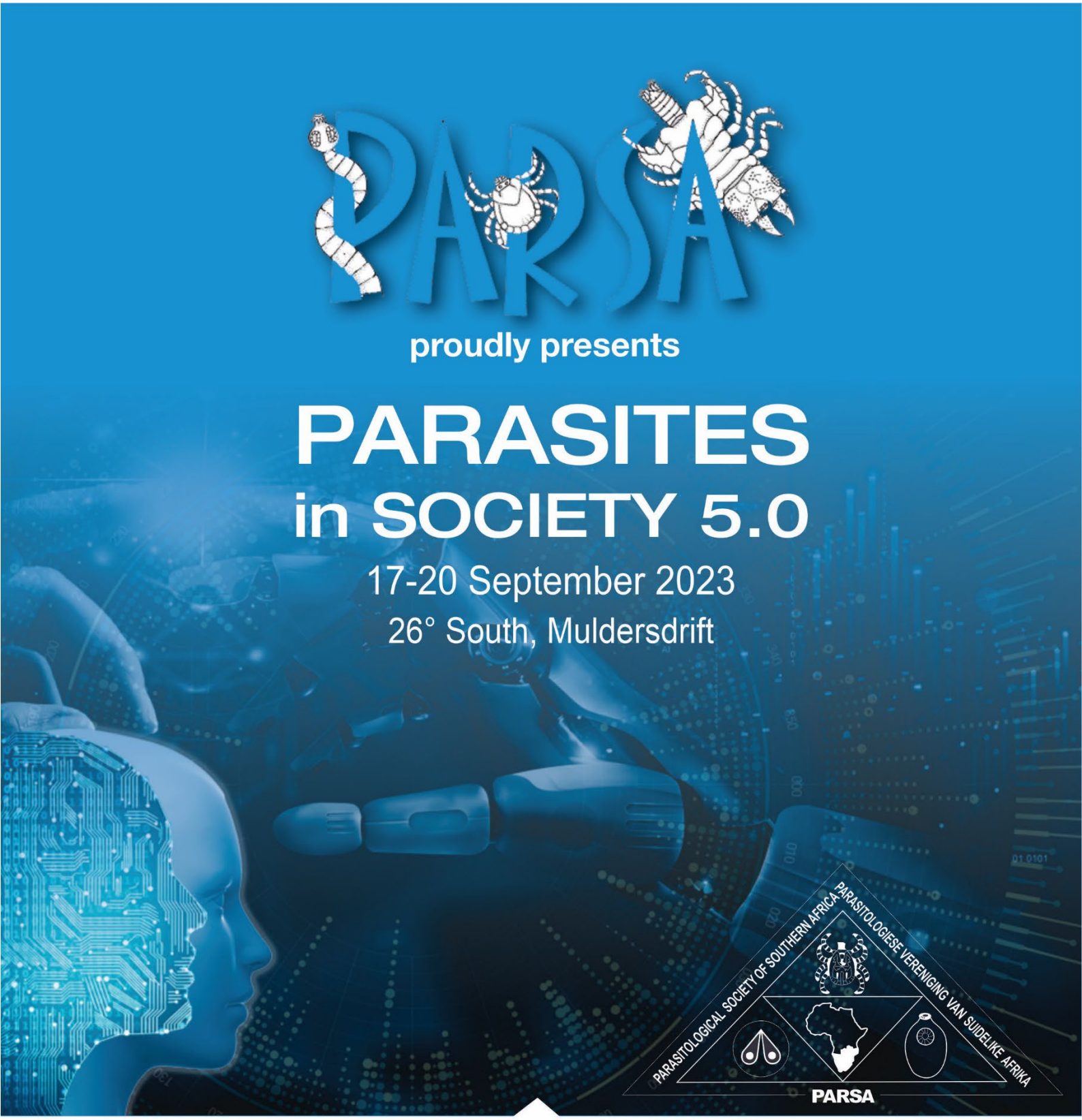

51ST ANNUAL PARSA CONFERENCE

PROGRAMME & ABSTRACTS

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Welcome note from the PARSA President

Dear PARSA Participants,

It is my absolute pleasure to welcome you to the 51st Annual Conference of the Parasitological Society of Southern Africa. This year the conference is held at the beautiful 26 Degrees South Hotel based in Muldersdrift, Gauteng. I would like to extend my gratitude to Prof. Tshepo Matjila (PARSA 2023 Conference Chairperson) and his team from the University of Pretoria, as well as SAVETCON, for arranging the conference with the exciting theme 'Parasites in Society 5.0'. Thank you for all the time and effort invested in making this conference enjoyable for all of the participants.

The programme is full of interesting talks and posters, and I am convinced we will be educated and stimulated with the work being done in southern Africa. Whether this is your first or fiftieth conference, I am sure you will find yourself surrounded by friendly faces and good conversation.

Thank you for taking time out of your busy schedules to attend this conference and share your research with fellow parasitologists. I trust you will all enjoy this time with like-minded colleagues. I hope this will be the perfect opportunity to forge new relationships and collaborations.

Enjoy the conference and the beautiful setting!

Best wishes,

Kerry

PARSA President

Welcome from the Conference Chairperson

On behalf of the Parasitological Society of Southern Africa and the University of Pretoria, it is with great pleasure that I extend a warm welcome to the 51st Annual PARSA Conference.

PARSA 2023 promises to be a truly exceptional event as we delve into the theme of 'Parasites in Society 5.0.' In this era of Society 5.0, characterized by the integration of cutting-edge technologies such as artificial intelligence, big data, and robotics, we find ourselves on the brink of a parasitology revolution. These innovations have the potential to transform our understanding of the intricate relationships between parasites and their hosts. Moreover, they can accelerate the development of more effective strategies for diagnosing, preventing, and treating parasitic diseases in both humans and animals. The ultimate goal is to enhance health outcomes and elevate the quality of life for individuals and communities worldwide.

As we gather for this significant event, I am filled with anticipation for the productive and interactive discussions that will undoubtedly shape the future of parasitology. Your participation and contributions are vital to the success of PARSA 2023, and I have no doubt that each of you will enrich our collective knowledge.

I look forward to meeting and engaging with all of you during this conference. Together, let us explore the exciting possibilities that await us in the realm of parasitology within the context of Society 5.0.

Welcome to PARSA 2023!

Prof. Tshepo Matjila
PARSA 2023 LOC Chairman

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Programme

Sunday 17 September 2023	
15h00	Registration Opens
15h00	Poster applications
17h30	Welcome Reception @ the Pool (*Theme: Business on Top, Party at the Bottom*)

Monday 18 September 2023			
Time	Abstract #	Description	Speaker
THEME: PARASITE DETECTION, CHARACTERIZATION AND CONTROL			
Session Chair: Tshepo Matjila			
08h00	Registration opens - arrival coffee and tea		
08h30	Welcome and Opening		Tshepo Matjila, University of Pretoria
08h45	**Keynote 1 - Oriental spices, the French Revolution and Babesia: What is the connection?**		Banie Penzhorn, University of Pretoria
09h15	003	Parasitic nematodes of *Pternistis swainsonii* from two northern regions in South Africa.	Andrea Spickett, ARC-Onderstepoort Veterinary Research
09h30	005	Prevalence of Gastrointestinal parasites and Molecular epidemiology of *Haemonchus contortus* in sheep in Lesotho.	Moeketsi S. Phalatsi, National University of Lesotho
09h45	010	Evaluation of the spherical body protein 4 (SBP4)-encoding gene for molecular typing of *Babesia caballi.*	Alicia Venter, University of Pretoria
10h00	Mid-morning refreshments		
Session Chair: Kgomotso Sibeko-Matjila			
10h30	013	Infection rates and genotyping of *Ehrlichia ruminantium* detected in *Amblyomma* species from Southern Africa.	Andeliza Smit, University of Pretoria
10h45	015	Detection of *Theileria haneyi* in South African equids using a newly developed quantitative real-time PCR assay.	Tshenolo V. Mbaba, University of Pretoria
11h00	031	A review on the genetic diversity of *Toxoplasma gondii* from an African perspective.	Ilze du Plooy, University of South Africa
11h15	037	The complete Mitochondrial Genomes of species of *Haemogregarina* (Adeleorina: Haemogregarinidae), parasitising the Serrated hinged terrapin *Pelusios sinuatus.*	Tiaan P. Haarhoff, North-West University
11h30	038	Frogs and their blood parasites: A biodiversity survey of the Soutpansberg mountain range.	Joretha du Buisson, North-West University
11h45	044	Assessing dairy farm personnel's knowledge of the aetiology, risk factors, clinical signs, zoonotic potential and control of bovine fasciolosis in the Eastern Cape province, South Africa.	Munyaradzi C. Marufu, University of Pretoria
12h00	045	Under the Dragon's Veil: investigating the diversity of blood parasites in the Flat dragon lizard (*Smaug depressus*) from the Soutpansberg mountain range.	Edward C. Netherlands, University of the Free State
12h15	Poster Session 1		
13h00	Lunch & Exhibitor Networking		

Monday 18 September 2023			
Time	Abstract #	Description	Speaker
Session Chair: Ed Netherlands			
14h00	048	Molecular detection of a novel *Rickettsia* species in a rural community in South Africa: Insights from rodent flea samples.	Dina M. Fagir, University of Pretoria
14h15	051	Identification and characterization of ticks and tick-borne parasites of wild felids in South Africa.	Mamohale Chaisi, South African National Biodiversity Institute
14h30	060	Avian haemosporidia in native and invasive sparrow at an Afrotropical region.	Tshifhiwa C. Nangammbi, Tshwane University of Technology
14h45	080	Evaluation of knowledge, attitudes and practices regarding neosporosis and toxoplasmosis among farmers and animal health practitioners in Namibia.	Tshepo Matjila, University of Pretoria
15h00	Mid-afternoon refreshments & Posters		
THEME: PARASITE ECOLOGY AND HOST-PARASITE INTERACTIONS			
Session Chair: Ard Nijhof			
15h30	002	Old data, new insights: NMDS, DSPCA and NNODF provide a fresh take on parasite community patterns in nyalas in South Africa.	Kerstin Junker, ARC-Onderstepoort Veterinary Institute
15h45	021	The Living Collections Cluster - a platform for the management of living collections in South Africa.	Mamohale Chaisi, South African National Biodiversity Institute
16h00	043	Aspects of the histopathology associated with *Rhabdochona* infecting smallmouth yellowfish, *Labeobarbus aeneus* (Burchell, 1822) in the Vaal River System.	Nonkcubeko Masango, University of Johannesburg
16h15	Close of Day 1		
19h00	Potjiekos Dinner @ the Boma		

Tuesday 19 September 2023			
Time	Abstract #	Description	Speaker
06h30	Yoga on the lawns		
THEME: VACCINES, GENOMICS AND NOVEL DIAGNOSTICS IN PARASITOLOGY			
Session Chair: Mamohale Chaisi			
08h30	**Keynote 2 - Advances in the genetic manipulation of ticks**		**Ard Nijhof, Freie Universität Berlin**
09h00	009	Identification and gene expression profiling of subunit vaccine candidates in cattle- and buffalo-derived *Theileria parva* isolates.	Lauren-Leigh Borchers, University of Pretoria
09h15	018	A gene drive that reduces the fertility of malaria parasites.	Geoffrey I. McFadden, University of Melbourne
09h30	041	Detection of bacterial tick-borne pathogens in two provinces of South Africa using a microbiome sequencing approach.	Bongekile L. Khoza, University of Pretoria
09h45	042	Rodents as potential reservoir hosts for *Anaplasma* spp. at the human-livestock-wildlife interface of the Mnisi community, South Africa.	S. Marcus Makgabo, University of Pretoria

Tuesday 19 September 2023			
Time	Abstract #	Description	Speaker
10h00	052	Development and validation of a real-time PCR assay, and phylogenetic classification of *A. platys.*	Nokuzola F. Nkosi, University of Pretoria
10h15	Mid-morning refreshments & Posters		
THEME: PARASITES IN MARINE AND FRESHWATER SYSTEMS			
Session Chair: Liesl van As			
10h45	004	Assessment of anthropogenic impacts on the aquatic environment and biodiversity in the Katangese Copperbelt Area (DR Congo): a parasitological approach.	Gyrhaiss K. Kasembele, Université de Lubumbashi
11h00	007	Rare findings in neglected freshwater limpets: integrated characterisation of *Sanguinicola* spp. (Digenea) cercariae and a monoxenous nematode in *Burnupia* spp. from South Africa.	James O. Outa, University of Johannesburg
11h15	~~022~~	~~An overview of fish parasite diversity in Botswana~~	~~Maxwell Barson, University of Botswana~~
11h30	023	New reports of Pennellidae Burmeister, 1835 metamorphosed females infecting marine Teleostei off Southern Africa.	Melita M. Sebone, University of Limpopo
11h45	030	Trace element sequestration in *Lamproglena clariae* from Lake Heritage (Crocodile River) and the Vaal River.	Lutfiyya Latief, University of Johannesburg
12h00	033	Aspects of the histopathology of the stomach of *Clarias gariepinus* (Burchell, 1822) infected by *Procamallanus (Procamallanus) pseudolaeviconchus* Moravec & Van As, 2015.	Kenneth Matea, University of Johannesburg
12h15	Poster Session 2		
13h00	Lunch		
Session Chair: Kerry Malherbe			
14h00	035	Ectosymbiotic fish peritrichs (Ciliophora: Peritrichia) and their suctorian (Ciliophora: Suctoria) predators.	Linda Basson, University of the Free State
14h15	046	Parasite diversity of *Chiloglanis pretoriae* from the Limpopo river system.	Thabelo Maginya, University of Limpopo
14h30	081	To like or dislike the alien and invasive common carp as a parasite "taxi".	Liesl van As, University of the Free State
14h45	024	Worms, worms and more worms: Advances in knowledge regarding the richness of South African fish-infecting digenean fauna.	Russell Qi-Yung Yong, Water Research Group, North-West University (Potchefstroom)
15h00	036	Untangle the knot: Global turtle polystomatid flatworm diversity.	Louis H. du Preez, North-West University
15h15	Mid-afternoon refreshments & Posters		
THEME: PARASITE TAXONOMY AND SYSTEMATICS			
Session Chair: Andrea Spickett			
15h45	012	Aspects of the morphology and taxonomy of *Dactylogyrus* Diesing, 1850 species parasitising cyprinids in the Vaal River system, Gauteng, South Africa.	Mpho Maduenyane, University of Johannesburg
16h00	016	The Diplozoinae of Africa: Revision of two taxa.	Quinton M. dos Santos, University of Johannesburg
16h15	027	Another fish parasite invasion?	Annemarie Avenant-Oldewage, University of Johannesburg

Tuesday 19 September 2023			
Time	Abstract #	Description	Speaker
16h30	034	Development of an interactive electronic identification key for South African *Culicoides* species.	Karien Labuschagne, ARC-Onderstepoort Veterinary Research
16h45	040	*Tetracampos ciliotheca* and *Glossidium pedatum* from *Clarias gariepinus* (Burchell, 1822) in Lake Ol'Bolossat, Kenya.	Joan M. Maraganga, Kisii University
17h00	047	Scanning electron microscopy and molecular data for a *Lamproglena* sp. from *Labeobarbus altianalis* in Kenya.	Nehemiah M. Rindoria, University of Limpopo
17h15	Close of Conference		
17h30	PARSA AGM		
19h00	Conference dinner & awards (Theme: Sophiatown)		

Posters

Monday 18 September 2023		
POSTER SESSION 1: 12h15-13h00		
Abstract #	Description	Speaker
017	Detection of the Brown Ear tick, *Rhipicephalus appendiculatus*, in the Free State province.	Elizna Terblans, University of the Free State
029	Geographic distribution of boophilid ticks in communal grazing cattle in the north-eastern region of the Eastern Cape Province, South Africa.	Mandla Yawa, DRDAR
039	Revisiting the diversity and phylogenetic relationships of trypanosomes (*Trypanosoma*) infecting pelomedusid (Pelomedusidae) freshwater turtles in Southern Africa.	Bernard J. Jordaan, University of the Free State
049	Metazoan parasites of the southern mouthbrooder *Pseudocrenilabrus philander* (Weber, 1897) from Nwanedi and Luphephe rivers in Limpopo province, South Africa.	Collins N. Mashilwane, University of Limpopo
054	Evaluation of host metabolome in goats following infection with *Haemonchus contortus.*	Ontiretse B. Kube, University of Pretoria
055	Evaluation of immune response and gut microbiome in *Haemonchus contortus infected goats.*	Busisiwe Q. Maphangela, University of Pretoria
056	Parasites of the Mozambique tilapia (*Oreochromis mossambicus*) from a natural system and fish farm in Namibia.	Willem J. Smit, University of Limpopo
057	Redescription of the parasitic copepod *Rhinergasilus piranhus* Boeger & Thatcher, 1988 (Cyclopoida: Ergasilidae) based on an integrative approach.	Rodrigo B. Narciso, Universidade Estadual Paulista "Júlio de Mesquita Filho" – Unesp
058	Risk assessment for three *Dactylogyrus* species in South Africa: Prospects for management and policy implications.	Lwendo Rasifudi South African National Biodiversity Institute
061	Morphological and molecular characterisation of a species of *Longicollum Yamaguti*, 1935, a fish parasitic acanthocephalan infecting two species of sea breams off the South Coast of South Africa.	Angela A. Minnie, North-West University
062	Molecular and morphological characterisation of four species of fish parasitic *Trypanosoma Gruby*, 1843 from the South Coast of South Africa.	Chandra le Roux, North-West University, Potchefstroom Campus

Abstract #	Description	Speaker
063	Water quality and parasite diversity of Mozambique tilapia from the Limpopo River System.	Lola Singo, University of Limpopo

