserved for molecular characterisation, targeting the 28S rDNA, ITS and *cox1* gene regions. This study provides only the second documented life cycle of a liolopid trematode based on natural infections and the first complete life cycle for freshwater trematodes from southern Africa.

084 – Parasite Diversity of *Clarias gariepinus* from Tzaneen Dam, Limpopo Province, South Africa

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Aquatic parasites play an essential role in ecosystems, offering insights into biodiversity, food web dynamics, ecosystem function, and environmental degradation. This study investigated metazoan parasites associated with the African sharp-toothed catfish *Clarias gariepinus* Burchell, 1822, from Tzaneen Dam in Limpopo Province following an environmental parasitology approach. Eight fish were sampled from November 2024 to March 2025 using gill nets and longlines. Following euthanasia, fish were dissected and examined for metazoan parasites. Monopisthocotyleans from the gills were mounted in glycerin ammonium picrate, while all other parasites were preserved in ethanol for morphological and molecular analyses. Larger helminths and muscle tissue were frozen for future analysis of pesticide and metal accumulation. The following parasites were recorded: Monopisthocotylea (*Macrogyrodactylus clarii*, *Quadriacanthus clariadis*, *Quadriacanthus aegypticus*) from the gills (prevalence [P]=50%, Mean Intensity [MI]=12); Digenea (*Tylodelphys metacercariae*, unidentified digenea) from the brain and eye (P=88%, MI=150.57); Branchiura (*Dolops ranarum*) from the skin (P=88%, MI=6.26); and Nematoda (*Contracaecum* larvae, *Procamallanus* sp.) from the body cavity and intestine (P=88%, MI=18.26). Digeneans showed the highest mean intensity. As parasites are known to bioaccumulate pollutants, they hold promise as long-term bioindicators of aquatic contamination. This study contributes baseline data for future environmental monitoring and supports integrative approaches to freshwater ecosystem health assessment in southern Africa. This research is supported by the DSTI-NRF SARChI Chair in Ecosystem Health (UID 101054).

087 - Unravelling the development of anuran trypanosomes in mosquito vectors

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Trypanosomes are widespread protozoan parasites that infect all vertebrate groups. While research has been extensively focused on species affecting humans and livestock because of their medical and economic impact, amphibian *Trypanosoma* species remain largely neglected. Our study examines the development of anuran trypanosomes in potential insect vectors by experimentally infecting three mosquito species (*Culex quinquefasciatus*, *Cx. molestus* and *Aedes aegypti*). Based on our results, three out of the eight tested *Trypanosoma* species successfully survived defecation, attached to the hindgut wall via their flagella to form hemidesmosomes, and proliferated. However, migration into the salivary glands was not observed, indicating that transmission to amphibians is likely to occur via contaminative routes rather than through direct injection. These findings offer new insights into parasite-vector interactions and contribute to our understanding of trypanosome development and transmission strategies. Furthermore, our study provides valuable insights into the

evolutionary transition of trypanosomes from aquatic to terrestrial hosts and sheds light on their broader evolutionary history of trypanosomes.

088 - Molecular detection and risk factors of fasciolosis in sheep, snails and the environment in the Eastern Cape, South Africa

