

3rd International Congress on PARASITES OF WILDLIFE 2017

24 – 27 September 2017 Kruger National Park
28 September 2017 Workshop

**3rd International Congress
on PARASITES OF
WILDLIFE
Kruger National Park
South Africa**

24 – 27 September 2017



PROGRAMME & ABSTRACTS



3rd International Congress on PARASITES OF WILDLIFE Kruger National Park South Africa

24 – 27 September 2017

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Africa

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Welcome

Dear Fellow Parasitologists

On behalf of the Parasitological Society of Southern Africa, I wholeheartedly welcome you to the 3rd International Congress on Parasites of Wildlife in Skukuza. It is PARSA's pleasure to host this event for a third time! For participants who are here for the first time, you are all very welcome and will definitely, as those of us who are attending for a second and third time, discover why we decided to have this congress every three years.

For this 3rd ICPOW there are 182 registered participants representing 23 countries, including South Africa. I am convinced that you are all going to thoroughly enjoy the packed programme and the presentations during the three days, especially the three keynote speakers. I think an advantage of the congress is the variety of presentations that include parasites of different groups, different habitats and also the variety of research methods used in studying these parasites. This is the perfect platform to stimulate interest and learn something new, even if it is only out of curiosity.

On behalf of all participants I want to thank the local organizing committee chaired by Prof Sonja Matthee and SAVETCON for all their hard work to organize the congress and all accompanying events. I want to urge you to make the most of the opportunity to strengthen existing, and to form new, friendships and collaborations but also to enjoy the tranquil atmosphere of the park and its inhabitants. Hopefully the event will persuade you to diarise it in your calendars as a "not to be missed" congress in future.

Hope to see you all again in 2020!

Sincerely

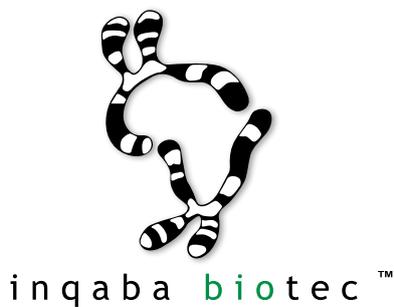


Susan Dippenaar



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International Congress on Parasites of Wildlife: A history

Based on the recollections of Professor Jo van As

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

During September 2014, PARSA hosted the 2nd International Congress on Parasites of Wildlife, in Kruger National Park. This meeting coincided with the 43rd Annual meeting of PARSA. Almost 150 delegates, from 19 countries (including South Africa), attended the meeting. The programme comprised 83 oral and 37 poster presentations. Kerstin Junker from Onderstepoort Veterinary Institute (South Africa), Serge Morand jointly from Centre Christophe Mérieux (Lao PDR) and CIRAD (France) and Ute Mackenstedt from University of Hohenheim (Germany) gave keynote addresses. The days again ended with game drives and informal social events. At the 2014 meeting it was decided that PARSA will continue to host an International Congress on Parasitology of Wildlife every three years, with 2017 identified as the year for the 3rd International Congress on Parasites of Wildlife in Kruger National Park.