Tuesday 18 September 2023

POSTER SESSION 2: 12h15-13h00

Abstract #	Description	Speaker
064	Occurrence of *Lamproglena cleopatra* Humes, 1957 parasitizing gills of *Labeo victorianus* Boulenger,1901 in Kenya.	Redson T. Nkhumeleni, University of Limpopo
065	Metazoan parasites of canary kurper, *Chetia flaviventris* in the Limpopo and Olifants river systems: new locality records.	Fhulufhelo Mulaudzi, University of Limpopo
066	Parasite diversity of *Coptodon rendalli* from Doorndraai Dam, Nwanedi-Luphephe Dam and Nwanedi River, South Africa.	January N. Seabela, University of Limpopo
067	The effect of larval exposure to plastic pollution on the life history of the major malaria vector *Anopheles arabiensis* (Diptera: Culicidae).	Shristi Misser, University of the Witwatersrand/ Wits Research Institute for Malaria/Vector control reference laboratory
068	Digenean trematodes from North African catfish *Clarias gariepinus* in Lake Naivasha, Kenya.	Ornah Shiburi, University of Limpopo
069	Life cycle stages and molecular phylogeny of *Hepatozoon fitzsimonsi* (Dias 1953) (Adeleorina: Hepatozoidae) in tortoises *Stigmochelys pardalis* (Cryptodira: Testudinidae) and ticks of the genus *Amblyomma* (Acari: Ixodidae) from South Africa.	Courtney A. Cook, North-West University
070	Borneo's hidden connections: unveiling the enigmatic Corallanidae isopods and their elasmobranch hosts.	Kelsey Longstaff, North-West University
071	Parasite diversity and community structure of the Cape Stumpnose, *Rhabdosargus holubi*, from the Groot River estuary, South Africa.	Charles de de Beer, North-West University
072	A first insight into the application of the historical ecology of parasitism on the parasitological communities of *Labeobarbus marequensis* in the Letaba River, South Africa.	Tshenolo Masilo, Northwest university (Potch campus)
073	Molecular characterization and phylogeny of two South African fish haemogregarines – *Haemogregarina curva*ta and *Haemogregarina koppiensis* (Adeleorina: Haemogregarinidae).	Zandile Dhlamini, North-West University
074	The biodiversity and host utilisation of gnathiid isopods parasitising elasmobranchs from Borneo.	Hesmarié Botha, North-West University
075	Diversity of freshwater snail vectors and associated trematode cercariae from the lowveld and highveld regions.	Marcel Kruger, North-West University Water Research Group
076	Preliminary study on the effect of using single and combined dipping compounds to control *Rhipicephalus* (*Boophilus*) *spp* on Bhisho Thornveld in the Eastern Cape, South Africa.	Mlungisi Jansen, DRDAR (Dohne)
077	Encroachment and adaptation of the *Rhipicephalus microplus* on camps grazed by sheep in the Eastern Cape Province, South Africa.	Nkululeko Nyangiwe, Dohne ADI & University of South Africa
079	First integrated taxonomy study for characterisation of gill copepod *Ergasilus mirabilis* Oldewage & van As, 1987 (Ergasilidae: Cyclopoida).	Precious P.Fikiye, North-West University, Potchefstroom
082	Exploring helminth parasitic diversity in South African estuarine fish: a case study of the full moony, *Monodactylus falciformis* Lacépède, 1801.	Jodi Gallop, North-West University

Keynote Presentations

Oriental spices, the French Revolution and *Babesia*: What is the connection?

Prof. Banie Penzhorn

Emeritus Professor, Faculty of Veterinary Science, University of Pretoria - banie.penzhorn@gmail.com

Looking back on more than 50 years of research in biological sciences, most of which was in parasitology, I would like to share some basic insights that I learned, often the hard way.

1. Things are interconnected in unexpected ways
2. Be familiar with the original literature in your field of interest
3. Network, network, network
4. Keep an open mind and respect the scientific insights of others

Although the examples cited all relate to my specific interest in tick-transmitted haemoparasites, the basic principles are valid in all branches of science.

Biography:

- BVSc(Pret), MAgric(Wildlife Science)(Texas A&M), DSc(Wildlife Management)(Pret)
- Retired at the end of 2011, after a 31-year academic career at the Faculty of Veterinary Science, University of Pretoria, South Africa
- Part-time senior research fellow at the Faculty of Veterinary Science until February 2021.

After an honours degree in Wildlife Management (University of Pretoria), Banie Penzhorn joined South African National Parks where he worked as researcher in the Eastern Cape Province. During this period, he was granted study leave and obtained an M. Agric. (Wildlife Science) at Texas A&M University. He used his research on ecology and behaviour of Cape mountain zebras for a Doctorate (Pretoria). Dr. Penzhorn resigned after 8 years with SANParks to study veterinary science. He taught at the Faculty of Veterinary Science, University of Pretoria, from 1981 to 2011. His current research focus is tick-transmitted haemoprotozoa of wildlife and domestic animals. Dr. Penzhorn's list of publications in refereed journals has surpassed 160. He supervised or co-supervised many MSc, MMedVet and PhD candidates. In recognition of his contribution to veterinary parasitology, Dr Penzhorn was recently awarded honorary membership by the World Association for the Advancement of Veterinary Parasitology.

MONDAY, 08h45

Advances in the genetic manipulation of ticks

Prof. Ard Nijhof, DVM, Ph.D

Professor at the Institute for Parasitology and Tropical Veterinary Medicine, Freie Universität Berlin, Robert-von-Ostertag-Str. 7, 14163 Berlin, Germany - Ard.Nijhof@fu-berlin.de

Recent years have seen an enormous increase in genomic data on ticks and tick-borne pathogens. Unravelling tick gene function may advance the development of novel tick control methods to improve human and animal health. Currently, gene silencing by RNA interference (RNAi) is the most widely used tool to examine tick gene function. Despite its many advantages, RNAi does have some limitations, as it is for instance not easily applicable to all tick life stages, its knockdown effect is transient and typically not complete. CRISPR-Cas9 based gene editing has the potential to overcome these disadvantages and has found wide use in other arthropods such as mosquitoes. Successful gene editing in ticks by microinjection of CRISPR/Cas9 components in dewaxed tick eggs or through the ReMOT control technique was recently reported. We here examined the possibility of inducing CRISPR-Cas9 based gene editing in one-host *Rhipicephalus australis* ticks by delivery of the CRISPR/Cas9 ribonucleoprotein complex (RNP) by injection in engorged females followed by electroporation. The distalless (*dll*) gene was used as a target, as studies in other arthropods showed that it is essential for limb development during embryogenesis. Transovarial RNAi studies in *R. australis* confirmed that *dll* gene silencing during embryogenesis resulted in aberrant larvae with missing or malformed legs. Combinations of the Cas9 protein with single sgRNAs or sgRNA mixtures in different mole ratios were subsequently injected in groups of engorged *R. australis* females. These groups were exposed to different electroporation conditions and subsequently allowed to oviposit. Up to 12% of the larvae that hatched from females injected with Cas9 and *dll* sgRNAs showed aberrant phenotypes such as missing or malformed legs that were not found in the control groups. DNA sequencing confirmed mosaic mutations including insertions and deletions at the expected cutting sites. These results demonstrated that CRISPR-mediated genome editing can be performed by the injection of Cas9 protein with sgRNAs in engorged female ticks followed by electroporation. Further studies are required in order to optimize this method and to determine its suitability for knock-in editing in ticks.

Biography: Ard Nijhof is a veterinarian with a specialist degree in Parasitology. After completion of his PhD at Utrecht University, the Netherlands, he moved to the Freie Universität Berlin in Germany. His current research focus is on the development and exploitation of novel research tools to increase our knowledge of ticks and the pathogens they transmit. This includes studies on basic tick biology, tick-pathogen interactions, the optimization of artificial tick feeding methods and functional tick genomics. Dr Nijhof is the co-editor-in-chief of the journal 'Ticks and Tick-borne Diseases' since 2021.

TUESDAY, 08h30

Oral Presentations

in order of appearance as on the programme

THEME: Parasite detection, characterization and control

(003) Parasitic nematodes of *Pternistis swainsonii* from two northern regions in South Africa

Andrea Spickett[1], Kerstin Junker[1] & Boris R. Krasnov[2]

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[3]*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, 84990 Midreshet Ben-Gurion, Israel krasnov@bgu.ac.il*

Swainson's spurfowl, *Pternistis swainsonii* (Phasianidae), are restricted to the northeastern areas of South Africa. To date, little is known with regard to the helminth diversity associated with these birds and the present study discusses their nematode assemblages and diversity. The birds were acquired through donation from the South African Wingshooters association at their organised events. Seventy-eight spurfowl were obtained from two localities, 69 from Settlers in Limpopo Province and nine from Rustenburg in North-West Province. Sampling took place during June and July 2019. Hosts were dissected on site where the gastro-intestinal tracts were removed and later examined for helminth parasites. In total, 11 nematode species, representing five families, were recorded i.e. *Gongylonema congolense*, *Tetrameres swainsonii*, *Tetrameres numida*, *Tetrameres* sp., *Acuaria gruveli*, *Cyrnea eurycerca*, *Cyrnea parroti*, *Dispharynx nasuta*, *Stellocaronema* sp., *Allodapa suctoria* and *Allodapa dentigera*. The most prevalent and abundant species was *Allodapa suctoria* with a prevalence of 79.7% and mean abundance of 16.68 ± 4.67 at Settlers, and a prevalence of 55.6% and mean abundance of 5.33 ± 2.47 at Rustenburg. Five species occurred at both localities and six were exclusive to the Settlers hosts. In particular, adult female bias was seen with regard to *T. swainsonii*, and counts of *Acuaria gruveli* were markedly higher in adult than juvenile spurfowl. *Cyrnea eurycerca, D. nasuta*, *Stellocaronema* sp. and *Tetrameres numida* presumably comprise new parasite records for spurfowl. It is evident that Swainson's spurfowl harbour a large nematode species richness that might be due to them being well adapted to seasonal food availability and exploiting agricultural landscapes with the associated crops and insects. Despite high worm burdens in individual hosts these hosts did not appear to be adversely affected.

MONDAY, 09h15

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(005) Prevalence of Gastrointestinal parasites and Molecular epidemiology of *Haemonchus contortus* in sheep in Lesotho

Moeketsi Solomon Phalatsi[1,2], Philip Makama Dawuda[1], Adeniyi Charles Adeola[3], Mabusetsa Joseph Raporoto Makalo[4], Lineo Bohloa[4] & Oriel Matlhahane Molefi Thekisoe[5]

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[2]*Department of Biology, Faculty of Science and Technology, National University of Lesotho, P.O Roma 180, Lesotho*
[3]*State Key Laboratory of Genetic Resources and Evolution, Kunming Institute of Zoology, Chinese Academy of Sciences, Kunming, Yunnan, China*

[4]*Central Veterinary Laboratory. Department of Livestock Services, Ministry of Agriculture and Food Security, Private Bag A82, Maseru 100, Lesotho*
[5]*Unit for Environmental Sciences and Management, North-West University, Private Bag X6001, Potchefstroom 2520, South Africa*

Small ruminant production is the main agriculture sector contributor to Lesotho's GDP through wool, mohair, and animal sales in Lesotho. Gastrointestinal parasites are an unceasing threat, causing major economic losses and limiting factors for the small ruminant industry worldwide, especially in resource-poor communities. *Haemonchus contortus* is the most pathogenic and economically restrictive gastrointestinal nematode of small ruminant industry globally. Morbidity, poor cross-bodily state, and mortality of sheep in Lesotho suggest infection by *H. contortus.* The present cross-sectional study investigated the gastrointestinal parasites, morphological and molecular characterization, and population genetics of *H. contortus* third-stage larvae infecting sheep in four ecological zones of Lesotho. The McMaster method of fecal egg count was used for the analysis of gastrointestinal diversity and intensity. Coprocultures were prepared for larval morphological identification and PCR determination. The overall prevalence rates for strongyles, *Eimeria spp.,* and *Monezia spp.* were 64%, 18%, and 1.3%, respectively. The Highlands recorded the highest strongyle burdens (1170.97±113.134), which were also significantly different ($p<0.05$) across ecological zones. *Eimeria spp.* prevalence and intensity did not record any significant difference ($p>0.05$) between age groups. The present study recorded an average STE of 81.7±1.3 µm and an STE value (´X´) of 2.4752±0.03953, values typical of *H. contortus*. Larval identification from coprocultures revealed 100% *H. contortus* in the study area. The Second Internal Transcribed Spacer (ITS-2) gene of the ribosomal DNA of H. contortus isolates in the present study revealed nucleotide homology ranging from 97 to 100% when compared with selected GenBank reference sequences. Pairwise evolutionary divergence among *H. contortus* isolates was low, with 0.01318 recorded as the highest in the present study. Five haplotypes resulted from 14 Lesotho sequences. Haplotype diversity and nucleotide diversity were 0.76923 and 0.00590, respectively. Genetic differentiation among isolates was low but not statistically significant. An analysis of molecular variance found that most molecular variation was distributed within topographic populations at 94.79% (F_{ST} = 0.05206, $p > 0.05$) and 5.21% among populations. There was high gene flow and no definite population genetic structure among Lesotho isolates.

MONDAY, 09h30

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(010) Evaluation of the spherical body protein 4 (SBP4)-encoding gene for molecular typing of *Babesia caballi*

Alicia Venter[1], Nokuzola F. Nkosi[1], Kgomotso P. Sibeko-Matjila[1] & Raksha. V. Bhoora[1]

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Babesia caballi is an intra-erythrocytic protozoan parasite causing equine piroplasmosis. Three *B. caballi* genotypes (A, B, and C) have been identified based on the heterogeneity in the 18S rRNA and rhoptry-associated protein-1 (*rap*-1) gene sequences. These variant parasite genotypes compromise the diagnostic utility of the OIE-recommended serological assays used in declaring horses free of the disease. The spherical body protein 4 (SBP4) was recently identified as a potential antigen for serological detection of *B. caballi*. However, it remains uncertain whether this antigen can effectively detect the various geographical strains of *B. caballi*. The molecular distinction between variant *B. caballi* parasite genotypes is limited; therefore, we developed *sbp*4 gene-based quantitative real-time polymerase chain reaction (qPCR) assays for the rapid distinction and quantification of *B. caballi* parasite genotypes. Retrospective DNA samples from horses and zebras were screened for the presence of *B. caballi* using an established 18S rRNA-based multiplex equine piroplasmosis qPCR assay. Phylogenetic analysis of the

amplified *sbp*4 and 18S rRNA genes confirmed the groupings of the South African isolates into either *B. caballi* genotypes B or C. The *sbp*4 gene sequences obtained in this study were aligned with published reference sequences representing *B. caballi* genotype A. This alignment allowed the identification of conserved regions within the gene, which were used to design three primer pairs and three genotype-specific TaqMan minor-groove binder (MGB™) probes. The qPCR assays showed to be specific and efficient in the detection and differentiation between *B. caballi* genotypes A, B and C and can be considered for improved diagnosis of *B. caballi* genotypes, to prevent the unintentional spread of equine piroplasmosis globally.

MONDAY 09h45

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(013) Infection rates and genotyping of *Ehrlichia ruminantium* detected in *Amblyomma* species from Southern Africa

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Ticks are haematophagous ectoparasites of domestic and wild animals. With their vast geographical distribution and aptitude as vectors of a large variety of pathogens; they are ranked amongst the top two arthropod families of veterinary and medical concern. *Amblyomma*, the third largest genus in the Ixodidae, is important in southern Africa due to its vector competence for *Ehrlichia ruminantium* and other pathogens. *E. ruminantium,* the causative agent for heartwater, a lethal disease in ruminants, is recognised by the World Organization for Animal Health as a notifiable disease. *Amblyomma* ticks were collected in five southern African countries from livestock and wildlife. They were morphologically identified to species level with taxonomic keys. Species identity was confirmed with molecular assays targeting the *16S* and *12S* rRNA genes. Preliminary screening for *E. ruminantium* was conducted by targeting the *pCS20* gene fragment. Genotyping of a 100 *E. ruminantium* positives was done using Ampliseq technology. In total, 7,773 *Amblyomma* ticks were collected and identified as belonging to four species: *A. eburneum*, *A. hebraeum*, *A. pomposum* and *A. variegatum*. *E. ruminantium* tick infection rates per country ranged from 7.7% to 36.5%. The genotyping analysis indicated the clustering of our sequences with several strains, including the Gardel, Grootvallei and Springbokfontein1. The Ampliseq analysis was effective in differentiating between strains found in southern Africa. This study is one of the largest performed in this region of Africa, illustrating the variability of *E. ruminantium*. Pathogen

diversity studies, such as this one, provides essential information to guide vaccine design as well as research into new polymorphic genes for either phenotypic or genetic characterization.

MONDAY 10h30

(015) Detection of *Theileria haneyi* in South African equids using a newly developed quantitative real-time PCR assay

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Theileria haneyi is an apicomplexan parasite that is closely related to *Theileria equi*, a known causative agent of equine piroplasmosis. Preliminary studies in South Africa have indicated an association between *T. equi* genotype C and *T. haneyi* infections. The molecular distinction between these parasites is reliant on a nested PCR assay, which has been reported to be unreliable. A recently reported indirect ELISA based on the equi merozoite antigen (*Th*EMA-11) of *T. haneyi* is capable of detecting geographically diverse *T. haneyi* strains. Based on its exclusivity to *T. haneyi*, we developed *a* TaqMan minor groove binder (MGB™) quantitative real-time PCR (qPCR) assay to amplify and detect the *ema*-11 gene. Published *T. haneyi ema*-11 gene sequences were used to design primers for the amplification of the *ema*-11 gene from South African samples. The amplicons were cloned and sequenced. An alignment of the South African *ema*-11 gene sequences with published sequences enabled the identification of a conserved region for the design of the real-time assay. The *T. haneyi ema*-11 qPCR assay was shown to be rapid, specific, and sensitive in detecting *T. haneyi* infections. The diagnostic utility of the *T. haneyi ema*-11 qPCR assay was evaluated together with a *T. equi ema*-1 specific qPCR assay. *Theileria haneyi* was detected in 75% of the South African field samples screened, while the occurrence of *T. equi* based on the quantitative amplification of the *ema*-1 gene was much higher (94%). These results suggest that, used in combination, the *T. haneyi ema*-11 qPCR assay, and the *T. equi ema*-1 qPCR assay could be used to detect and differentiate between *T. haneyi* and *T. equi* infections.