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Fasciolosis is a global economically significant disease of livestock, with emerging zoonotic implications. Livestock production is heavily burdened by fasciolosis in South Africa, particularly in smallholder farming regions with restricted levels of knowledge, awareness and limited control measures. In South Africa, Eastern Cape Province where sheep farming underpins the rural economy, fasciolosis threatens productivity exacerbated by inadequate epidemiological data and limited on-farm investigations, especially in smallholder farming settings. Conventional diagnostic approaches for the final host often have low sensitivity, while research on environmental contamination remains scarce. A cross-sectional study was conducted to detect and identify *Fasciola* infection in sheep, snails and contamination of the environment (drinking water sources) in six smallholder farms in the Chris Hani and Amathole Districts, Eastern Cape Province. Faecal samples were collected from sheep (n=355) of various breeds, age groups, and both sexes. Furthermore, snails (n=49) and water samples (n=9) were collected from drinking water sources at each farm. Faecal samples were first analysed by the sedimentation technique. Then, the faecal sediments as well as snail and water were analysed with a quantitative real-time polymerase chain reaction (qPCR) and conventional PCR targeting the internal transcribed spacer 2 (ITS-2), cytochrome c oxidase subunit 1 (CO1), and fatty acid-binding protein (FABP) type 1 genes for genus or species-specific identification. The faecal sedimentation identified 58/355 (16.3%) *Fasciola* positive sheep, while qPCR detected 43/355 (12.1%) positive sheep. The Cohens kappa test showed a slight agreement (kappa=0.183, p<0.01) between qPCR and sedimentation in the detection of *Fasciola* infection. For the snails, 3/49 (6.1%) were positive, whereas 1/9 (11.1%) water samples were positive for *Fasciola*. The ITS-2 and CO1 conventional PCR and sequencing resulted in sequences that were 99.1-100% identical to previously published *F. hepatica* sequences. Mixed effects Generalized Linear Models showed that breed was significantly associated with infection (p<0.05), whilst no significant associations (p>0.05) were observed by sex, district or age. This study confirmed the presence of *Fasciola* species within sheep farms in the Eastern Cape Province. There is, therefore, a need to promote appropriate control practices amongst farmers, given the zoonotic nature of fasciolosis, awareness should be created amongst the communities.

089 - Metazoan parasites of the Mozambique tilapia *Oreochromis mossambicus* (Peters, 1852) from Loskop Dam in Mpumalanga Province, South Africa

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Metazoan parasites can serve as valuable bio-indicators, providing insight into the health status of their host organisms and the surrounding aquatic ecosystem. The purpose of the current study was to examine and identify metazoan parasites associated with Mozambique tilapia *Oreochromis mossambicus* at Loskop Dam, Mpumalanga Province. To achieve this, fish ($n=34$) were sampled in May 2024 and March 2025 using gill nets of different mesh sizes. The sampled fish were then placed in tanks containing aerated dam water and transported to the field laboratory for the parasitological examination. Fish were examined for any noticeable ectoparasites, euthanised, dissected and examined for parasites. Based on morphological characteristics, parasites identified included ectoparasites: *Argulus japonicus* from the skin and fins, *Neogergasilus japonicus* from the fins and *Cichlidogyrus halli* from the gills. Endoparasites recorded were: *Enterogyrus* sp. from the stomach, digenean larvae (*Euclinostomum* sp.) from the muscle, *Neogryporhynchus* sp. from the intestinal wall and *Contracaecum* sp. from the body cavity. The results indicate that *O. mossambicus* from Loskop Dam harbours a diverse range of parasites, including both ecto- and endoparasites. Indices in terms of percentage prevalence, mean intensity, and mean abundance are indicated for each species. These findings highlight the need for ongoing research of this host-parasite system to inform management strategies for the ongoing protection of the aquatic fauna of Loskop Dam.

095 - New species of *Gastronodus* Singh, 1934 (Nematoda: Spirocercidae) discovered in a South African rodent

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The nematode diversity associated with wildlife in South Africa remains poorly researched. To address the paucity in data four rodent species (*Rhabdomys intermedius*, *Rhabdomys pumilio*, *Micaelamys namaquensis*, and *Otomys unisulcatus*) were trapped at 12 localities in the WCP during the summer months of 2023 to 2025. Five females and 14 males of *Gastronodus* sp. were recovered from the stomach of a single *M. namaquensis* female in the Nama Karoo biome. All females and 11 males were slide-mounted in lactophenol and examined under a compound light microscope. The specimens were assigned to the genus *Gastronodus* Singh,

1934 based on the buccal capsule armed with six teeth: three pairs of pedunculate, postcloacal papillae in males and the vulva situated at the level of the anterior part of the glandular oesophagus in females. The three pairs of postcloacal, pedunculate papillae distinguish our specimens from the closely related genera *Cylicospirura* Vevers, 1922 and *Skrjabinocercina* Matschulsky, 1952. The five pairs of pedunculate, precloacal papillae distinguish them from their single congener, *G. strasseni* Singh, 1934, suggesting that our specimens represent a new species. Graphic illustrations were prepared, and scanning electron micrographs will be taken to visualize and characterize morphological features. The COX1 gene region of the remaining males was sequenced and compared to reference sequences of closely related nematode species. Based on our assessment of the literature, this is the first recording of the genus *Gastronodius* in Africa. The discovery of a new parasitic nematode species confirms that the nematode diversity in South Africa and Africa is currently underestimated.

096 - Batload of parasites: investigating the drivers of ecto- and endoparasite infracommunity composition in the Natal long-fingered bat (*Miniopterus natalensis*) in South Africa

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Bats and their associated parasites have garnered much research globally, given the importance of parasites in structuring communities. Furthermore, the close proximity of humans to bat communities necessitates understanding the determinants, both host and environmental, of their parasite communities. Little is known about the drivers of the parasite communities belonging to bats in Africa. Here, we investigated the effect of host sex and body condition on ecto- and endoparasite infracommunity composition of the Natal long-fingered bat (*Miniopterus natalensis*). Bats were sampled across seven sites in South Africa, and all ecto- and endoparasites were removed, identified and counted after euthanasia. Nineteen species of parasites comprising helminths (represented by nematodes, cestodes and trematodes), as well as ectoparasites (represented by flies, mites, ticks and fleas) were recovered from 96 bat individuals. Across the most prevalent parasite species, abundance alone was largely driven by environmental factors, with only one ectoparasite species being influenced by bat body condition. Significant drivers of infracommunity composition were found only for helminths, with host sex influencing the composition of parasite species. Interestingly, the parasite communities of male bats appear to be a subset of the female bat parasite communities. Overall, our findings support the ephemerality of ecto- and endoparasite infracommunities. Variable drivers were identified for different parasite species, as well as between levels of diversity, where environmental factors largely shaped the abundance of

parasites per species, while bat-specific factors influenced the composition of these diverse infracommunities.

097 - Molecular detection and characterisation of *Theileria parva* in selected buffalo populations in Zambia

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Corridor disease, caused by buffalo-derived *Theileria parva*, is neglected in Zambia and many other African countries where East Coast fever (ECF), caused by cattle-derived *T. parva*, is endemic. Although Corridor disease is fatal, there is no record of the molecular occurrence and characterisation of *T. parva* in Zambian buffalo populations. The efficacy of the infection and treatment method (ITM) vaccine stocks, Chitongo and Katete, used to immunise cattle against ECF in Zambia, has yet to be evaluated against Corridor disease. This study used molecular tools to detect *T. parva* DNA from buffalo blood samples collected from selected provinces of Zambia, and to characterise the parasites, in comparison to cattle-associated parasites and the ITM vaccine stocks. Majority of buffalo samples (>75%) tested positive for *T. parva*. The p67, Tp1 and Tp2 antigen gene and protein sequences revealed extensive genetic and antigenic diversity in buffalo-associated parasites. Median-joining networks revealed a close antigenic relationship of some of the buffalo-derived isolates with the cattle-derived, especially those closely related to the Chitongo vaccine stock. Genotypic diversity analysis, based on mini-satellite markers, showed that *T. parva* populations from the study areas are not distinctly different from one another. Although the populations are composed of similar genotypes, there is a state of non-panmixia in all the populations. These findings suggest that the cattle populations in Zambia are at risk of infection with Corridor disease. The close antigenic relationship of some of the buffalo-derived parasites with the Chitongo vaccine stock suggests that this vaccine stock may provide protection against infection with some of the buffalo-associated parasites. However, the extensive diversity in the latter remains a concern as the current vaccine stocks may not provide protection against all buffalo-derived parasites.