MONDAY 10h45

(031) A review on the genetic diversity of *Toxoplasma gondii* from an African perspective

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Toxoplasma gondii is an obligate intracellular apicomplexan protozoan parasite causing toxoplasmosis, a priority zoonotic disease of One Health importance. Countless species of warm-blooded vertebrates including humans are susceptible to infection. Different genotypes of *T. gondii* have been linked to disease severity with a variance in virulence among the genotypes. Determining which genotypes of *T. gondii* are prevalent in Africa can aid in its prevention and control. A systematic review of literature was conducted to investigate the present status of *T. gondii* genetic diversity in African countries and among host species on the continent. A total of 885 *T. gondii* isolates from 20 countries and 21 different host species were characterized into archetypal clonal lineages (type I, II, III), clonal variants, regional or local clonal lineages (*Africa 1-4*), unique strains, mixed types, recombinant strains and unknown types. The PCR-RFLP ToxoDB genotypes of 203 of these isolates, originating from 10 of the countries and four of the host species were identified as ToxoDB #1, #2, #3, #6, #15, #20, #41/#145, #132, #137, #168, #169, #176, #203, atypical strains, mixed types and unique types. North-, South -and East Africa showed more

of a clonal structure when compared to Central -and West Africa. The distribution of local clonal lineages *Africa 1, 2 and 3* and unique genotypes to Africa seems to overlap with the countries that have tropical rainforest biomes, near the equator. Whereas *Africa 4* genotype was more widespread. A possible connection between genotypes and congenital toxoplasmosis as well as ocular toxoplasmosis is seen in this review. Congenital toxoplasmosis cases were primarily linked to type I, recombinant and atypical strains. In the ocular toxoplasmosis group, apart from 1 atypical isolate, all other strains were type I. This review shows that connections exist between specific *T. gondii* genotypes, disease manifestations and severity as well as geographic locale. There is a severe lack of genotype information on *T. gondii* in Southern Africa. Future studies should not only focus in determining the prevalence of *T. gondii* infection in Africa but also on the genotypes involved. This research has been published and can be viewed at https://doi.org/10.1017/S0031182023000252.

MONDAY 11h00

(037) The Complete Mitochondrial Genomes of species of *Haemogregarina* (Adeleorina: Haemogregarinidae), parasitising the Serrated hinged terrapin *Pelusios sinuatus*

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The genus *Haemogregarina* belongs to one of seven genera of blood parasites collectively referred to as haemogregarines. Species of *Haemogregarina* follow a heteroxenous life cycle between turtles and leeches, however, studies have shown *Haemogregarina* infection in lungfish, hinting at a larger unknown host variety. Molecular data from these parasites are lacking in South Africa, especially those from the mitochondrial genome. In this study, we sequenced the 18S rDNA sequences of two previously unidentified *Haemogregarina* species from the serrated hinged terrapin (*Pelusios sinuatus*), in addition to those already known. One of these species shares a close molecular resemblance (98.2%) to *Haemogregarina cylemydis*, while the other remains unidentified. We obtained and compared the complete mitochondrial genome of both species, revealing a significant degree of sequence variability with the protein-coding genes. Previous studies have reported high sequence variability in the mitochondrial protein-coding genes of *Haemogregarina*, but the extent of this variability remains unclear. Our findings suggest that this sequence variability may be a common occurrence or even unique to *Haemogregarina*.

MONDAY 11h15

(038) Frogs and their blood parasites: A biodiversity survey of the Soutpansberg mountain range

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The Soutpansberg mountain range forms part of the Vhembe Biosphere Reserve, an area known to harbour at least 35 species of anurans. Anurans are known to host a variety of intra- and extracellular haemoparasites. In the present study, we show that the rich anuran diversity found within the Vhembe Biosphere also host a variety of haemoparasite species. Blood samples were collected, prepared, and screened for the presence of haemoparasites from 387 individual frogs. Molecular characterisation and phylogenetic analysis were conducted for positive samples and statistical analysis of the anuran parasite fauna calculated. Overall, 89% (31/35) of expected anuran species were observed of which blood samples were collected from 25 species of anuran. A total of 10% (38/387) of the anuran specimens were found infected within 20% (5/25) of the frog species observed. This includes trypanosomatids, haemogregarines, haemococcidians, and filarial nematodes. These results demonstrate a diverse parasite community across the Vhembe Biosphere providing insight to understanding the diversity and distribution of South African anuran blood parasites.

MONDAY 11h30

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(044) Assessing dairy farm personnel's knowledge of the aetiology, risk factors, clinical signs, zoonotic potential and control of bovine fasciolosis in the Eastern Cape province, South Africa

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Dairy farm personnel's knowledge levels on bovine fasciolosis are poorly understood. The current study investigated the knowledge and awareness of the aetiology, risk factors, clinical signs, zoonotic potential and control of bovine fasciolosis among dairy farm personnel in the Eastern Cape province, South Africa. A cross-sectional questionnaire-based survey, with 12 questions about knowledge and 27 questions about practices, was conducted amongst 152 randomly selected dairy farm personnel in coastal and inland regions of the province. The chi-square test was used to assess associations between demographic descriptors and knowledge on fasciolosis. The majority of respondents were below 40 years old (77.6%), males (65.8%), attained tertiary education (64%), had more than 6 years of experience (65%) and lived in the inland regions (65.4%). Most of the respondents (62.5%) were not knowledgeable about fasciolosis ($P < 0.001$). About half of the respondents from coastal regions possessed knowledge about the aetiology and zoonotic potential of fasciolosis compared to a third of the respondents in the inland areas. More respondents ($P < 0.05$) from the coastal regions correctly identified the clinical signs of fasciolosis than in the inland areas. Significantly more respondents ($P < 0.05$) possessing tertiary education qualifications were knowledgeable on the disease's zoonotic potential than those with primary or secondary education qualifications. It was concluded that the bulk

of dairy farm personnel in the Eastern Cape province lacked knowledge on the aetiology, risk factors, clinical signs, zoonotic potential and control of bovine fasciolosis. There is a need to improve farm personnel's knowledge through strategic agricultural extension services, community engagement, and enlightenment campaigns. Such awareness campaigns and training programmes may improve farmers' knowledge about and control of bovine fasciolosis in the Eastern Cape province.

MONDAY 11h45

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(045) Under the Dragon's Veil: investigating the diversity of blood parasites in the Flat dragon lizard (*Smaug depressus*) from the Soutpansberg mountain range.

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The Soutpansberg mountain range, located within the Vhembe Biosphere Reserve, boasts high biodiversity, including a diverse lizard community comprising over 30 species. Despite this diversity, knowledge about the blood parasites of lizards from this area remains limited. This is particularly true for understanding blood parasites in the Flat dragon lizard (*Smaug depressus*), an endemic lizard species inhabiting the Soutpansberg mountain range and surrounding regions in Limpopo, South Africa. Thus, this study aims to investigate the blood parasite diversity in *S. depressus* specifically in the eastern section of the mountain range. To achieve this objective, we collected blood samples from 20 *S. depressus* individuals and conducted morphological and molecular analyses to identify the presence of blood parasites. Our findings reveal a striking variety of blood parasites hosted by *S. depressus*, encompassing trypanosomatids, haemosporidians, haemogregarines, haemococcidians, and filarial nematodes. These results represent valuable baseline data regarding the blood parasite diversity within cordylid lizards. Furthermore, this study bridges the knowledge gap regarding blood parasite infections in *S. depressus* and sheds light on the interaction between reptilian hosts and their associated blood parasites. Ultimately, this research aids the broader conservation efforts to preserve the unique reptilian biodiversity and their parasites within the Soutpansberg mountain range.

MONDAY 12h00

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(048) Molecular detection of a novel *Rickettsia* species in a rural community in South Africa: Insights from rodent flea samples

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Zoonotic diseases are caused by pathogens transmitted directly or indirectly (by vectors) between animals (domestic and wild) and humans. Zoonoses are appraised to account for one quarter of the disease burden in low-income countries. Furthermore, poverty increases the risk of zoonotic diseases in communities living at the interface with livestock and wildlife. Rickettsioses are a group of infectious diseases caused by bacteria of the order Rickettsiales. They are transmitted by arthropod vectors including fleas, lice, ticks and mites. The present study was carried out in the Mnisi Community, located in north-eastern South Africa, in the Bushbuckridge Municipality, Mpumalanga Province. The community is surrounded by game reserves, and rodents are widespread, and are frequently seen in and around households. The present study investigated fleas infesting rodents in different localities in the area, and aimed to identify *Rickettsia* spp. in the fleas. A total of 255 rodents were captured from four villages (houses and croplands) and a natural area (game reserve). A total of eight flea species were recorded from 986 flea individuals, in order of overall abundance: *Xenepsylla frayi, Echidnophaga gallinacea, X. bechuanae, X. brasiliensis, Dinopsyllus lypusus, Nosopsyllus fasciatus, Chiastopsylla godfreyi* and *Ctenocephalides connatus*. Female specimens of the same flea species from individual rodents were pooled (n = 278 pools of fleas), DNA was extracted and screened using a *Rickettsia*-specific real-time PCR. *Rickettsia* positive flea pools were seen from 1) *E. gallinacea* collected from *Rattus* spp. from houses 2) *X. bechuanae* collected from *Saccostomus campestris* from the natural habitat and 3) *Ctenocephalides connatus* collected from *Mastomys* spp. from the natural habitat. *GltA, ompA and ompB* genes sequences with 92-95% identity to *Rickettsia asembonensis* were identified from *X. bechuanae. Rickettsia asembonensis,* a flea-borne rickettsia closely related to *Rickettsia felis,* was first detected in cat fleas in Kenya and subsequently reported worldwide. The infectivity and pathogenicity of *R. asembonensis* in humans is largely unknown.

MONDAY 14h00

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(051) Identification and characterization of ticks and tick-borne parasites of wild felids in South Africa

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Ticks are ranked second to mosquitoes as vectors of animal and human pathogens globally. However, there are gaps in the knowledge and impact of ticks and tick-borne pathogens in the conservation of wild animals in South Africa. Thus, this study aimed to determine the occurrence and diversity of ticks and tick-borne pathogens of selected species of wild felids and their associated ticks using morphological and molecular assays. A total of 93 ticks collected opportunistically from 30 cheetahs and four lions in four game reserves in South Africa during routine health checks, were identified morphologically. Blood in EDTA was also collected from each animal. Genomic DNA was extracted from 87, ticks and blood samples of 33 hosts (30 cheetahs and 3 lions) using the Zymo Quick DNA Miniprep

kit. Six ticks were donated to the Gertrud Theiler Tick Museum as voucher specimens; blood was not collected from one lion. Additionally, 84 archived blood samples from the SANBI Biobank were included in the study. The samples originated from wild felids (lions, cheetahs, servals, caracals) in different localities in South Africa and were stored at the SANBI Biobank. The *CO1*, 16S rRNA, and *nad5* genes from ticks, and the 18S rRNA gene from Apicomplexan parasites (*Babesia*, *Theileria,* and *Hepatozoon* spp.) were amplified and sequenced. Tick species of four genera, namely *Amblyomma*, *Haemaphysalis*, *Hyalomma,* and *Rhipicephalus* were identified from the study. *Haemaphysalis elliptica* was the most common species (53.7%) collected from lions and cheetahs. Parasitic infections were identified in 67% (22/33) of host DNA from field samples, 24.1% (21/87) ticks, and 11.9% (10/84) of archived blood samples. BLASTN results indicated that the obtained sequences were 98 – 100% identical to published sequences of *Babesia felis*, *B. lengau, Hepatozoon felis, H. luiperdjie*, and an uncharacterized *Babesia* sp. from lions in Botswana. This study confirms previous reports of infections by *Babesia* and *Hepatozoon* spp. in wild felids in South Africa and highlights the importance of monitoring these infections in wild animals prior to translocation to prevent transmission of ticks and pathogens to new hosts and localities.

MONDAY 14h15

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(060) Avian haemosporidia in native and invasive sparrow at an Afrotropical region

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Bio-invasions are a major threat to biodiversity and ecosystems globally and may contribute to the proliferation of emerging infectious diseases. We examined the prevalence and phylogenetic diversity of avian haemosporidian parasites infecting the non-native house sparrows (*Passer domesticus*) and the native southern grey-headed sparrows (*Passer diffusus*). Blood samples from 104 sparrows (74 house sparrows and 30 southern grey-headed sparrows) mist-netted inside and around the Kruger National Park were used. Genomic DNA was extracted from each blood sample and subjected to nested PCR analyses, Sanger sequencing and phylogenetic analyses. Overall, 35.57% (37/104) of the birds sampled were infected with at least one haemosporidian parasites. Southern grey-headed sparrows had a higher parasite prevalence (60%) than house sparrows (24.3%). A total of 16 parasite lineages were identified, of which eight were novel lineages. Whereas *Haemoproteus* spp. showed the highest lineage diversity, *Leucocytozoon* spp. were the most prevalent parasites, albeit with significant differences between sparrow species. A single Plasmodium sp. infection was recorded in a southern grey-headed sparrow. In support of the enemy release hypothesis, we found that prevalence on non-native house sparrows was lower than prevalence recording their region of origin and also that they were infected only by indigenous parasites lineages.

MONDAY 14h30

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(080) Evaluation of knowledge, attitudes and practices regarding neosporosis and toxoplasmosis among farmers and animal health practitioners in Namibia

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This study assessed the knowledge, attitudes and practices of livestock farmers in Namibia's Khomas region and animal health practitioners (veterinarians and animal health technicians) in the whole country concerning neosporosis and toxoplasmosis. Structured questionnaires were used, and a total of 63 farmers and 51 animal health practitioners responded out of an estimated 560 farmers in the Khomas region and 300 veterinarians and veterinary technicians in the country. Only 15.9% of the livestock farmers (n = 63) had heard about neosporosis or toxoplasmosis or knew how animals get infected ($p < 0.0001$). Only 5% of the farmers knew the risks associated with keeping dogs and cats concerning neosporosis and toxoplasmosis, respectively ($p < 0.0001$). None of the 51 animal health practitioners routinely requested *Neospora caninum* or *Toxoplasma gondii* laboratory tests in cases of cattle, sheep or goat abortions. Although all animal health practitioners indicated they routinely interacted with livestock farmers, none regularly discussed neosporosis or toxoplasmosis. Only 3.9% of animal health practitioners (n = 51) indicated that they had ever discussed either neosporosis or toxoplasmosis at a farmers' gathering ($p < 0.0001$), and only 21.6% had talked to at least one cat owner about toxoplasmosis in the previous 12 months ($p < 0.0001$). The authors concluded that farmers in the Khomas region were generally unaware of neosporosis and toxoplasmosis but could change their attitudes and practices if educated. The animal health practitioners lacked a deeper understanding and appreciation of the two diseases, which is required to cultivate enough confidence to educate farmers. Sharing this research and other relevant information on the two diseases at farmers' meetings, veterinary congresses, journals and newsletters could help educate farmers and animal health practitioners. Such platforms are likely to succeed because both these groups use these forums to get new information.

MONDAY 14h45

THEME: PARASITE ECOLOCY AND HOST-PARASITE INTERACTIONS

(002) Old data, new insights: NMDS, DSCPA and NNODF provide a fresh take on parasite community patterns in Nyalas in South Africa

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While recent years have seen a number of studies exploring the impact of host sex and age on processes and patterns within parasite communities, little is known about the effect of host variables on the structure of host-parasite networks. Many of these studies concentrated on small mammals, whereas large terrestrial mammals have remained largely unstudied. A comprehensive data set of the internal parasites of 74 nyalas (*Tragelaphus angasii*), compiled in KwaZulu-Natal Province during 1983–1984, allowed us to investigate the effects of host age and sex on the parasite infra- and component communities of these hosts and on the structure of individual-based nyala-endoparasite networks. The provenance of the nyalas from three different game reserves also allowed us insights into the spatial

variability of these effects and the possible influence of conservation management interventions. Nyalas are intermediate mixed feeders, whose helminth communities are moderately species rich with a predominance of directly transmitted parasites. Across all localities, the nematodes *Ostertagia harrisi*, *Paracooperia horaki* and *Cooperia rotundispiclum*, together with paramphistomine trematodes were the most prevalent species. Apart from this, however, environmental conditions contributed to varying infection patterns in the three reserves, influencing transmission pathways, likely via survival rates of free-living infective stages or the presence/absence of suitable intermediate or final hosts. Our results clearly illustrated that pooling data from different localities for host-parasite network analyses could skew data by masking locality specific trends. Host age, more so than host sex, was the main driver of the structure of parasite communities and parasite-host networks in nyalas. Behavioural, dietary and physiological changes throughout a nyala's lifespan are likely contributing factors to these age-related differences, as well as a stochastic increase in the likelihood of exposure to parasites with an increase in a nyala's age. In conclusion, our study emphasizes the complex interactions between parasites and their hosts, and the far-reaching impact environmental changes, including man-made interventions, can have on the same.

MONDAY 15h30

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(021) The Living Collections Cluster- a platform for the management of living collections in South Africa

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Scientific collections are valuable for addressing global challenges such as climate change, food security, health and emerging diseases, illegal wildlife trade, and biodiversity conservation. However, these collections are scattered and poorly organised globally to provide optimal access for research purposes. This leads to them being considered of limited use and value for innovative and problem-solving research. South Africa has a huge wealth of Living Collections located in zoological and botanical gardens, captive facilities, aquaria, agricultural facilities, and research laboratories used by scientists for cutting-edge research and include both marine and terrestrial plants and animals. Within these collections are plants and animals of high conservation value (some are extinct in the wild), and representatives of flora and fauna from different habitats and biomes that contribute to distinctive landscapes across the country. However, the management of Living Collections in South Africa is not well coordinated to ensure their long-term preservation and use for multi-disciplinary research that can contribute to and stimulate economic development. As such, the Department of Science and Innovation (DSI) has established a National Scientific Research Collections Platform (NSRCP) that provides strategic guidance and financial resources to facilitate a coordinated structure for the management of scientific collections in South Africa. The role of the South African Living Collections Cluster (SALCC) is to coordinate the establishment of a network of custodians of Living Collections within the biodiversity conservation, agriculture, and higher education and training (academic) sectors in South Africa to ensure that the collections are well-managed and curated, and are accessible to the scientific community, and to determine their sustainability and use for multi-and trans-disciplinary research. Progress towards these goals and planned activities for the cluster is discussed.