098 - Larval cestodes and a poisonous host: Implications for marine cestode transmission pathways and host adaptability

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Cestodes play a significant role in shaping intricate marine food webs, with their larval stages found in various intermediate hosts, such as bivalves, crustaceans and teleost fish. Investigating these larval forms is essential for understanding transmission pathways and host specificity related to adult cestodes. This study examined the larval cestodes parasitising the evil eye blaasop, *Amblyrhynchote honckenii* (Teleostei: Tetraodontidae), a poisonous pufferfish species. A total of 55 *A. honckenii* specimens were collected from five locations along the South African coast and screened for cestodes. Three abundant larval forms were identified through morphological and genetic analyses, linked to the elasmobranch-infecting cestode genera *Acanthobothrium*, *Nybelinia*, and *Kotorella*. Adult forms of these genera have only been recorded in elasmobranchs, indicating that, despite being poisonous and generally avoiding predation by other fish or elasmobranchs, *A. honckenii* still serves as an intermediate host. One intriguing possibility is that certain elasmobranchs have developed physiological adaptations that allow them to consume poisonous prey without harm, thus enabling a direct transmission route for larval cestodes to their definitive hosts. Alternatively, *A. honckenii* may act as a reservoir for these larval forms, supporting their development and persistence in the ecosystem without direct predation. This suggests that some larval stages can survive in non-predated hosts, revealing a complex ecological strategy that facilitates host switching. These findings emphasise the importance of further research into parasite interactions in marine food webs and their adaptability to environmental changes, contributing to a deeper understanding of the intricate relationships between marine fish and their parasites.

106 - Socio-economic characteristics associated with animal husbandry practices, particularly the control of tick-borne diseases, for the production of red meat by small-scale farmers in the Eastern Cape Province of South Africa

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Socioeconomic characteristics have been highlighted as some of the most influential aspects in the farmers' decision-making processes, including their adoption of farming practices, the type of farming systems utilised, and even what is farmed. This study presents an integrated examination of livestock production constraints associated with communal farming in six district municipalities (DMs) of the Eastern Cape Province. We collected data on demographic and socio-economic factors from 271 farmers randomly given questionnaires. About 26 Land Redistribution for Agricultural Development (LRAD) owned by communal farmers were surveyed to ascertain the condition of grazing land, meanwhile, tick species and distribution

on cattle and goats found in 158 sampling sites of the study area were also recorded. From the results, a total of 34,929 adult ticks belonging to five genera and 10 species were encountered. The most abundant tick genera were *Rhipicephalus* of the subgenus *Boophilus* (68.91%), *Amblyomma* (20.72%), *Hyalomma* (8.64%), *Ixodes* (1.22%), and *Haemaphysalis* (0.51%). From the map plotted for 16 custom feeding centres, lack of marketing channels (23%), poor animal conditions (20%), lack of infrastructure (19%), high price of medicine (14%), shortage of feed (10%), stock theft (8%), and age of animals (too old) to be marketed (6%) are the major shortcomings in red meat production. We found that the associations between gender ($\chi^2 = 31.3481$, $p < 0.0001$), age ($\chi^2 = 32.4889$, $p < 0.0001$), and farming experience ($\chi^2 = 52.7556$, $p < 0.0001$) were significantly ($p < 0.05$) higher. Inferences from the data indicate the need for government and stakeholder intervention to farmers through the provision of infrastructure, marketing channels, and training on livestock-based programs. The study outlined constraints faced by low input-farming areas and brought solutions that can be used to improve the farming conditions.

108 - From internet fame to scientific fact: the tale of *Ceratothoa famosa*

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Ceratothoa famosa is a parasitic isopod of the family Cymothoidae, commonly known as a tongue-replacement isopod due to its remarkable ability to replace the tongue of selected marine fish hosts. Officially described in 2014, this species had previously been misidentified as *C. imbricata* or *C. exigua*. Remarkably, *C. famosa* gained international recognition prior to its formal description, largely due to a widely circulated and frequently misattributed photograph taken by one of the authors. This image appeared across social media, films, books, and popular science magazines, inspiring the species name "famosa" in recognition of its fame. To date, *C. famosa* is known only from the south coast of South Africa, where it parasitises sparid fishes, particularly the Cape white seabream (*Diplodus capensis*) and musselcracker seabream (*Sparodon durbanensis*). The isopod exhibits a direct lifecycle: free-swimming mancae temporarily attach to a host before migrating into the buccal cavity, where they establish themselves on the tongue. The first individual to settle undergoes protandrous hermaphroditism, transforming into a female, while subsequent individuals remain male in the presence of a female. Removal of the female often results in the death of both host and parasite. The isopod causes mechanical damage to the host's buccal cavity, occasionally destroying the tongue, reducing feeding efficiency, and potentially leading to mortality. As haematophagous parasites, they can induce anaemia and secondary infections. With its unique biological traits, noteworthy ecological impact, and global public interest, *C. famosa* stands out as an engaging topic for both scientific investigation and other interested parties.

110 - Morphological and molecular characterisation of two *Lamproglena* species from cyprinid fishes in South Africa and Kenya

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Parasitic copepods of the genus *Lamproglena* von Nordmann, 1832 have been reported infecting the gills of various fish species across different regions of the world. The genus comprises 38 nominal species, with 12 species described from Africa. The material for this study was collected from the gills of three cyprinids: *Labeo victorianus* and *Labeobarbus altianalis* from Nyando River in Kenya, and *Labeo rosae* from Flag Boshielo Dam, Limpopo Province, South Africa. An integrated systematic approach was used to study these copepods. Morphological analyses using scanning electron microscopy (SEM) revealed that the copepod from *L. victorianus* was morphologically similar to *Lamproglena cleopatra* Humes, 1957 in most taxonomic aspects. Copepods associated with *L. rosae* in South Africa and *L. altianalis* in Kenya displayed distinctive taxonomic characteristics that have not been described before. The morphology visible on SEM images of *Lamproglena* sp. from *L. rosae* was notably distinct, particularly the position of the first thoracic segment, when compared to *L. cleopatra*, originally described from the same fish species and locality. Phylogenetic trees generated using Maximum Likelihood analyses of the 18S, 28S rDNA, and COI datasets revealed a distinct clade comprising sequences of *Lamproglena* spp. The *Lamproglena* sp. from *L. altianalis* in Kenya formed a clade with *Lamproglena hoi* from South Africa, with the COI showing 146 nucleotide base pair difference and a pairwise distance of 23.25%. Ongoing molecular studies using the COI marker aim to facilitate the accurate identification of *Lamproglena* sp. from *L. rosae* in Flag Boshielo Dam. This study was partly supported by the DSTI-NRF SARCHI Chair (No.101054).

125 - Parasite, Vector, Prey: looking into the different ecological roles of *Gnathia africana*

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Gnathia africana is a temporary ectoparasite within the family Gnathiidae, parasitising both teleost and elasmobranch fish. Its biphasic life cycle is characterised by polymorphic larval stages, alternating between the unfed, host-seeking zuphea and the engorged praniza stage. Zuphea larvae attach to hosts using hooked gnathopods and feed using specialised mouthparts. During feeding, the hindgut expands, transforming them into praniza larvae, which detach to moult in sheltered environments after feeding. This cycle repeats twice more, producing first male, then female adults. The gnathiid's frequent host interactions and blood-feeding behaviour make it an effective vector for blood parasites, specifically the apicomplexan *Haemogregarina bigemina* in South African waters. Although the precise mechanism of transmission is still under investigation, it is hypothesised that the parasite may be passed via the gnathiid's salivary gland during feeding, or when infected gnathiids are consumed by the host. Developmental stages of *H. bigemina* have been documented in both fish and gnathiid

hosts. Other gnathiid species are also suspected vectors of haemogregarines and potentially other viruses, such as viral erythrocytic necrosis (VEN). Gnathiid infestations pose a threat to aquaria and aquaculture health, potentially leading to anaemia, secondary infections, and mortality in smaller hosts. Nonetheless, gnathiids serve an ecological role as a primary food source for cleaner fish, driving cleaning mutualisms in diverse marine environments. The noteworthy interaction of these gnathiids—functioning as fish parasites, vectors for blood parasites, and essential prey for cleaner fish—highlights the importance of these often-overlooked ectoparasites and their contribution and impact on marine ecosystems.