MONDAY 15h45

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(043) Aspects of the histopathology associated with *Rhabdochona* infecting smallmouth yellowfish, *Labeobarbus aeneus* (Burchell, 1822) in the Vaal River System

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Labeobarbus aeneus is a freshwater fish endemic to South Africa and naturally occurs in the Orange-Vaal river system. Despite the social, economic and environmental importance of *L. aeneus*, there is only a limited number of studies on its biology and ecology, and even fewer on the endoparasites it hosts. Nematodes, preliminarily identified as *Rhabdochona* Railliet, 1916, were found in *L. aeneus* in the Vaal River system. There are no prior studies on the pathology associated with *Rhabdochona*, which often infects economically important freshwater fishes. This study aimed to describe the histopathological effects associated with *Rhabdochona* sp. in the intestine of *L. aeneus.* Furthermore, their wound-inflicting structures were described. The pathology caused by *Rhabdochona* sp. to the intestine of *L. aeneus* was studied using standard histological techniques, light microscopy (LM) and scanning electron microscopy (SEM). The wound-inflicting structures of the nematodes were described using LM and SEM. Prevalence, abundance and mean intensity, and the confidence intervals and standard errors were calculated. An inflammatory response, granulomatosis and loose tissue were observed around the regions where the parasite was attached. The teeth-like longitudinal projections present in the buccal cavity are likely the primary wound-inflicting structures. *Rhabdochona* has been reported to occur in masses. The results from the current study could indicate an early infection or the influence of low infection intensity.

MONDAY 16h00

THEME: VACCINES, GENOMICS AND NOVEL DIAGNOSTICS IN PARASITOLOGY

(009) Identification and gene expression profiling of subunit vaccine candidates in cattle- and buffalo-derived *Theileria parva* isolates

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Bovine theileriosis caused by *Theileria parva* kill more than one million cattle annually in affected African countries, largely affecting smallholder farmers. The disease is currently managed by tick control with expensive acaricides often ineffective in altering disease progression, and immunization using the infection and treatment method which is associated with a range of limitations including limited protection against field strains. Therefore, the search is ongoing for antigens that can provide broad protection against field strains, especially buffalo-derived *T. parva* infections, for consideration in the development of a subunit vaccine. Thus, in this study, reverse vaccinology and transcriptome analyses were respectively employed to identify *T. parva* schizont antigens and profile their expression in cattle- and buffalo-derived *T. parva* isolates. The *T. parva* proteome was screened using a combination of bioinformatics tools for secreted proteins with predicted glycosylphosphatidylinositol anchor and ≤ 1 transmembrane domain, which were further evaluated for solubility and antigenicity properties prior to T-cell and B-cell epitope prediction analysis. Eighteen proteins had good binding affinity to MHC class-

I BoLA alleles. Comparative transcriptome analysis between three cattle- and three buffalo-derived *T. parva* isolates showed that 12 of the predicted antigens were expressed in both parasite groups during the schizont stage. Seven of these were expressed at similar levels in both groups and had no homologs or orthologs to the host *(Bos taurus)* proteome. The seven predicted antigens include four that have been previously reported as antigens, namely p104, p32, p67 and a hypothetical protein, and three novel antigens that are hypothetical proteins. Six of these have been reported to be expressed in the host infective stage, the sporozoite. Thus, these antigens can be considered for the development of a subunit vaccine that will target both the inoculation and the pathogenic phases of infection; moreover, provide protection against both cattle- and buffalo-derived *T. parva* isolates.

TUESDAY, 09h00

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(018) A gene drive that reduces the fertility of malaria parasites

Geoffrey McFadden[1], Dean Goodman[1], Anton Cozijnsen[1], Sophie Collier[1] & Benjamin Cam[1]

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Gene drives could alter or even eradicate an entire target population. We built a homing gene drive and introduced it into *P. berghei* disrupting the *male development 4* gene (*md4*), which is essential for male gamete production[1]. Disruption of *md4* by the gene drive cassette rendered this "gene drive line" female-only and unable to self-fertilise, as expected. Our gene drive cassette includes Cas9 endonuclease and a guide RNA (gRNA) targeting *md4*. The next objective was to test if the gene drive cassette would home to *md4* at the zygote/ookinete stage when a homologous chromosome containing the *md4* target was introduced by syngamy. We infected mice with two lines: i/ our *md4*- gene drive line, and ii/ a line that produces only male gametes because it has the *female development 1* (*fd1*) gene deleted (i.e., *md4+/fd1-*). Mosquitoes were allowed to bite these dual infected mice and became infected. Oocysts and sporozoites were produced efficiently and were genotyped. Crossing had occurred, and all progenies had the gene drive cassette inserted into the *md4* locus. A control gene drive line with an irrelevant gRNA did not result in homing of the drive into *md4* in cross progenies. The gene drive homes as directed by the gRNA, efficiently. Sporozoites from the cross of our gene drive line (*md4-*) with the *fd1-* line, successfully infected naïve mice. Mosquitoes were allowed to bite these mice, but they did not become infected. No oocysts or sporozoites were produced, likely because the gene drive cross progenies were all female-only (*md4-*) and unable to self-fertilise. Thus, our gene drive could ultimately cause sex bias and population collapse. We are also exploring multiplexed gRNAs to target other fertility genes, as well as versions that revert drug resistant alleles to sensitive genotypes. Deployment of a gene drive pathogen has massive safety, ethical, moral, social, and regulatory challenges. Nevertheless, malaria defies efforts at global eradication, and a gene drive strategy could be a decisive new tool to contribute to the battle against this devastating disease.

TUESDAY, 09h15

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(041) Detection of bacterial tick-borne pathogens in two provinces of South Africa using a microbiome sequencing approach

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Ticks are obligate ecto-parasites recognised worldwide as major vectors of several disease-causing pathogens and are good indicators of disease distribution and epidemiology. However, global warming

has effected climate change and consequently expanded tick distribution. As a result, there is a growing concern of emerging and re-emerging of tick-borne pathogens. This study seeks to identify ticks and detect bacterial tick-borne pathogens using a 16S rRNA next-generation sequencing approach in three neighbouring towns: Harrismith, Phuthaditjhaba and Bergville. A total of 50 blood samples were collected from cattle in each study site and 418 ticks collected from these cattle. Ticks were identified morphologically with Harrismith *(Rhipicephalus decoloratus,R. microplus, R.evertsi evertsi, Hyalomma truncatum, H. rufipes*), Phuthadithjaba *(R. appedndiculatus,R. simus, R.evertsi evertsi, R.turanicus, H.rufipes)* and Bergville (*R. evertsi evertsi, R. appendiculatus, H. truncatum*). *Rhipicephalus evertsi evertsi* was dominant in the three study sites, whereas *R. decoloratus and R. microplus* ticks were only present in Harrismith and Phuthaditjhaba. The 16S rRNA NGS was used to explore the bacterial pathogens transmitted by the ticks in cattle. A total 7,687,581 reads were obtained. Most pathogens belonging to the genera: *Anaplasma, Mycoplasma and Ehrlichia* were detected from bovine cattle blood. Species-level differences of microbial communities across the three localities, showed no significant differences (p=0.081, Kruskal Wallis test) in the microbiome relevant abundance. Of the 71 detected species (159 genera), 12.67%, 22.54% and 21.13% had a sole association with Phuthaditjhaba, Bergville and Harrismith localities respectively. *Anaplasma marginale* (relative abundance 56.2%, 43.5%, 54.2%, respectively) was the most abundant bacterial pathogen in the Bergville, Harrismith and Phuthaditjhaba samples, followed by *A. platys* (22.6%, 31.5%, 32.9%) and *Mycoplasma wenyonii* (14%, 19.6%, 7.8%). Bacterial composition at the three sites aligns with the presence of the biological vector ticks. Results obtained will contribute to current tick distribution and pathogens they transmit in the study sites. Moreover, improving strategies for prevention and control of tick-borne diseases.

TUESDAY, 09h30

(042) Rodents as potential reservoir hosts for *Anaplasma* spp. at the human-livestock-wildlife interface of the Mnisi community, South Africa

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Rodents represent the largest order of living mammals, comprising 42% of the global mammalian biodiversity with an almost worldwide distribution. Rodents are reservoir hosts for many pathogens of humans and livestock of importance and play a key role in the natural circulation of many viral, bacterial and parasitic infections. Species of the genus *Anaplasma* are widely distributed in a variety of vertebrate hosts and include species of veterinary and medical importance. Although *Anaplasma bovis* and *A. phagocytophilum* were previously reported in the eastern rock sengi and rodents, respectively in South Africa, the role of small mammals in the occurrence and distribution of *Anaplasma* spp. has not been extensively explored. In the Mnisi Community, located in Bushbuckridge Municipality, Mpumalanga, and in the surrounding game reserves, rodents are widespread and are frequently found in and around households. The presence of *Anaplasma* species in rodents in the Mnisi Community over a period of three years, from spring 2019 to spring 2021, was examined using a third-generation sequencing approach. Genomic DNA was extracted from blood collected from a total of 168 rodents of various species captured from villages, croplands and the Manyeleti Game Reserve. Barcoded 16S rRNA primers were used to amplify the full-length 16S rRNA gene. Libraries comprising equimolar amounts of 64 amplicons were prepared and sequenced on a Pacific Biosciences platform. Preliminary results from more than 31,000 sequence reads classified in the genus *Anaplasma* from 35 *Anaplasma*-positive samples, revealed the presence of 16S rRNA sequences with 99.77% and 99.85% sequence identity to

those from the *A. centrale* vaccine strain and *A. platys*, respectively, as well as a sequence closely related to the *A. bovis* 16S rRNA sequence, with 98.15% identity. Since some distinct *Anaplasma* spp. have more than 98.7% sequence identity, it is not clear if these sequences represent novel species or variants of known species. A multi-locus sequence typing (MLST) will be used to clarify the phylogenetic classification of the putative species identified. Our findings demonstrate an abundance of *Anaplasma* sequences in rodents and contribute to the limited information on rodents as potential reservoir hosts of *Anaplasma* spp. in South Africa.

TUESDAY, 09h45

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(052) Development and validation of a real-time PCR assay, and phylogenetic classification of *A. platys*

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Anaplasma platys, a tick-borne gram-negative bacterium (family Anaplasmataceae and order Rickettsiales) is of public health and veterinary importance. The pathogen is the main cause of anaplasmosis in dogs. In dogs, infection leads to canine thrombocytopenia and platelets are the target cells. Serological tests such as Immunofluorescence assay (IFA) and commercially available immunochromatography-based point-of-care (POC) tests are used as diagnostic tools on dogs presenting clinical signs. PCR methods are also available to detect pathogens in the blood or tissue of dogs. However, these tests have shortcomings such as cross-reactivity (serological tests) and lack of multiplexing capabilities (molecular tests). *A. platys* has not been successfully cultured to date therefore we developed *Ehrlichia/Anaplasma* group-specific primers for multiplexing purposes and *A. platys* specific TaqMan® minor groove binder probe. TaqMan® MGB probes allow shorter probe design, which is useful for shorter conserved regions identification in a variable region. The gene of interest for this assay is 16S rRNA and hypervariable region 1. We phylogenetically classified *A. platys* to increase knowledge about the South African strains. This assay will be a useful tool for early diagnosis of *A. platys* and prevent the inappropriate use of antibiotics as a result avoiding potential microbial resistance from emerging.

TUESDAY, 10h00

THEME: PARASITES IN MARINE AND FRESHWATER SYSTEMS

(004) Assessment of anthropogenic impacts on the aquatic environment and biodiversity in the Katangese Copperbelt Area (DR Congo): a parasitological approach

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The field of fish parasitology, which was unexplored for the Upper Congo Basin until a few years ago, has seen an increased interest in the last decade in monogenean fish parasites. These monogeneans are being included in policy-relevant studies as potential bio-indicators of pollution. The Upper Congo Basin is an area with high mining potential and exploitation and has particular interest in biomonitoring. Monogeneans are sensitive to environmental changes, highly host specific, ubiquitous and have a direct lifecycle. Unfortunately, they are not well studied in many ecoregions of the Upper Congo Basin. This study aims to use monogeneans as bio-indicators of water pollution in the Katangese Copperbelt Area (KCA). As a starting point, we carry out an inventory of the parasitological fauna of the fish with the highest economic value and most abundant in fishermen's catch in two ecoregions spanning the KCA. Two fish families, Cichlidae, three fish species (*Oreochromis mweruensis*, *Coptodon rendalli* and *Serranochromis macrocephalus*) and Clariidae, four fish species (*Clarias ngamensis*, *C. gariepinus*, *C. buthupogon* and *C. stappersii*), were selected. Monogeneans were isolated from the gills and mounted on glass slides with ammonium picrate-glycerin for identification based on morphological analysis. Species richness was reported and infection parameters of the retrieved parasites were calculated. A total of 13 parasite species were recorded on cichlid fishes, and ten monogenean species from clariids. The prevalence of monogeneans on cichlids ranged between 2 - 92%, while on clariids, it ranged between 7 - 67%. Mean intensities were between 1 - 17 ± 24 on cichlids, and 1 to 17± 21 on clariids. Based on preliminary results, monogenean species diversity and their respective epidemiological indices are low in sites near mining areas (source of pollution) and increase with increasing distance from them. This study highlights the potential biodiversity still to be explored in the Upper Congo Basin and it will serve as an important baseline for the assessment of water quality using bio-indicators in the KCA.

TUESDAY, 10h45

(007) Rare findings in neglected freshwater limpets: integrated characterisation of *Sanguinicola* spp. (Digenea) cercariae and a monoxenous nematode in *Burnupia* spp. from South Africa

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Fresh water snails have been the subject of numerous parasitological studies since they transmit diverse species of Digenea that infect aquatic and terrestrial fauna. Even though limpets belonging to the family Burnupiidae are abundant in Africa, they remain neglected in many parasitological surveys. *Sanguinicola* spp. (Aporocotylidae) are blood flukes of fish and are associated with losses in fisheries. Until now, only two species of *Sanguinicola* (from Egypt and Sudan)are known in Africa. Unfortunately, data on their genetic characteristics, intermediate hosts and descriptions of their larvae, are still lacking. Unlike gastropod-digenean associations which are relatively well documented, nematodes of snails are under studied worldwide. In the present study, *Burnupia stenochorias* (Melvill & Ponsonby, 1903) and *Burnupia capensis*(Walker, 1912) were collected in summer (2021-2023), from the Crocodile and Vaal River systems in South Africa.Overall,1637snails were examined, of which4.22% harboured digeneans, while 28.0% were infected with nematodes. Characterisation of the helminths was based on DNA analyses and morphometric data obtained from light and scanning electron microscopy. Four morphotypes of *Sanguinicola* cercariae were distinguished by overall body size, number of penetration glands, patterns of tegumental spines and relative size of the fin folds on the body and furcae. Genetic analyses showed that the morphotypes were distinct from each other and from their congeners whose genetic data are available, for 18Sand28S rDNA. This study also reports on a new host and locality for the recently described nematode, *Daubaylia burnupiae* Outa & Avenant-Oldewage, 2023 (Daubayliidae).The nematode was originally reported in *B. stenochorias* from the Vaal River and has now been found in *B. capensis* from the Crocodile River, in the Limpopo River system as well. *Daubaylia burnupiae*is the second daubayliid species in Africa, and the only one that is known to infect burnupiids.

In summary, the current study shows the hidden diversity of parasitic helminths in snail species that tend to receive little attention in parasitological surveys.

TUESDAY, 11h00

(023) New reports of Pennellidae burmeister, 1835 metamorphosed females infecting marine Teleostei off southern Africa

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Pennellidae (Copepoda: Siphonostomatoida) has 24 accepted genera and 147 species symbiotic on marine fishes and mammals. One feature that distinguishes pennellids from other siphonostomatoid families is their reliance on an intermediate host (either a teleost or an invertebrate) in their life cycle, where mating usually takes place. Adult metamorphosed female pennellids have large bodies, with loss of maxillipeds adapted to their mesoparasitic lifestyle. Morphologically, these organisms exhibit a wide range of variations, including variations in cephalothorax structure (ranging from simple to the development of a cephalic holdfast organ), trunk shape (ranging from straight to sigmoid), abdomen complexity (ranging from simple to having embedded posterior processes) and egg sacs shape (ranging from straight to curled). To date, only three genera and four species (*Pennella filosa* (Linnaeus, 1758), *Pennella balaenoptera* Koren & Danielssen, 1877, *Cardiodectes bellottii* (Richiardi, 1882) and *Lernaeenicus kabatai* Oldewage, 1989) were reported from South African marine waters. This study includes the first reports of *Lernaeenicus longiventris* Wilson C.B., 1917, *Pennella instructa* Wilson C.B., 1917, *Propeniculus stromatei* (Gnanamuthu, 1951) and *Sarcotretes longirostris* Ho, Nagasawa & Kim I.H., 2007 off South Africa, and *Sarcotretes scopeli* Jungersen, 1911 off Namibia. Morphological re-descriptions of *P. stromatei* and *S. scopeli* are done while new hosts are reported for *Pennella instructa*, *Propeniculus stromatei*, *Sarcotretes longirostris* and *Sarcotretes scopeli*.