126 - A holistic parasite survey of juvenile *Enteromius trimaculatus* from the Mooi River, South Africa

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This study presents a preliminary parasitological survey of juvenile threespot barb (*Enteromius trimaculatus* Peters) (Pisces: Cyprinidae) from the Mooi River in Potchefstroom, North-West, South Africa. The main objectives were to document parasite diversity, identify host-parasite associations, and quantify infestation metrics including prevalence, intensity, and abundance. Sampling took place in May 2025 using a backpack electrofishing unit, resulting in the capture of 16 juvenile *E. trimaculatus* (<10 cm). Each fish was examined in full, maximising scientific value by screening all external and internal anatomical regions for parasitic infections. External surfaces and mucus smears were examined to detect ectoparasites, while detailed dissections of gills, liver, gastrointestinal tract, kidneys, and muscle tissue were performed under a stereomicroscope to identify endoparasites. Parasites were identified using morphological criteria, fixed in hot or boiling saline and preserved in 70% or 96% ethanol for further taxonomic and molecular analyses. Parasites observed included nematodes, cestodes, monogeneans and metacercariae (immature trematodes), and were recovered from multiple organs (gills, intestine, kidney, liver, and muscle). Additionally, host tissue samples were collected for potential future ecotoxicological assessments, which will enable the assessment of contaminants such as heavy metals or pesticides. This fully integrated, cross-disciplinary approach enhances the utility of each specimen and contributes to both parasitological and environmental datasets. By establishing a detailed baseline of parasite diversity and host susceptibility, this study supports long-term ecological monitoring and strengthens our understanding of host-parasite-environment interactions in southern African freshwater systems.

130 - Seasonal variations of *Haemonchus contortus* species affecting communal sheep grazing at Tsomo grassland in the Eastern Cape, South Africa

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Every sheep grazing on the pasture is infested with one type of worm or the other. Warm, humid climates are ideal for worms and therefore, animals will have more problems with internal parasites in these climates. The objectives of the study were to establish seasonal changes of *Haemonchus contortus* species in communal sheep and to develop a health management guide for controlling roundworm infestations. The study was conducted at Warburg community, which is situated in Stutterheim on the sourveld (humid) and it is 899 m above sea level. Faecal samples were collected monthly for four years (January 2012–December 2015) with a total number of 1188 samples. During the experiment, the animals were only dosed when the *H. contortus* egg per gram (e.p.g) counts exceeded the levels above 3000 e.p.g. Significantly higher levels of *H. contortus* were seen during winter (2347.14 ± 3543.5) than spring (980.88 ± 1405.8) for the study period. During the late winter months (August), higher levels of *H. contortus* were observed. Summer *H. contortus* levels were significantly higher (1226.1 ± 701.3) compared to winter (597 ± 628.4). Significantly higher levels of *H. contortus* were observed in spring (1467.61 ± 1308.9) than in autumn (951.23 ± 1376). The study highlights that autumn and winter have lower *H. contortus* infestations than summer and spring. The higher the rainfall, the higher levels of *H. contortus* should be expected. Within the context of the study, season and management of the communal sheep are affected by the e.p.g. levels.

134 - Population dynamics of ticks (Acari: Ixodidae) infesting cattle in the central region of the Eastern Cape Province, South Africa

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Ticks are widely distributed throughout the world, especially in tropical and subtropical areas. Globally, costs associated with ticks and tick-transmitted pathogens in cattle range between US\$ 22-30 billion. This study was carried out from April 2016 to March 2017 to identify the tick species from 10 cattle and also from six drag samples during the 12-month period. All ticks collected per animal and from vegetation were stored in labelled sample tubes containing 70% ethanol. A total of 2 391 ticks were collected during the study. Based on morphological traits, 10 tick species were identified: *Amblyomma hebraeum* (36.6%), *Rhipicephalus evertsi evertsi* (18.0%), *R. (Boophilus) decoloratus* (16.3%), *Hyalomma rufipes* (12.7%), *R. appendiculatus* (8.9%), *R. simus* (6.7%), *Ixodes pilosus* (0.5%), *R. foliis* (0.3%), *Haemaphysalis elliptica* (0.04%) and *H. silacea* (0.04%). Significantly more larvae of *R. (B.) decoloratus* were collected from the vegetation than on cattle. No collection of the invasive cattle tick, *R. (B.) microplus*

was found in the study area. The absence of *R. (B.) microplus* is of epidemiological interest in terms of tick distribution, as this species is known to be highly resistant to numerous acaricide compounds.