TUESDAY, 11h15

(030) Trace element sequestration in *Lamproglena clariae* from Lake Heritage (Crocodile River) and the Vaal River

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Anthropogenic activities have a significant impact on the state of aquatic environments and the organisms inhabiting them. Parasites have been proposed as bioindicators due to their sensitivity to environmental changes and, in some cases, their ability to accumulate metals to higher concentrations than their host tissues. This study focused on investigating the sequestration of trace elements in the ectoparasite, *Lamproglena clariae* from Lake Heritage in the Crocodile River and in the Vaal River below the Vaal Dam, South Africa. Adult *L. clariae* were collected from the gills of *Clarias gariepinus*. Parasites were flash-frozen in liquid nitrogen and then sectioned using a cryo-microtome. After that sections were treated with Phen-Green FL Cell-permeant Diacetate to study metal sequestration. To correlate fluorescent signals and the specific metals present and their levels in sections of *L. clariae*, a scanning electron microscope equipped with an energy-dispersive spectroscope (SEM-EDS) was used. Fluorescence results showed more intense signals in the egg yolk and exoskeleton of the parasite

compared to the other tissues. SEM-EDS analysis showed that Al, Fe, Cu and Zn in parasites from both collection sites. Metal levels (wt%) in *L. clariae* from the Vaal River were higher than those in parasites from Lake Heritage, which corresponded to the differences in metal concentrations reported in literature for water from the sites. Therefore, based on fluorescence and SEM-EDS analyses, it can be concluded that metals such as Al, Fe, Cu and Zn are present at higher levels in the exoskeleton of the abdomen and eggs compared to the exoskeleton of the head and thorax of *L. clariae*. The presence of metals in the egg yolk suggests that the eggs may serve as a route for adults to eliminate metals from their bodies.

TUESDAY, 11h30

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(033) Aspects of the histopathology of the stomach of *Clarias gariepinus* (Burchell, 1822) infected by *Procamallanus* (*Procamallanus*) *pseudolaeviconchus* Moravec & Van As, 2015

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The effect of fish parasites on aquaculture has intensified studies on the ecto-and-endo-parasites of fish. Parasites have been associated with alterations to their host's organs and defence mechanisms. Cestodes, trematodes and nematodes of *Clarias gariepinus* are among the most studied fish endoparasites. These studies include parasite identification, taxonomy, and pathogenicity. *Procamallanus* (*Procamallanus*) *Pseudolaeviconchus* Moravec & Van As, 2015 (Nematoda) was recently described, and the morphology reported. The current study contributes additional information about feeding mechanisms and the pathological impact on *C. gariepinus* from the Vaal Dam. A total of 10 *C. gariepinus* were collected from the Vaal Dam and tissue samples (infected and uninfected) were collected from the stomachs and some were processed using standard histology protocols. Sections were stained with haematoxylin and eosin. Further/other specimens were prepared for scanning electron microscopy using standard techniques. Photomicrographs were taken to describe and quantify the pathology and feeding structures. Sections indicated that the parasites feed by sucking the tissue into the buccal capsule. This was linked to the morphology of the buccal capsule and muscular oesophagus of the parasite. There was limited penetration, trauma to the mucosal layer, cellular infiltration in the mucosal layer and cell hypertrophy in the mucosal layer were observed. It was concluded *P.* (*P*) *pseudolaeviconchus* use its muscular oesophagus in combination with the large, smooth buccal capsule to create a suction cup that allows it to ingest host tissue. This feeding mode is similar to that of other camallanids. The pathology is localised and limited to the mucosal layer. In high intensities, the effect may be severe.

TUESDAY, 11h45

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(035) Ectosymbiotic fish peritrichs (Ciliophora: Peritrichia) and their suctorian (Ciliophora: Suctoria) predators

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A variety of symbionts occur externally on freshwater fish, the most common being two closely related groups, i.e., the mobiline and sessiline peritrichs. Ectocommensal peritrichs sometimes have to deal with a predator that targets them. These predators are found in the ciliate subclass Suctoria. During fish parasitological surveys in Botswana and South Africa, several fish species harboured suctorians attached to sessiline peritrichs, in turn found on fish. Wet smears were prepared and sessiline and suctorians were studied live with the aid of light and scanning electron microscopy. Three genera of sessilines were commonly encountered on various fish, i.e., *Epistylis*, *Scopulata* and *Apiosoma*, but suctorians were found attached to the latter in the majority of cases, with only two records of them attached to *Epistylis*. In a single case, a suctorian was also found associated with the copepod parasite, *Lernaea cyprinacea*. Very little is known about this interesting group of predatory ciliophorans. Most work has been done on the genera found attached directly to either the skin or gills of fish, and this research mostly focused on their taxonomic status. All suctorians, whether attached to peritrichs or directly to fish, feed on ciliophorans. There is no evidence of any serious injuries caused by suctorians to the fish host. The question arises whether the peritrichs these suctorians attach to is utilised as a prey organism or merely serves as an attachment site whilst they target any of the other ciliophorans present on the skin and fins of the fish.

TUESDAY, 14h00

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(046) Parasite diversity of *Chiloglanis pretoriae* from the Limpopo river system

Thabelo Maginya[1] , Willem J. Smit[1], Humbulani E. Munzhelele[1,2] Piet H. King[3], Iva Přikrylová[1,4], Nehemiah M. Rindoria[1,5], & Wilmien J. Luus-Powell[1]

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Chiloglanis pretoriae Van der Horst, 1931 (Mochokidae) is an endemic freshwater fish species of Southern Africa with limited information regarding its parasite diversity. The aim of the study was to determine the parasite diversity of the host within the Limpopo River System. Between September 2021 and May 2022, a total of 127 specimens of *C. pretoriae* were collected from four rivers (Mutshundudi, Nwanedi, Lutanandwa and Politsi) using electrofishing. Standard methods were used for the collection, fixation, and preservation of parasites. Forty-seven fish (37%) were infected by at least one parasite. Three parasitic groups (monogeneans, digeneans and hirudineans) were recovered during the study with digeneans more abundant compared to the other groups. Four specimens of *C.*

pretoriae [Politsi: n = 1; Lutanandwa: n = 3] were infected by a new dactylogyrid from the gills [mean intensity (MI) = 5.3 and mean abundance (MA) = 0.41]. Twelve *C. pretoriae* from Politsi River were infected by an undescribed adult digenean from the Cephalogonimidae (MI = 5.51 and MA = 0.11) in the intestine and *Clinostomum* sp. (MI = 1 and MA = 0.03) from the body cavity. Digenean larvae from the Diplostomidae was the most abundant digenean infecting the body cavity, muscle, under the skin and gill cavity of 20 fish from Mutshundudi (n = 12), Lutanandwa (n = 3) and Nwanedi (n = 5) rivers. Results from this study include two new parasite species as well as new host and locality records contributing to global parasite distribution records. This work is based on research supported by the Department of Science and Innovation and the National Research Foundation of South Africa (Grant Number 101054).

TUESDAY, 14h15

(081) To like or dislike the alien and invasive common carp as a parasite "taxi"

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During fish biodiversity surveys conducted by FS DESTEA, in the Free State Province (FSP), parasitologists from UFS tagged along. Fish were collected using long lines, beach seine nets, gill and fyke nets. These surveys took place during 2012-2014, with sporadic fieldtrips thereafter and again on a more regular basis during 2018-2019. Field laboratories were set up close to the water edge and standard techniques were used for the collection and fixation of the different parasite taxa collected. The same applied to the fish data obtained, i.e., using standard techniques. This paper will focus on one fish only i.e., the common carp *Cyprinus carpio*. It is an alien and invasive fish species that has invaded most aquatic systems in South Africa, where it dominates fish communities. The species has also been responsible for the introduction of nine alien fish parasites. Despite all of this, the common carp supports a multi-billion-rand recreational fisheries sector. A study of recreational fisheries in the FSP from 1974-2014, has revealed that common carp dominated recreational fishers' catches, which made up between 42 and 98% of total weight, and 9-99% of total number of fish caught. Overall, carp comprised 81% of the weight and 77% of the number of all fish landed during angling tournaments. Carp of different sizes classes were collected from 21 impoundments and nine river systems in the FSP. The spectrum of parasites found included skin and gill protozoa (*Trichodina, Tripartiella, Apiosoma* and *Scopulata*), alien argulids from the skin, monogeneans from skin and gills, as well as a cestode representative in the digestive system. From the literature, the common carp appears to be only bad news in the eyes of fish parasitologists, however, from inland fisheries perspective, it is a completely different ball game.

TUESDAY, 14h30

(024) Worms, worms and more worms: Advances in knowledge regarding the richness of South African fish-infecting digenean fauna

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In the Indo-Pacific/global scheme of knowledge regarding digenean richness, South Africa lags behind many other regions. As of now, only 75 digenean species are known from South African waters and, prior to this year, only one species (from freshwater) had been described from the country in the 21st century. New research efforts, with a focus on the fish-infecting digeneans of South African marine waters, aim to drive straight to the heart of this knowledge gap. Recent surveys, which encompassed parasitological dissections of 59 fish species and were conducted in various locations along the South African coast ranging from the temperate waters off Cape Town to the subtropical reefs of Sodwana Bay, have uncovered at least 40 digenean species from 14 families. These include representatives of large families known to be widespread across the Tropical Indo-west Pacific but have never before been recorded from South Africa, including the Bucephalidae, Cryptogonimidae, Fellodistomidae and Haplosplanchnidae. I will expound on some of these discoveries, highlighting instances of interest in terms of new species discovery, systematic and phylogenetic advances and the implications under-surveying this fauna has for marine conservation in South Africa.

TUESDAY, 14h45

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(036) Untangle the knot: Global turtle polystomatid flatworm diversity

Louis du Preez

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Polystomatids are monogenetic flatworms infecting all three Orders of amphibia, freshwater turtles, the Australian lungfish and the common hippopotamus. Since 1939 Turtle polystomes (Polystomoidinae) have been lumped into three genera namely *Polystomoides* with two pairs of hamuli, *Polystomoidella* with one pair of hamuli and *Neopolystoma* with no hamuli. Over the past decade polystome taxonomy received a fair deal of attention and today 30 genera are recognised. Of these, nine are known from turtles. The genera *Aussietrema, Apaloneotrema* and *Fornixtrema* are known from the surface of the eye, *Polystomoidella* and *Uropolystomoides* from the urinary bladder; *Manotrema* and *Uteropolystomoides* from the oral region; and *Pleurodirotrema* as well as *Polystomoides* from both the urinary bladder and the oral region. Turtle polystomatids are known to have Small to large ovoid body; haptor discoid with three pairs of haptoral suckers bearing skeletal elements; one or two pairs of hamuli when present; mouth subterminal; eyespots absent; intestine bifurcate with caeca not diverticulated, not joining posteriorly showing no anastomoses; ovary small, pre-equatorial; uterus present in a single genus, sacciform, pre-equatorial, holding up to 20 eggs operculated; vaginae antero-lateral, pre-ovarian; small to big, genital bulb armed with as many as 130 genital spines; vitellarium throughout body proper or in two lateral columns along gut caeca; testis compact, smooth to lobed, midbody, post-equatorial; eyes.

TUESDAY, 15h00

THEME: PARASITE TAXONOMY AND SYSTEMATICS

(012) Aspects of the morphology and taxonomy of *Dactylogyrus* Diesing, 1850 species parasitising cyprinids in the Vaal River system, Gauteng, South Africa

Mpho Maduenyane[1], Quinton Marco Dos Santos[1] & Annemariè Avenant-Oldewage[1]

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The genus *Dactylogyrus* Diesing, 1850 consists of over 900 nominal species globally, however, the numbers continue to rise as more species are being described. In South Africa, 18 species have been

reported from cyprinid hosts six of these from the Vaal River system. The latter six species were only described with standard light microscopy (LM) and have never been studied with scanning electron microscopy (SEM), with the majority of these species lacking genetic data as well. The aim of this study was to conduct further morphological and molecular analyses of *Dactylogyrus* species infecting cyprinids in the Vaal River system, Gauteng. The methodology included LM, SEM and molecular analysis. Light microscopy comprised the examination of flattened whole worms mounted in glycerine ammonium picrate and generating point-to-point measurements and line drawings of the copulatory organs and haptoral sclerites. Scanning electron microscopy included the digestion of soft tissue and examination of isolated sclerotised structures. Molecular analysis included characterisation of the 18S and internal transcribed spacer (ITS) 1 to 5.8S rDNA regions. The current study presents the first SEM of sclerotised structures and additional or new genetic data for *Dactylogyrus* species from cyprinids in the Vaal River system contributing to the limited taxonomic information available. This study also includes an updated distribution status record and species-host checklist of *Dactylogyrus* species and their cyprinid hosts for the system.

TUESDAY, 15h45

(016) The Diplozoinae of Africa: Revision of two taxa

Quinton M. Dos Santos[1] & Annemariè Avenant-Oldewage[1*]

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Recently, four species of Diplozoinae have been described from Africa. Three of these species were described from South Africa, *Paradiplozoon ichthyoxanthon*; *Paradiplozoon vaalense* and *Paradiplozoon krugerense*, and one species from Morrocco, *Paradiplozoon moroccoense*. The descriptions or subsequent studies of these species provide sufficient morphometric data required to differentiate diplozoid taxa, as well as sequence data for the second internal transcribed spacer (ITS2) rDNA. However, two more species occur in Africa, *Paradiplozoon ghanense* and *Paradiplozoon aegyptense*, and their descriptions lack crucial morphometric data for comparative taxonomic studies. To revise and supplement the taxonomic data for these two species, specimens of both species from museum collections were studied using light microscopy. The type material for *P. aegyptense* was studied, alongside paratype and voucher material, but only vouchers of *P. ghanense* could be located. However, the voucher material of *P. ghanense* bore a striking resemblance to the illustrations in the description, promoting the designation of this material as type and paratype material. Additionally, a voucher specimen of *P. aegyptense* was more similar to *P. ghanense*, thus it is designated as a voucher of the latter species. Full morphometric accounts for both species were completed and compared to other diplozoid taxa. The result supported the distinctness of *P. ghanense* and *P. aegyptense* from other African Diplozoinae, but there was a high similarity between *P. aegyptense* and *P. krugerense*. The use of molecular approaches is required to support species distinctness further, but accessibility to fresh material for *P. aegyptense* and *P. ghanense* remain problematic.

TUESDAY, 16h00

(027) Another fish parasite invasion?

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Neoergasilus japonicus (Harada, 1930) (Crustacea: Copepoda), a fish ectoparasite indigenous to eastern and southern Asia, has been introduced to Europe and North and South America, where it is spreading at an alarming rate. It was reported that *N. japonicus* infected 88 species and 3 subspecies of fishes worldwide [1], confirming their opportunistic nature. Furthermore, they can swim efficiently, and even mature females can change hosts [2]. It was also collected from the Vaal and Limpopo river systems in South Africa. This presentation describes the morphology of the wound-inflecting structures in *N. japonicus* and connects their morphology to the pathological effect observed on *Tilapia sparrmanii* collected from the Padda Dam in the Braamfontein Spruit on the University of Johannesburg campus. The DNA profile of parasites collected in the Vaal and Limpopo river systems was compared to that of parasites collected in Japan, and it was confirmed that it is the same species. Host tissue with parasites attached to the host was prepared for histological sections in resin and subsequently stained with haematoxylin and eosin and studied with light microscopy (LM). Additional specimens were prepared for study with scanning electron microscopy (SEM) using standard techniques. Some specimens were removed from the host to expose the wound-inflicting structures and studied with LM and SEM. Adult females attach by inserting the hooked tips of the antennae into the epidermis. The maxillulae are minute and armed with sharp tips. The mandibles also have sharp tips on the endopodite and terminally on the exopodites, setae. The maxillae are much larger and equipped with setae arranged in a brush-like formation. These structures are used to strip the epidermis of the host and brush it into the buccal cavity. The presence of host cells in the intestine of the parasite confirms that adult females consume host tissue. Removing the epidermis leaves the dermis exposed to opportunistic secondary infections. The microscopic size of the parasite prevents casual observation, even for the keen, trained eye, and its occurrence in Africa is, therefore, probably underreported.

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TUESDAY, 16h15

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(034) Development of an interactive electronic identification key for South African *Culicoides* species

Karien Labuschagne

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Correct identification of any species is a prerequisite of any biological study particularly for species comparative studies. Though morphological taxonomy is the most common identification method used by biologists worldwide, funding opportunities for pure taxonomic studies are limited. Morphological taxonomy also requires expertise that are unfortunately declining as existing taxonomists retire or leave due to funding constraints. Ideally a specimen should be compared with the original type specimen but often researchers are reliant on the published description or dichotomous identification keys. These descriptions and or identification keys rely heavily on good descriptions of comparative characteristics,

clear photographs or drawings of the characters depicted. The internet, software and coding advances has transformed taxonomy worldwide, through opening communication channels, open-access publication, and interactive identification keys. Mathieu *et al* [1] developed an interactive identification key for *Culicoides* females from the Western Palaearctic region based on Xper^2 version 2.0 software developed by Ung *et al* [2]. The Xper^2 software is used to edit and manage a morphological database and create interactive keys. It does not require advanced programming, is easy to use and can be freely downloaded. An interactive identification key, comparable to the one developed by Mathieu *et al* [1] and based on the same morphological characters were developed for South African female *Culicoides* species. The morphological characters broadly cover the wing, head, abdomen, and leg with sub characters for each of the main characters. Shortly, the key works by examining specific sub characters and choosing the correct characters for the specimen being examined. Only species with specific characters will remain within the species list while the others are eliminated from the list ultimately leaving the researcher with one species remaining as each relevant character is chosen. The ultimate goal is to expand the key to include all Afrotropical species before publication of it. This development represents the first electronic key for Afrotropical *Culicoides* species.

References:

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TUESDAY, 16h30

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(040) *Tetracampos ciliotheca* and *Glossidium pedatum* from *Clarias gariepinus* (Burchell, 1822) in Lake Ol'Bolossat, Kenya

Joan M. Maraganga[1] & Nehemiah M. Rindoria[2,4], George M. Morara[3] & Wilmien J. Luus-Powell[5]

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Platyhelminthes comprise over 13000 known species commonly referred to as flatworms and include several life forms of parasitic and free-living worms. These are often distinguished by their unique and diverse morphological features, some of which are still inadequately described. A parasitological study was carried out in May 2023 with an aim of identifying gastrointestinal platyhelminths infecting North African catfish *Clarias gariepinus* (Burchell, 1822) in Lake Ol'Bolossat, Kenya. The fish were collected with seine and gill nets and dissected for the examination of gastrointestinal parasites. The investigation revealed two platyhelminths: a bothriocephalidean tapeworm *Tetracampos ciliotheca* Wedl, 1861 and plagiorchioidean digenean *Glossidium pedatum* Looss, 1899 from anterior and posterior parts of intestine, respectively. Prevalence and mean intensity were calculated and recorded as 100%, and 3.9, respectively, for *T. ciliotheca* and 14.2%, and 4.0, respectively, for *G. pedatum*. The parasites were morphologically studied using light microscopy (LM) and scanning electron microscopy (SEM). The morphology of these parasites under LM and SEM, and distinctive differences on already described specimens are discussed. Genetic analysis of these parasites is under consideration. The findings of the

present work add additional information to existing morphological descriptions and extends the geographical records of the two parasites to Kenya.

TUESDAY, 16h45

(047) Scanning electron microscopy and molecular data for a *Lamproglena* sp. from *Labeobarbus altianalis* in Kenya

Nehemiah M. Rindoria[1, 2], George N. Morara[3], Willem J. Smit[1], Coret van Wyk[4], Nico J. Smit[4], & Wilmien J. Luus-Powell[1]

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Lamproglena von Nordmann, 1832 is the second largest group of Lernaeidae Cobbold, 1879, in which females are parasitic and males are usually found associated with females on the gills of most actinopterygians. Until now, morphological descriptions resulted in 38 nominal species of *Lamproglena*, out of which only four have been characterised genetically using small and large subunit ribosomal rDNA (18S, 28S rDNA), with no genetical record of cytochrome *c* oxidase subunit 1 (*cox*1). Between March and August 2022 parasitological surveys were caried out in River Nyando of Lake Victoria Basin, Kenya, where a parasite of the genus *Lamproglena* was collected from gills of a cyprinid, Ripon barbel, *Labeobarbus altianalis* (Boulenger, 1900). A combined approach of light, scanning electron microscopy and molecular techniques were employed in studying this copepod. Morphological analyses revealed similarity of the present material with *Lamproglena barbicola* Fryer, 1961 in most aspects but differed by possessing a fringe of setae on the antennule. Bayesian inference and maximum likelihood analyses of the 18S and 28S rDNA dataset placed the species within the genus *Lamproglena* but it also revealed that this species is genetically distinct from the four known *Lamproglena* taxa available on GenBank. No comparison for mitochondrial *cox*1 sequences generated during this study could be made as there is no data currently available from GenBank for this gene region. This study adds new taxonomic information on morphology using scanning electron microscopy and provides the first ribosomal and mitochondrial genetic data for this parasitic copepod. Further, this study also adds to the available molecular data for *Lamproglena* and forms baseline data for the phylogeny of this genus. This work is based on the research supported in part by the Department of Science and Innovation and the National Research Foundation of South Africa (Grant Number 101054).

TUESDAY, 17h00

-- END ORAL PRESENTATIONS --

Poster Presentations

in order of appearance as on the programme

POSTER SESSION 1 – MONDAY 18 SEPTEMBER, 12h15

(017) Detection of the brown ear tick, *Rhipicephalus appendiculatus*, in the Free State province

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Hard ticks are haematophagous ectoparasites that feed on a wide range of hosts including cattle. They are responsible for substantial economic losses in the livestock industry worldwide due to a decrease in production performance by the host as well as increased costs associated with acaricides for control and remedies to treat tickborne diseases. One of these tick species is the brown ear tick, *Rhipicephalus appendiculatus*, which is an important vector of Corridor disease and East Coast fever in South Africa. Both diseases are controlled by the state according to the Animal Disease Act 35 of 1984. Therefore, it is important to know the distribution of the brown ear ticks to prevent economic losses. This study determined the tick composition on Paradys Experimental farm in Bloemfontein by collecting ticks from 30 cross-bred animals once a month for a 12-month period. All the collected ticks were identified up to species level with a dissection microscope. The following tick species were observed *Rhipicephalus appendiculatus*, *Rhipicephalus evertsi eversiti*, *Hyalomma rufipes* and *Hyalomma truncatum*. Three of the species are known to occur in the Free State. Previously, *R. appendiculatus* has been known to occur along the coast of South Africa from the Eastern Cape to KwaZulu-Natal and adjacent inland areas. To date it was only speculated that these ticks occur in the Free State province. Studies have noted the existence of *R. appendiculatus* in Parys and Kroonstad in the Free State. This study showed that the brown ear ticks was either introduced to the Free State or it has always been there but have not been recorded. Due to climate changes and movement of cattle, ticks can be found in new areas. This poses a great risk for animal health and food security especially in close proximity of buffaloes.

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(029) Geographic distribution of boophilid ticks in communal grazing cattle in the north-eastern region of the Eastern Cape Province, South Africa

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The boophilid ticks are regarded as highly adaptive tick species in tropical and subtropical regions and considered to be the most economically important ectoparasites to cattle worldwide. To that, a geographical survey to investigate the distribution of boophilid ticks on grazing cattle was conducted

seasonally between October 2018 and September 2019 at Elundini, Senqu and Walter Sisulu Local Municipalities in the north-eastern region of the Eastern Cape Province (ECP). Ten cattle were selected randomly during the tick sampling at each locality. Ticks were carefully removed from cattle and placed into sampling tubes containing 70% ethanol. During tick sampling, special attention was paid to the tick predilection sites such as lower perineum, neck, dewlap and ventral body parts which are the preferred sites for blue ticks. Based on the morphological traits, a total of 6176 ticks belonging to two boophilid tick species of Rhipicephalus were identified: *Rhipicephalus decoloratus* (98.30%) and *Rhipicephalus microplus* (1.70%). Locality and season significantly influenced boophilid tick distribution ($P < 0.05$). *Rhipicephalus decoloratus* had a significantly higher prevalence ($P < 0.05$) in Elundini during the hot-dry (3.37 ± 0.121) and hot-wet (3.35 ± 0.121) seasons compared to other localities. In Senqu, *R. microplus* had high counts ($P < 0.05$) during the post-rainy season (1.06 ± 0027) compared to other localities. Interestingly, the current study recorded Asiatic invasive pantropical blue tick (*R. microplus*) for the first time in the north-eastern region of the ECP. This tick is of great veterinary economic importance locally and globally, and thus necessitates continuous monitoring and control.

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(039) Revisiting the diversity and phylogenetic relationships of trypanosomes (*Trypanosoma*) infecting pelomedusid (Pelomedusidae) freshwater turtles in Southern Africa

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Species of *Trypanosoma* infecting reptiles are poorly understood and understudied. The study of trypanosomes infecting turtles could lead to a greater understanding of the genus and its evolutionary history. The present study re-evaluates and classifies previously described species of *Trypanosoma* in freshwater pelomedusid turtles and characterises a new species using morphological and molecular data. The trypanosome sequences from the present study clustered together within a phylogenetic clade with other freshwater turtle, platypus, and clawed frog trypanosomes. Three distinct genotypes were observed, while being supported with morphometric characterisation. This study provides the first morphological descriptions and molecular data of South African turtle trypanosomes, setting a base for future research on the reptile trypanosomes of Africa.

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(049) Metazoan parasites of the southern mouthbrooder *Pseudocrenilabrus philander* (weber, 1897) from Nwanedi and Luphephe rivers in Limpopo province, South Africa

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Metazoan parasites can provide a perspective on the health status of their host and surrounding ecosystem. In recent years, there has been increasing interest in using metazoan parasites as bio-indicators of aquatic systems. The current study focused on examining the metazoan parasites associated with the southern mouthbrooder *Pseudocrenilabrus philander* (Weber, 1897) as a means to determine the ecological state of Nwanedi and Luphephe rivers, in the Limpopo River System. Using electroshocking a total of 38 specimens were caught from Nwanedi (n = 28) and Luphephe (n = 10) rivers during a summer 2021 and winter 2022 survey. The morphometrics of fish specimens including the presence of ecto- and endoparasites, observed using a stereo microscope, were recorded. Based on morphological characteristics, parasites identified were the monogenean; *Cichlidogyrus philander* from the skin and gills, the cestode; *Neogryporhynchus lasiopeius* and the nematode; *Rhabdochona* sp. both extracted from the intestine. *Cichlidogyrus philander* and *N. lasiopeius* were recorded from both rivers during each survey, whereas *Rhabdochona* sp. and digenean larvae were recorded during the summer and winter surveys, respectively. *Cichlidogyrus philander* and *Rhabdochona* sp. represent new host and distribution records from Luphephe River. To identify *Rhabdochona* specimens to species level scanning electron microscopy and molecular characterisation will be done. This research was financially supported by the Department of Science and Innovation and National Research Foundation, SARChI Chair in Ecosystem Health (Grant Number 101054).

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(054) Evaluation of host metabolome in goats following infection with *Haemonchus contortus*

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Haemonchus contortus is regarded as one of the most pathogenic gastrointestinal nematodes (GIN) causing major economic losses worldwide in the production of small ruminants especially sheep and goats. Anthelmintic drugs have been used for decades to treat *H. contortus* infections, however, the excessive use of these drugs led to the anthelmintic resistance. The current commercial vaccine (Wirevax) available against *H. contortus* infection, is licensed for use only in sheep, and it has been shown to be effective after repeated administration, making the vaccine expensive. Both the anthelmintic drug resistance, and the drawbacks of the current vaccine show an urgent need for alternative measures to control *H. contortus* infections including new drugs, diagnostic markers and/or improved vaccines. Several Omics approaches including metabolomics have been applied to studying host-pathogen interactions with the aim of identifying new drug targets, new diagnostic markers and/or new vaccine candidates. Metabolomics, is a high throughput omics approach where all the metabolites in a biological sample can be profiled, thus describing the metabolome of a particular host. This approach has been used to study the effect of other helminth species on the metabolome of hosts like humans, mice and pigs. However, this approach has not yet been applied to investigating the effect of *H. contortus* infection on the metabolome of the ruminant host, hence, the aim of our study is to evaluate the global metabolome of goats following experimental primary and secondary infection with *H. contortus*. To achieve this aim, serum samples will be collected weekly from infected and uninfected goats for five weeks to profile serum metabolites using Two–Dimensional Gas Chromatography and Time-of-Flight Mass Spectrometry. Metabolome data will be analysed using MetaboAnalyst 5.0 and Pathway Analysis (MetPA) to identify metabolites and metabolic pathways affected by *H. contortus* infection respectively.

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(055) Evaluation of immune response and gut microbiome in *Haemonchus contortus* infected goats

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Haemonchosis is a highly pathogenic disease of small ruminants, including sheep and goats, caused by the gastrointestinal nematode (GIN), *Haemonchus contortus*. This parasite feeds on blood, causing anaemia, weight loss, and reduced productivity, eventually leading to the death of these animals. The deaths of livestock and the cost of treatment and other preventative measures result in major economic losses globally. Currently, *H. contortus* infections are controlled using anthelmintic drugs; however, there is a growing widespread resistance to the available drugs. This necessitates the need for the development of alternative control measures, like new therapeutics. The gut microbiome, which is responsible for stimulating mucosal and systemic immune development and preserving natural immune homeostasis, has been explored as a potential target for the development of therapeutics. During *H. contortus* infection, the ruminant gut microbiome co-exists with the nematode. Several studies performed in sheep and goats showed that *H. contortus* infection alters the composition, structure, and function of the gut bacterial microbiome. However, no study has investigated how these alterations influence the host immune response to the *H. contortus* infection. Studying how alterations in the gut microbiome affect the host immune responses during infection can help identify gut microflora that are essential for immune modulation, which can then be explored as possible targets for new therapeutics. Thus, this study aims to evaluate the gut microbiome and immune responses of goats after primary and secondary experimental infection with *H. contortus*. To achieve this aim, faecal samples will be collected before infection (day 0) and 3, and 21 days post primary and secondary infection for microbiome analysis using 16S rRNA gene sequencing. Blood samples will also be collected at the same time points for haematological and cytokine expression analysis. At the end of the experiment, all goats will be euthanized, and abomasum fluids will be collected for microbiome analysis, while lymph nodes and abomasum mucosa will be collected for cytokine analysis as above.

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(056) Parasites of the Mozambique tilapia (*Oreochromis mossambicus*) from a natural system and fish farm in Namibia

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A parasitological study was conducted on commercially farmed *Oreochromis mossambicus* (Mozambique tilapia) from Hardap Inland Aquaculture Centre (HIAC) and wild fish from a natural system, Hardap Dam (HD). Fish were collected in November 2021 and August 2022 using a scoop net at the farm and gill nets in the natural system. Monogeneans were mounted on slides in glycerine ammonium picrate, whereas all other parasites were fixed and preserved according to standard methods for each parasite group. Representatives of all parasites were stored in 96% ethanol for molecular characterisation. Numerous ecto- and endoparasites were recorded from this fish species including trichodinids, monogeneans, digenean larvae, larval nematodes and copepods. The prevalence (P) for each is indicated. The recorded parasites included eight different species. Ectoparasites comprised of trichodinids (HD, P=20,0%; HIAC, P=66,6%) from the skin, two monogenean species e.g.

Cichlidogyrus halli (HD, P=23,3%; HIAC, P=33,3%) from the gills and *Gyrodactylus thlapi* (HD, P=13,3%; HIAC, P=20,0%;) from the skin and the copepod *Neoergasilus japonicus* (HD, P=40%; HIAC, P=3,3%) from the skin and fins. Endoparasites comprised of the monogenean *Enterogyrus* sp. (HIAC, P=10,0%) from the stomach, the larval nematode *Contracaecum* sp. (HD, P=63,3%; HIAC, P=10,0%) from the body cavity, gryporhynchid cestode larvae from the intestinal layer (HD, P=20,0%; HAIC, P=26,6%) and unidentified digenean metacercaria (HD, P=3,3%; HAIC, P=3,3%) encysted on the fins. All parasites except for *Enterogyrus* sp. occurred in both the natural system and fish farm. The prevalence and intensity of trichodinids was significantly higher in farmed fish whereas *N. japonicus* was more prevalent in the natural system. The infestation levels of none of the parasites were alarming, however, it can increase and become detrimental if fish become stressed, especially in aquaculture facilities. The study includes new host and distribution records for Namibia. This work was partly funded by the DSI-NRF SARChI Chair in Ecosystem Health (101054).

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(057) Redescription of the parasitic copepod *Rhinergasilus piranhus* Boeger & Thatcher, 1988 (Cyclopoida: Ergasilidae) based on an integrative approach

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In Brazil, the copepod family Ergasilidae Burmeister, 1835 represents the most specious taxa among parasitic crustaceans with over 70 reported species from 19 different genera, mostly endemic to the country [1]. Although most ergasilids are found attached to the gills, there are several species that specialize in parasitizing the nostrils [2]. The freshwater ergasilid, *Rhinergasilus piranhus* Boeger & Thatcher, 1988 is one of the oldest Brazilian species, it was originally described based on specimens found inside the nostrils of the sarralmid fish *Pygocentrus nattereri* Kner, 1858 or "red piranha" sampled in Marchantaria Island, Amazonas state, Brazil. Since then, this species has been reported in different locations and hosts throughout the country [3]. During a parasitological survey of fishes from the Pardo River, São Paulo state, Brazil (June 2020 to December 2022), we detected several ergasilids parasitizing the nostrils of two small characids or "lambaris", namely: *Astyanax lacustris* (Lütken, 1875) (n = 93) and *Psalidodon bockmanni* (Vari & Castro, 2007) (n = 142). In the laboratory, copepods were carefully removed using fine needles and then stored in glass vials filled with 70% ethanol for morphological identification. Some copepods were also preserved in 96% ethanol for molecular characterization (in progress). Type specimens of *R. piranhus* (including Holotype and Paratypes) were borrowed from scientific collections, but the poor condition of the specimens prevented the visualization of most diagnostic features. A morphological analysis of these copepods allowed us to identify them as *R. piranhus*, however, we also observed several discrepancies regarding the original description, such as: cephalosome and first somite not fused, different number of setules on legs/antennules, and egg sacs multiseriate. Previous features are usually difficult to visualize in ergasilids, especially in old and/or small species like *R. piranhus*, and therefore do not indicate the need to designate a new species. Additionally, the present specimens also showed new diagnostic features not describedqoberserved in the original description such as spine-like structures on cephalosome/antenna, pores distributed throughout the body, claw's tip with rounded projection, among others. The present study aids in improving the knowledge about ergasilids in Brazil through the redescription of this important species.
Reference

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2. R.B. Narciso, and R.J. Silva, "Two *Gamispatulus* Thatcher & Boeger, 1984 (Cyclopoida: Ergasilidae) from *Schizodon intermedius* Garavello & Britski (Actinopterygii: Anostomidae), with description of a new species", Zootaxa, 4803, June 2020, pages 463 to 482.
3. R.B. Narciso, et al, "A New Species of *Rhinergasilus* Boeger et Thatcher, 1988 (Copepoda: Ergasilidae) from Gills of *Astyanax fasciatus* (Cuvier, 1819) (Actinopterygii: Characidae)", Acta Parasitologica, 65, January 2020, pages 327 to 334.