135 - The South African Living Collections Cluster (SALCC) project - managing and preserving living collections for the future

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South Africa boasts a diverse array of living collections in national and private zoological and botanical gardens, captive facilities, aquaria, agricultural facilities and research laboratories. Within these collections are plants and animals of high research and conservation value (with some extinct in the wild), and representatives of flora and fauna from different habitats and biomes that contribute to distinctive landscapes across the country. These collections are valuable resources for cutting-edge research addressing global challenges, including climate change, food security, emerging infectious diseases, the illegal wildlife trade and biodiversity conservation. However, their management is not well-coordinated to ensure their long-term preservation and use for transdisciplinary research. This results in them being considered of limited use and value for innovative and problem-solving research. As such, the Department of Science, Technology and Innovation (DSTI) has established the South African Living Collections Cluster (SALCC), a network of custodians of living collections, to ensure that living collections are well managed, curated, comply with relevant national and international standards and legislation, and are accessible to the scientific community for multi-disciplinary research and capacity building. The role of the SALCC is to establish a coordinated network of custodians of Living Collections within public and private institutions and sectors in South Africa to achieve the objectives of the National Scientific Research Collections Platform (NSRCP) of the DSTI. Stakeholders and custodians of living collections across different spheres of government and sections of the public are invited to join this initiative and contribute to its targets.

137 - Seroprevalence and associated risk factors for *Toxoplasma gondii* infection of goats and sheep in the Khomas region of Namibia

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This study aimed to determine the seroprevalence levels of *Toxoplasma gondii* in small ruminants (goats and sheep) and the associated risk factors in the Khomas region of Namibia. A total of 299 and 345 sheep and goat sera from 22 farming establishments were tested, respectively. An IDEXX Toxotest Ab[®], a commercial ELISA kit, was used to screen for IgG antibodies to *T. gondii*. Overall, 3.68% (11/299) of the sheep sera were positive, and 61.54% (8/13) of the sheep flocks tested had at least one positive animal. Only one of the 345 goat sera from 19 flocks was positive, giving animal-level and herd-level prevalences of 0.29% and 5.26%, respectively. Sheep flocks had significantly greater animal-level and flock-level prevalences than goats ($p < 0.05$) and were 13.14 times more likely to be seropositive (OR = 13.14; CI 95%: 1.686–102.382) than goat flocks. A questionnaire was also administered to identify any putative risk factors associated with seropositivity. Eight risk factors were evaluated, including the total number of goats, total number of sheep, farm size, average rainfall, presence of wild Felidae (African lions, caracals, cheetahs and leopards), presence of domesticated and stray cats and history of abortions in the flocks. Seropositivity to *T. gondii* in sheep was positively associated with the total number at the farming establishment, history of abortions and farm size ($p < 0.05$), but not with goats. The study determined that sheep in the Khomas region were probably more exposed to *T. gondii* infection than goats. It also found *T. gondii* seroprevalences that were much lower than those in similar studies from other countries in the sub-region and elsewhere.

142 - Genomic insights into *Plasmodium vivax* and *Plasmodium simium* host shifts in Latin America

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Plasmodium vivax causes >70% of malaria cases in Latin America. The emergence of *Plasmodium simium*, transmitted from humans to monkeys, increased the malaria burden, notably after an outbreak in 2015 in Brazil. To investigate *P. simium* evolutionary history, we screened 646 monkey samples and analyzed whole genome variations for 19 *P. simium* and 408 *P. vivax* isolates. *P. vivax* strains were identified in Colombian (n=3) and Brazilian monkeys (n=1), suggesting host reinvasion in Colombia and genetic exchange between *P. vivax* and *P. simium* in Brazil. Genetic analysis indicates that *P. simium* originated from a host jump approximately a century ago, possibly linked to *P. vivax* migration from Mexico to Brazil. Genome-wide scans identified selection in genes interacting with primate hosts and vectors. These findings highlight *P. simium* evolutionary history and zoonotic malaria risks and underscore the need to include monkeys in malaria prevention measures while ensuring human-wildlife coexistence.

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