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(058) Risk assessment for three *Dactylogyrus* species in South Africa: Prospects for management and policy implications

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The utilization of non-native fish is a common practice to enhance aquaculture and fisheries. Although these fishes may be introduced into the natural environment, their impact on native biodiversity is insignificant. However, evaluating the risk associated with introducing generalist parasites that are more likely to be transported with non-native fishes, establish, and infect new hosts is crucial. Non-native parasites possess the potential to adversely affect native hosts, leading to negative consequences such as stunted growth, diminished condition, and reduced energetics. Therefore, it is essential to evaluate the risk associated with these parasites. In this study, we employed an innovative non-native pathogen risk assessment scheme designed to support the management of non-native fish parasites during both pre- and post-introduction phases. Specifically, we assessed the invasion risk posed *by Dactylogyrus lamellatus*, *Dactylogyrus extensus,* and *Dactylogyrus minutus* using four modules: Initial hazard identification, Long-term impact assessment, Management and regulation of assessed risk, and Risk communication. Our assessment revealed that all three species are highly susceptible to native species, displaying substantial colonization potential and posing a significant risk of disease introduction. Additionally, there is a moderate potential for disease introduction from *Dactylogyrus minutus*. Regarding the impact of parasites, the three species under study would have severe consequences upon invasion, as indicated by Module 3b on Parasite impact. Consequently, effective long-term management strategies for non-native fish parasites, based on parasite impact and distribution, necessitate developing and implementing fisheries management practices that minimize their impact (referred to as D in the scheme). It is essential to maintain controls, if necessary, to protect specific sectors of fisheries, defined geographical localities, or susceptible host species. In conclusion, we provide recommendations for managing and regulating alien hosts and parasites under the National Environmental Management: Biodiversity Act 10 of 2004 alien and invasive species regulations. These recommendations aim to ensure the preservation of native biodiversity and the sustainable functioning of aquatic ecosystems.

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(061) Morphological and molecular characterisation of a species of *Longicollum* Yamaguti, 1935, a fish parasitic acanthocephalan infecting two species of sea breams off the South Coast of South Africa

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The current knowledge of acanthocephalans from marine fish in South Africa is limited to six species from five families reported from marine and brackish fishes. These species include representatives of the genera *Bolbosoma* Porta,1908, *Corynosoma* Lühe, 1904, *Longicollum* Yamaguti, 1935, *Rhadinorhynchus* Lühe, 1911 and *Transvena* Pichelin et Cribb, 2001. Two records exist for the genus *Longicollum* Yamaguti, 1935 in South Africa. The first is of *Longicollum chabanaudi* Dolfus & Golvan, 1963 described from the Lemon sole, *Barnardichthys fulvomarginata,* and the second a *Longicollum* sp. from the Blackhand sole, *Pegusa nasuta*, both collected off the West Coast of South Africa. During parasitological surveys on the South Coast of South Africa, acanthocephalans were found in two species of seabreams: the Zebra, *Diplodus hottentotus*, and the Cape white seabream, *Diplodus capensis.* Acanthocephalans were morphologically characterised with the aid of differential interference contrast compound microscopy and scanning electron microscopy. Morphometrical data was obtained by measuring morphologically relevant internal structures and based on both morphology and morphometrics, the species was identified as a member of the genus *Longicollum.* Molecular characterisation was done by amplifying the 18S rRNA and CO1 genes, which were sequenced and subsequently aligned for the construction of a phylogenetic tree. Molecular results of both genes grouped the present species with other members of the family Pomphorhynchidae Yamaguti, 1935 supporting its morphological identification as a species of *Longicollum*. This study expands the knowledge on the occurrence of marine acanthocephalans in South Africa by using an integrated approach consisting of morphological and molecular characterisation and is also the first molecular characterisation of any species of *Longicollum* from southern Africa.

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(062)Molecular and morphological characterisation of four species of fish parasitic *Trypanosoma* Gruby, 1843 from the South Coast of South Africa.

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The genus *Trypanosoma* comprises a range of unique flagellate and unicellular obligatory haemoparasites. Species of this genus have been identified in all vertebrate classes on every continent (including their water bodies), excluding Antarctica. They are causative agents of trypanosomiasis, a serious and occasional fatal disease in domesticated animals and humans. However, the trypanosomes of fishes are largely understudied, with few studies focusing on their complete life cycles and ecological interactions. Moreover, the phylogenetic position of several species is yet to be confirmed. Piscine hosts have the potential to facilitate the transmission of zoonotic trypanosomiases and provide important insights into the species descriptions of the genus *Trypanosoma*. In general, the parasites of marine

fishes in the South African biogeographical regions are considered to be understudied. In particular, marine fish trypanosomes are greatly underrepresented in the few parasitological studies, with only two marine fish trypanosomes known from this region. Thus, the aim of this project was to elucidate the biodiversity and systematics of marine fish trypanosomes along the southern African coast by providing detailed molecular and morphological characterisation of these trypanosomes. Blood was collected from 379 individual host fishes representing 31 species at the Tsitsikamma section of the Garden Route Nation Park and Chintsa East from 2020 to 2023. Giemsa-stained thin blood smears were screened for trypanosomes and were morphologically characterised. Molecular analyses of the 18S rRNA gene region were performed on the whole blood for smears that were positive with trypanosome infection. Using complementary morphological and molecular data, four *Trypanosoma* species, most probably new to science, are herein described from the South African mullet (*Chelon richardsonii*), Barehead goby (*Caffrogobius nudiceps*), Klipfish (*Clinus superciliosus*) and Sand steenbras (*Lithognathus mormyrus*).

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(063) Water quality and parasite diversity of Mozambique tilapia from the Limpopo River System

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The present study deals with determining the water quality and parasite diversity of Mozambique tilapia, *Oreochromis mossambicus*, at two localities in the Limpopo River System, Nwanedi-Luphephe Dam and Nwanedi River. Sixteen specimens were collected from the Nwanedi-Luphephe Dam and 11 specimens from the Nwanedi River and examined for metazoan parasites. Fish specimens were collected in June 2022 using gill and seine nets and sacrificed by cutting the spinal cord behind the head. All endo- and ectoparasites were fixed and preserved using standard methods and stored in 70% ethanol. *In situ* water parameters were measured using a handheld multi-parameter instrument taking three replicate readings for each parameter at the two different localities. In addition, water samples were collected at both localities and sent to an accredited laboratory where selected metals and nutrients were analysed. The majority of the water quality parameters, metals, and nutrient concentrations for both localities were within the Target Water Quality Range (TWQR) for aquatic ecosystems. Parasitological data from Nwanedi-Luphephe Dam includes *Cichlidogyrus halli* (prevalence (P) 37%, mean intensity (MI) 18), *Enterogyrus* sp. (P 6%, MI 1), unidentified digenean larvae (P 93.8%, MI 32), *Amirthalingamia macracantha* (P 6%, MI 1) and *Neogryporhynchus lasiopeius* (P 6%, MI 1) *Contracaecum* sp. (P 25%, MI 2), *Neoergasilus japonicus* (P 38%, MI 15) and *Dolops ranarum* (P 31%, MI 2). Nwanedi River: *Cichlidogyrus halli* (18% P, MI 2), unidentified digenean larvae (P 64%, MI 3), *Clinostomum* sp. (P 55%, MI 3) and *Contracaecum* sp. (P 9%, MI 1). The fish collected from Nwanedi-Luphephe Dam had a higher parasite species richness compared to the fish from the Nwanedi River. The highest prevalence levels were recorded for the unidentified digenean larvae from fins of the fish at both localities. Several parasites recorded from this study represent new host and locality records contributing to biodiversity and distribution records. This work is based on research supported by the Department of Science and Innovation and the National Research Foundation of South Africa (Grant Number 101054).

POSTER SESSION 2 – TUESDAY 19 SEPTEMBER, 12h15

(064) Occurrence of *Lamproglena cleopatra* Humes, 1957 parasitizing gills of *Labeo victorianus* Boulenger,1901 in Kenya

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This study reports on a crustacean parasitising the gills of *Labeo victorianus* Boulenger, 1901 collected between May 2022 and March 2023 from River Nyando, Kenya. Using scanning electron microscopy (SEM) and comparisons with previous literature the parasite was identified as *Lamproglena cleopatra* Humes, 1957. Detailed SEM images revealed additional taxonomic features which are discussed in comparison with previously available records. Molecular analysis using genetic markers of 18S, 28S rDNA and cytochrome *c* oxidase subunit 1 were done. The results obtained from 18S and 28S rDNA showed that the present specimens were distinct from all other members of the same genus downloaded from GenBank with genetic pairwise distances of 0.1–2.0% (1-30bp) and 7.1–23.1% (47–159bp), respectively. The two ribosomal DNA markers produced nearly similar topologies with insignificant intraspecific branching. Since there was no *cox*1 sequences in GenBank it became impossible to construct a phylogeny tree for this gene region. This study adds new genetic data to existing phylogeny. This work is based on the research supported in part by the Department of Science and Innovation and the National Research Foundation of South Africa (Grant Number 101054).

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(065) Metazoan parasites of canary kurper, *Chetia flaviventris* in the Limpopo and Olifants River Systems: new locality records

Fhulufhelo Mulaudzi[1], Willem J. Smit[1], Andre C. Hoffman[2], Iva Přikrylová[1,3], Nehemiah M. Rindoria[1,4] & Wilmien J. Luus-Powell[1]

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The study focused on evaluating the diversity of metazoan parasites infecting *Chetia flaviventris* Trewavas, 1961 in two impoundments within Limpopo Province. A total of 72 fish specimens were collected from Doorndraai Dam (Limpopo River System) and Rust de Winter Dam (Olifants River System). The latter locality serves as an extralimital distribution record for this fish species. Parasites were collected, fixed, and preserved using standard methods for each parasite group. Infection indices and parameters of species diversity and richness were evaluated. The following parasites were recovered: nematode *Contracaecum* sp., metacercarial stage of digenean *Diplostomum* sp. and gryporhynchid metacestode *Neogryporhynchus lasiopeius*, monogenean *Cichlidogyrus* sp., and a copepod *Neoergasilus japonicus* were found from *C. flaviventris* from both localities. Monogenean *Enterogyrus coronatus*, gryporhynchid metacestode *Paradilepis scolecina* and two ectoparasitic branchiurans (*Argulus japonicus* and *Dolops ranarum*) were limited to Doorndraai Dam. *Neoergasilus japonicus* infected 90% of the fish with a mean intensity of 34.08 at Doorndraai Dam, while *Cichlidogyrus* sp. infected 75% of the fish with a mean intensity of 4.29 at Rust de Winter Dam. Relatively low mean intensity levels (between 1.00 and 10.86) for all endoparasites in this study indicate that the parasite infections for endoparasites did not reach alarming high numbers. Diversity and richness parameters showed a greater diversity and richness at Doorndraai Dam, yet species were more evenly distributed at Rust de Winter Dam. The water quality was in an oligotrophic condition which is associable with the variety of parasites on the hosts. The study reports new locality records for *N. lasiopeius* and *P. scolecina*. This work is based on the research supported by the Department of Science and Innovation and the National Research Foundation of South Africa (Grant Number 101054).

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(066) Parasite diversity of *Coptodon rendalli* from Doorndraai Dam, Nwanedi-Luphephe Dam and Nwanedi River, South Africa

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Diversity records of fish parasites are important for future biomonitoring of aquatic ecosystems. Limited information is available for the parasite diversity of smaller cichlids in South Africa. This study investigated metazoan parasites associated with Redbreasted tilapia, *Coptodon rendalli* (Boulenger, 1897). A total of 35 fish were sampled using gill nets, a seine net and conventional fishing gear at three localities: Doorndraai Dam (n=20), Nwanedi-Luphephe Dam (n=5) and Nwanedi River (n=10) all in Limpopo River Basin within the Limpopo Province. Fish were sacrificed by cutting through the spinal cord, dissected, and examined for metazoan parasites. The monogeneans from skin and gills were mounted on slides in glycerine ammonium picrate. Other parasites were fixed and preserved using standard methods and stored in 70% and 96% ethanol for morphological and molecular analysis, respectively. The following parasites were recorded from Doorndraai Dam: *Cichlidogyrus* sp. from the gills (prevalence (P)=70%, mean intensity (MI)=5.43), *Neoergasilus japonicus* from the fins (P=95%, MI=29.05), unidentified digenean larvae from the fins (P=5%, MI=1.0), *Dolops ranarum* from inside the operculum (P=5%, MI=1.0), gryporhynchid cestode larvae in the intestinal layer (P=10%, MI=1.0), unidentified nematode larvae from the body cavity (P=5%, MI=14.0), *Contracaecum* larvae from the body cavity (P=5%, MI=1.0) and *Clinostomum* metacercaria in the body cavity (P=5%, MI=7.0). Nwanedi-Luphephe Dam: *Cichlidogyrus* sp. from the gills (P=80%, MI= 10.0) and *N. japonicus* from the fins (P=100%, MI=109.80). The parasitological data from Nwanedi River: *Cichlidogyrus* sp. from the gills (P=30%, MI= 1.0) and *N. japonicus* from the fins (P=30%, MI=1.33). The high intensity levels recorded

for some parasites may have a negative effect on the host but none of the fish showed severe health problems. This work is based on the research supported by the Department of Science and Innovation and the National Research Foundation of South Africa (Grant Number 101054).

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(067) The effect of larval exposure to plastic pollution on the life history of the major malaria vector *Anopheles arabiensis* (Diptera: Culicidae)

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Microplastic pollution is a major concern for bodies of water worldwide. These common pollutants are a serious concern for aquatic organisms. Although most studies have focused on the effect on aquatic organisms, it is important to consider the short- and long-term effects on freshwater invertebrates. Mosquitoes spend their immature stage in water, and the larval environment is a critical determinant of adult life history. *Anopheles arabiensis* is a dominant vector species and a member of the *An. gambiae* complex. These species breed in clean, clear, temporary bodies of water. However, they are adapting to breeding in polluted water. One of the most common pollutants in their breeding sites, particularly in South Africa, are disposable nappies. In this study, we examined the effect of larval exposure to artificially degraded disposable nappies on two laboratory strains of *An. arabiensis.* One strain was insecticide resistant and the other insecticide susceptible. The insecticide resistant strain was more successful at breeding in polluted water, with a faster development time and higher pupation success. Exposure to this plastic pollutant significantly retarded development in both strains compared to untreated controls. The effect on adult longevity, insecticide resistance and microbiome composition were also examined. The findings suggest that larval exposure to plastic pollutants can alter the life history of this major malaria vector in an epidemiologically significant manner.

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(068) Digenean trematodes from North African catfish *Clarias gariepinus* in Lake Naivasha, Kenya

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Digeneans are endoparasitic flatworms in the Platyhelminthes with complex life cycles and distinct life stages that parasitise different host species. Members of this class have two suckers (oral and ventral) and the adult parasites live mostly within the digestive tract of vertebrates. A parasitological study was carried out in May 2023, in Lake Naivasha, Kenya with the objective of identifying digenetic trematodes

of a clariid North African catfish, *Clarias gariepinus* (Burchell, 1822). A total of 44 specimens of *C. gariepinus* were collected from Lake Naivasha using gill nets. The fish was euthanised by cervical dislocation posterior to the skull and dissected for examination of digeneans. Standard methods were used for fixation and preservation of parasites. A total of 474 digenean parasites were collected from the brain, eyes, and intestine. Infection parameters [prevalence (P) and mean intensity (MI)] were calculated for various parasites: *Diplostomum* sp. with P=72.73% and MI=13.63 (cranial cavity), *Tylodelphys* sp. P=40.91% and MI=1.44 (vitreous humor), and unidentified digenean with P=15.91% and MI=1.71 (intestine). The findings from this study shows that *Diplostomum* sp. was the most prevalent and the unidentified digenean least prevalent. Scanning electron microscopy and molecular analysis for these parasites are to be considered. This work is based on research supported in part by the Department of Science and Innovation and the National Research Foundation of South Africa (Grant Number 101054).

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(069) Life cycle stages and molecular phylogeny of *Hepatozoon fitzsimonsi* (Dias 1953) (Adeleorina: Hepatozoidae) in tortoises *Stigmochelys pardalis* (Cryptodira: Testudinidae) and ticks of the genus *Amblyomma* (Acari: Ixodidae) from South Africa

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Haemogregarines (Apicomplexa: Adeleorina) are commonly encountered haemoprotozoan parasites of reptiles, of which, the genus *Hepatozoon* appears to be the most prevalent. Species display a heteroxenous life cycle, requiring a vertebrate and invertebrate host. Based on relationships of haemogregarine genera inferred using the 18S rRNA gene, the genus *Hepatozoon* remains paraphyletic, which lead to a new genus being erected *Bartazoon* Karadjian et al., 2015, with solely haematophagous insects acting as vectors. *Hepatozoon fitzsimonsi* was one of the species proposed to be a member of *Bartazoon*. However, past research done on *H. fitzsimonsi* observed a close association with tortoises and ticks, observing what appeared to be sporogonic stages in ticks collected from tortoises. The present study aimed to revisit the potential of ticks as vectors for *H. fitzsimonsi* in tortoises, by (i) collecting tissue and ticks from tortoises, (ii) screening both microscopically for the presence of development stages respectively, and (iii) molecularly characterising these stages using fragments of the 18S rRNA gene to determine if they are that of *H. fitzsimonsi*. Fourteen tortoises were collected, including nine individuals of *Kinixys* spp. and five *Stigmochelys pardalis*. Ten of the 14 (71%) tortoises were infested with ticks belonging to three species of *Amblyomma*. As *Kinixys* spp. are known to harbour both *H. fitzsimonsi* and *Hemolivia parvula* concurrently, three of the *S. pardalis* were selected, two of these showing a peripheral blood infection with *H. fitzsimonsi*. Impression slides from ticks showed sporogonic stages within the haemocoel, molecularly comparing to *H. fitzsimonsi*. Furthermore, merogonic stages were observed in the liver of one *S. pardalis* infected with *H. fitzsimonsi.* The present study thus provides further support for ticks acting as the vectors of *H. fitzsimonsi* based on observation of its development stages in tortoises as well as the invertebrate (*Amblyomma* spp.), with these stages linked molecularly. This would be the second haemogregarine of tortoises for which ticks are the vector, and the first species of *Hepatozoon* infecting chelonians for which ticks have been identified as a definitive host. This will hopefully encourage further research into chelonian *Hepatozoon*, a research area that remains largely neglected at present.

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(070) Borneo's hidden connections: unveiling the enigmatic Corallanidae isopods and their elasmobranch hosts.

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Within Isopoda, representatives of four families have associations with fishes: Cymothoidae (obligatory parasites), Gnathiidae (only juvenile stages parasitic), Aegidae, and Corallanidae (adults are temporary parasites). Corallanidae includes parasitic isopods found in marine and freshwater ecosystems. These isopods exhibit micro-predatory behaviour, feeding on blood before detaching. While mainly present in tropical and subtropical regions, research on Corallanidae biodiversity and biogeography remains limited. Although some records of Corallanidae hosts exist, information regarding their association with elasmobranchs is lacking. Therefore, this project aims to contribute to the knowledge of Corallanidae species diversity in one of the world's most biodiverse oceans off Borneo and shed light on their host species interactions. The project objectives involve morphological and molecular characterization of Corallanidae specimens collected from Borneo, as well as identification of their host species. As part of a larger study on cestodes from Borneo elasmobranchs, 185 individuals from 33 different species were also screened for isopods. Out of the 33 elasmobranch species sampled, 3 were infested with Corallanidae isopods: Hasselt's bamboo shark (*Chiloscyllium hasseltii*), the brownbanded bamboo shark (*Chiloscyllium punctatum*), and the darkfinned numbfish (*Narcine maculata*). Among the 10 sampled individuals of Hasselt's bamboo shark, only one was infested with two corallanids. Out of the 30 sampled brownbanded bamboo sharks, three individuals had infestations ranging from 1–4 corallanids. Additionally, the single darkfinned numbfish collected harboured one corallanid. To identify the isopod species, morphological and molecular analyses were conducted. Based on morphological characterisation, all 12 corallanid specimens from the three hosts conformed to the morphology of species in the *Argathona macronema* (Bleeker, 1857) species complex. This is the first record of an *Argathona* species from Borneo, the first record of corallanids as parasites of elasmobranchs, and the first molecular analysis of a species of *Argathona*. Overall, this project will contribute to our understanding of Corallanidae host associations, specifically among elasmobranchs, and aid in resolving the taxonomy of the *Argathona macronema* complex. The collections for this work were supported by funds from US National Science Foundation grant award Nos. DEB 0103640, DEB 0542846, and DEB 0542941 to Janine N. Caira and Kirsten Jensen.

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(071) Parasite diversity and community structure of the Cape Stumpnose, *Rhabdosargus holubi*, from the Groot River estuary, South Africa

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Fish utilize estuaries as important feeding and breeding grounds, as well as nursing homes for juvenile fish. Such an example is the ecologically important Cape stumpnose, *Rhabdosargus holubi*, (Steindachner, 1881). Although the ecology of *R. holubi* is well known, limited research has been conducted on this species parasite community composition, especially while inhabiting estuaries. Parasites play an important role in ecosystem functions, biodiversity, and their ecological roll in the health of host populations, and energy flow. The only study that examined parasites on juvenile *R. holubi* was conducted in St. Lucia estuary, South Africa. That study found only copepods (*Caligus* sp.)

infesting this host. The St. Lucia estuary is known to be impacted by anthropogenic activities, therefore raising an interesting question on whether there will be a different parasite community structure in juvenile *R. holubi* from pristine estuaries. The Groot River estuary is classified as a quiet zone, and it is protected from infrastructure development and excessive tourist impacts, and it can be considered a relatively pristine environment. Thus, the aim of the present study was to investigate the parasite community composition of *R. holubi* from the Groot River estuary. A total of 17 fish were collected with seine nets, dissected, and screened for ecto- and endoparasites. During the present study six parasitic taxonomic groups were identified with 11 of the 17 fish infested with ergasilid copepods (65%), 8 infected with digeneans (47%), 8 infested with leeches (47%), 13 with monogeneans (at least two different species) (77%), 2 infected with myxozoans (12%) and 8 infected with nematodes (47%). The mean intensity ranged from 2.3 to 50.6, with leeches at the lowest intensity and monogeneans the highest. *Rhabdosargus holubi* from the Groot River estuary thus host a large diversity of monoxenous and heteroxenous parasites. Previous studies found that impacted ecosystems cannot support complex parasite lifecycles and monoxenous parasite species are more prevalent. These results reflect near natural conditions and indicates the probability of the Groot River estuary to be a healthy estuarine ecosystem.

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(072) A first insight into the application of the historical ecology of parasitism on the parasitological communities of *Labeobarbus marequensis* in the Letaba River, South Africa

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The historical ecology of parasitism (HEP) is a new subdiscipline where preserved specimens are mined for data, such as fish parasites preserved within fish hosts in museum collections. In South Africa, the South African Institute of Aquatic Biodiversity houses the National Fish Collection (NFC) that potentially has a great number of parasitic species previously not reported. To determine the value and application of HEP in the South African context, a database search for fish present in the NFC collection was conducted. The search revealed that the Largescale yellowfish, *Labeobarbus marequensis* (Smith, 1841), is well represented for the past 60 years (1960 to 2017), thus, there is great potential for historical data mining. Additionally, *L. marequensis* still persists in the natural environment, enabling the collection of present-day data for comparison on a temporal scale. *Labeobarbus marequensis* is a freshwater fish species with a wide distribution from the middle and lower Zambezi River south to the Phongolo System and have been reported to host representatives of the Monogenea, Trematoda, Cestoda, Nematoda, and parasitic Crustacea. To get a first insight into the current day parasite community composition, 17 *L. marequensis* from the Letaba River were collected using cast nets and electrofishing. Individuals were humanely killed by blunt force trauma followed by severance of the spinal cord. A full parasitological screening for ectoparasites from the external body surface (skin smear), fins, and gills was done followed by an endohelminth screening of all internal organs. Overall, prevalence was 65% and infection intensity ranged between 1 and 27 with any parasitic taxon. Parasitic taxa were represented by myxozoan plasmodia, monogeneans, bivalve larvae, pre-metamorphic copepods on the gills, and digenean metacercariae encysted on the fins, free in the eye and cranial cavity, and nematodes from the intestine. This parasitological study represents the first of its kind from the Letaba River and provides novel

geographic records of these parasites in South Africa. In addition, this is also the first record of myxozoans and larval stages of bivalves parasitising *L. marequensis*.

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(073) Molecular characterization and phylogeny of two South African fish haemogregarines – *Haemogregarina curvata* and *Haemogregarina koppiensis* (Adeleorina: Haemogregarinidae)

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Haemogregarines are obligatory parasitic haemoprotozoans within the phylum Apicomplexa. These parasites are often reported from the blood of both ecto- and endothermic vertebrates but follow a heteroxenous life cycle, which includes developmental stages in both vertebrate and invertebrate hosts. In fishes, the majority of these parasites belong to the haemogregarine genus *Haemogregrina*, transmitted by a leech vector. To date, these parasites in fishes have been largely described using morphology of blood stages alone. Recently, two species of *Haemogregarina*, *Haemogregarina bigemina* and *Haemogregarina daviesensis*, have been molecularly characterized using fragments of the 18S rRNA gene and their phylogenetic placement estimated. Whilst the latter specie's sequences clustered with other species of *Haemogregarina*, *H. bigemina* clustered with unknown apicomplexan parasites and symbionts of fishes and corals respectively in a clade basal to sequences of members of the coccidia, and as such outside of the *Haemogregarina* and larger adeleorine clade. The taxonomy of this species has been questioned before as it is strongly suggested that the vector is a gnathiid isopod, which does not conform to the typical leech vector of members of the *Haemogregarina*. The aim of this study is to molecularly characterize and provide a phylogenetic estimate for the 18S rDNA sequences of both *H. curvata* and *H. koppiensis*. Blood was collected from the type host (*Clinus cottoides* for *H. curvata* and *Amblyrhyncotes honkenii* for *H. koppiensis*) and locality (De Hoop Nature Reserve, Western Cape) for both species. Thin blood smears were prepared, fixed in absolute methanol, and stained in a solution of Giemsa stain, with the remaining volume fixed in 96% ethanol for molecular analysis. Smears were screened and parasite stages micrographed and measured, comparing to the original descriptions of the above species. Upon completion of the molecular aspect, it is hypothesized that the sequences of *H. curvata* will cluster within the *Haemogregarina* clade as it is likely vectored by a leech, and *H. koppiensis* will cluster within the same clade as *H. bigemina*, even though its vector is unknown. These will represent the first haemogregarines molecularly characterized for teleost fishes in South Africa.

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(074) The biodiversity and host utilisation of gnathiid isopods parasitising elasmobranchs from Borneo

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Parasites in terrestrial and freshwater settings are more frequently studied as they are usually easier to access, however, research on marine parasites is relatively limited due to several sampling constraints. Recent advancements have begun to bridge this gap, leading to the growth of marine parasitology and among the globally distributed parasites, gnathiid isopods have garnered significant interest. These temporary ectoparasites feed on the blood, plasma, lymph, and tissue fluid of teleost and elasmobranch

hosts. Furthermore, the morphology of these organisms has proven difficult as their physical characteristics differ between all life stages, in addition to the sexual dimorphism displayed by adults. Subsequently, male morphology alone has been used to identify gnathiid species, using their prominent features, and limited descriptive information is available for females and larvae. Additionally, the study of gnathiids within biological hotspots, like the Indo-Pacific Ocean, remains scarce, indicating a significant information deficiency. To address these shortcomings, this project focused on gnathiids parasitising elasmobranchs in Borneo. Samples were separated based on different morphotypes, using morphometrics and relevant morphological characteristics. Molecular analyses utilising genetic markers, such as 16s rRNA, 18s rRNA, and mitochondrial cytochrome c oxidase subunit I (cox1), facilitated the identification of gnathiids at the genus and species levels through comparison with previously identified specimens. The combination of both morphological and molecular techniques (integrated taxonomy) confirmed distinct species for different morphotypes. The project also investigated host utilisation by analysing the meal content of the gnathiids and comparing it with data collected from host specimens. Overall, this project expanded our knowledge of gnathiid biodiversity in the Borneo region and enhanced our understanding of the region's biodiversity.

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(075) Diversity of freshwater snail vectors and associated trematode cercariae from the lowveld and highveld regions

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Parasites are abundant and important components of freshwater ecosystems and their complex life cycles depend extensively on the occurrence and distribution of their intermediate hosts, such as certain molluscs. However, in South Africa, snails and bivalves have been understudied in terms of their distribution and occurrences. Moreover, the occurrence of parasitic trematodes in these vectors has been understudied in the past. Therefore, the aim of this study was to determine the presence and prevalence of trematode vectors and their associated trematode parasites in the highveld and lowveld regions of South Africa. Field sampling took place during March 2023 across Gauteng, Mpumalanga, North-West, and Limpopo provinces. A total of 30 different sites were sampled using handpicking and sweep nets to collect molluscan taxa from the available habitats. Gastropoda were kept alive in site water until cercarial shedding experiments were conducted at the North-West University laboratories. During these experiments, snails were kept in individual containers and checked every 24 hours for the presence of cercariae. Following shedding (96 hours), each snail was dissected for the presence of any additional trematode infections. Cercariae were preserved in 4% formalin and 96% ethanol for morphological identification and molecular analyses, respectively. The field sampling yielded at least 19 species, including 12 Gastropoda and 7 Bivalvia. The dominance of taxa varied extensively across the sampled sites. Dominant taxa for the populations included *Corbicula africana*, *Pseudosuccinea columella*, *Tarebia granifera*, and *Bulinus* spp. Trematode cercariae were found in *Biomphalaria pfeifferi*, *Radix natalensis*, and *Bulinus* spp. from three sites in the Luvhuvhu and Klein Letaba Rivers. The prevalence of trematode parasites ranged from 1% to 3%, with the exception of *Bulinus* spp. from the Klein Letaba River, which had a prevalence of 10%. A total of eight trematode species were identified based on molecular evidence from the nuclear 28S, ITS and mitochondrial *cox*1 gene regions, two with zoonotic potential, namely *Schistosoma mattheei* found in *Bulinus* sp. and *Fasciola gigantica* from *Radix natalensis*.

(076) Preliminary study on the effect of using single and combined dipping compounds to control *Rhipicephalus* (*Boophilus*) spp. on cattle in the Eastern Cape, South Africa

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Boophilids are some of the most important tick species in the world from an economical point of view. In South Africa, only two of the boophilids that are present, namely *Rhipicephalus decoloratus* and *Rhipicephalus microplus*. The aim of this research was to evaluate the effect of using single and combined dipping compounds to control *R. (B) spp*. A total of 192 *R. (B.) spp* were counted on 12 Bonsmara cattle for the period of 21 days. The cattle were divided into three groups of four animals per group, group one was treated with Dectomax, group two was spot treated with Bayticol, and group three was treated with Dectomax and Batyicol. An expressively higher count of *R. (B) spp* was observed in Dectomax group one (91), followed by Bayticol group two (76), and much lower counts of *R. microplus* was observed in Dectomax & Bayticol group three (25). From the study, it is evident that the combined treatment with Dectomax and spot treatment with Bayticol is more effective in the control of *R. (B.)* spp on cattle. Therefore, the combined treatment with Dectomax and spot treatment with Bayticol can provide baseline information that can be used to control infections of *R. (B.) spp*. However, these are preliminary results that can form basis of building a comprehensive survey in future.

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(077) Encroachment and adaptation of the *Rhipicephalus microplus* on camps grazed by sheep in the Eastern Cape Province, South Africa

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The objective of this study was to establish the seasonal abundance and species richness of questing ixodid ticks on Amathole Montane Grassland camps grazed by sheep. Ticks questing for hosts were collected monthly for a period of three years by dragging flannel strips attached to a wooden spar over the vegetation. At each occasion, six replicate drag-samples were made in camps grazed by sheep. Of the questing ticks (n = 14 891) collected from the vegetation, the most abundant larvae were those of *Rhipicephalus microplus* (95.04%) followed by *Rhipicephalus appendiculatus* (2.32%), *Rhipicephalus evertsi* (1.56%), *Rhipicephalus decoloratus* (1.03%), *Rhipicephalus simus* (0.03) and *Amblyomma hebraeum* (0.02%). Comparing the two *Rhipicephalus* (*Boophilus*) spp., *R. microplus* (98.9%) outcompete the indigenous tick, *R. decoloratus* (1.1%). The *R. microplus* larvae were significantly higher ($P < 0.05$) in 2015 (2.11±0.108), 2016 (2.02 ± 0.076) and 2017 (1.94±0.075) during spring than any other season. There were no significant differences ($P > 0.05$) from *R. appendiculatus* questing ticks collected in autumn (0.27±0.007; 0.30±0.052) and spring (0.33±0.007; 0.20±0.052) for 2015 and 2016, respectively. The study showed that the cattle tick, *R. microplus* adapted very well on host species, in this case sheep, and encroached to areas that were too cold for its adaptation.

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(079) First integrated taxonomy study for characterisation of gill copepod *Ergasilus mirabilis* Oldewage & van As, 1987 (Ergasilidae: Cyclopoida)

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Ergasilids are external parasites typically found on the gills and fins of their fish hosts This group holds economic significance as some *Ergasilus* species have been observed to detrimentally impact fish populations. Among the 19 reported *Ergasilus* species in Africa, *Ergasilus mirabilis* Oldewage & van As, 1987 is considered one of the least host-specific, with a wide distribution across southern Africa. Following its description in 1987, the latest record of this parasite was in 1994 by Douëllou and Erlwanger, from Lake Kariba, Zimbabwe. As with most other species of *Ergasilus*, there is a lack of genetic data available to support the morphology of this species. Consequently, the present study aims at applying an integration of morphology and molecular techniques in the characterisation of this African *Ergasilus* species. As a part of an ongoing project, 159 *Clarias gariepinus* (Burchell, 1822) were caught in several localities around South Africa and Zambia. Adult female copepods were collected from two localities in South Africa (the Kushokwe Pan in the Phongolo Floodplain and the Vaal River) and from the Zambezi River, in Zambia. Fish were dissected and gills screened following standard techniques. Parasites were morphologically examined using light and scanning electron microscopy. Molecular analyses were performed using specific gene regions, including partial ribosomal RNAs genes (18S and 28S) and partial mitochondrial DNA (COI) genes. A total of 151 adult female ergasilids were collected. Parasites were morphologically and molecularly identified as *Ergasilus mirabilis.* Six new sequences were generated (two each for 18S, 28S, and COI) and new distribution records in the Phongolo Floodplain and the Vaal River are reported. Therefore, this study, carried out more than four decades after the initial species description, is the first integrated study of the African *Ergasilus* species, *E. mirabilis*, with the provision of supporting genetic data for partial 18S, 28S, and COI gene regions. Additionally, novel distribution records of *E. mirabilis* are reported from South Africa and Zambia.

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(082) Exploring helminth parasitic diversity in South African estuarine fish: a case study of the Full moony, *Monodactylus falciformis* Lacépède, 1801

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Research on fish populations in South African estuaries showed that these ecosystems are predominantly inhabited by marine species, particularly in permanently open estuaries, where juvenile fish heavily rely on them as nursery grounds. However, the parasitic communities associated with estuarine fish species along the South African coast have been poorly studied. To address this knowledge gap, the present study investigated the helminth parasitic community of *Monodactylus falciformis,* Lacépède, 1801 commonly known as the Full moony. Juveniles of *M. falciformis* prefer the middle and upper reaches of the estuaries as nursery areas where they form large shoals. Copepods is

the dominant component in the diet of the post larval moonies, whereas juveniles larger than 50 mm feed mainly on small crabs, isopods, amphipods, and insects. The diet of the moony in estuarine environments renders it a potential host to a diverse parasite community as the copepods, crabs, isopods, and amphipods are all suitable intermediate hosts for complex life cycle parasites such as helminths. Fish specimens were collected using seine nets from the Groot River Estuary, located on the southern coast of South Africa. A total of 14 individuals were screened for helminth parasitic infection. Prevalence of infection was 100%, with infection intensity ranging from 1–21 for various parasitic taxa. The helminth parasites identified belonged to the Monogenea (1), Cestoda (1), Nematoda (1) and Acanthocephala (1). This is the first study to investigate *M. falciformis* in estuaries along the coast of South Africa, shedding light on its parasitic associations in these environments.

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