Banie Penzhorn



Claude Comes & Mary Beverly-Burton



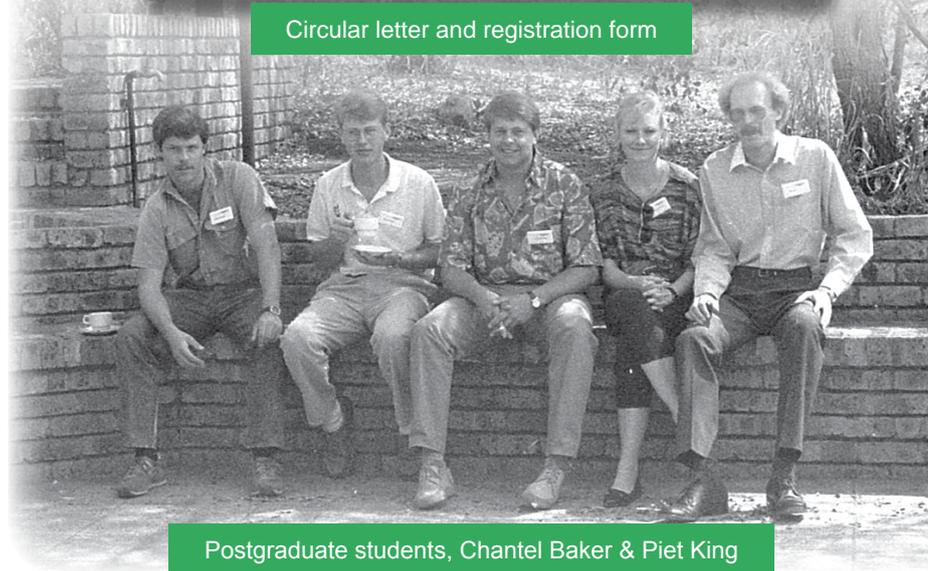
Linda Basson & Stanislav Kazubsi



Jo van As (l) & Anna Verster (r)



Circular letter and registration form



Postgraduate students, Chantel Baker & Piet King



Piet Joubert

Programme

Day 1 (24 September 2017)						
16:00-18:00	Registration					
18:00	Welcome Reception @ Conference Centre					
Day 2 (25 September 2017)						
07:30-08:00	Registration					
	Venue 1					
08:00	Keynote 1 - Tom Cribb - The nature and implications of trematode host-specificity: meaning from the muddle Chair: Nico Smit					
	Venue 1			Venue 2		
	Session 1.1.1			Session 1.2.1		
	Parasites in marine systems Chair: Nico Smit			Diversity & Distribution of mammalian parasites Chair: Andrea Spickett		
	Presenter	Title	Abstr	Presenter	Title	Abstr
08:45	Yong, Russell	Advances in understanding of fish blood flukes (Aporocotylidae) infecting tetraodontiform fishes: taxonomy and systematics	29	Modrý, David	Diversity and host specificity of stronglylid nematodes in primates: lessons learned from a next generation sequencing approach	77
09:00	Laubscher, Mariska	Biosecurity and treatment of fungal pathogens infecting Loggerhead sea turtles (<i>Caretta caretta</i>) in South Africa	76	Romig, Thomas	Taeniid cestodes in African mammals - an unrecognized aspect of biodiversity	53
09:15	Lempereur, Laetitia	<i>Crassicauda boopis</i> in a fin whale (<i>Balaenoptera physalus</i>) ship-struck in the eastern North Atlantic Ocean	6	Thompson, Andrew	Parasites lost - lessons learned from a critically endangered Australian marsupial – the woylie	14
09:30	Svavarsson, Jörundur	Species richness of gnathiids (Crustacea, Isopoda) on the Australian Great Barrier Reef and surrounding habitats – estimates based on adult males	16	Cervena, Barbora	Diversity and host specificity of <i>Mammomonogamus</i> in domestic and free-living animals	71
09:45	Dippenaar, Susan	Siphonostomatoids collected from White Sharks (<i>Carcharodon carcharias</i>) during the OCEARCH project in South Africa	44	Mihalca, Andrei	Wild carnivores of Europe as reservoirs of vector-borne nematodes	57
10:00	Georgieva, Simona	A complex of <i>Macvicaria</i> Gibson & Bray, 1982 (Digenea: Opecoelidae) in Mediterranean sparids	45	Cohen, Carmit	<i>Mycoplasma</i> bacteria in the wild: From patterns to mechanisms	139
10:15	Martin, Storm	Sucker stalk length is not important; it's which fishes you infect with it that matters! Polyphyly among species of <i>Podocotyloides</i> Yamaguti, 1934 (Trematoda: Opecoelidae)	28	-	-	-
10:30	Tea & Poster viewing Session I					
	Session 1.1.2			Session 1.2.2		
	Taxonomy & Systematics of parasites in marine and freshwater systems Chair: Susan Dippenaar			Ecology of small mammal parasites Chair: Heike Lutermann		
11:00	De Jager, Gerhard	The Great American Trichodinid?	72	Krasnov, Boris	Host identity and parasite performance: phylogenetic distance, co-occurrence and implications for evolution and conservation	4
11:15	Honka, Katrin	Experimental proof of the 'Trojan horse' strategy applied by the swim bladder nematode <i>Anguillicola crassus</i>	124	Warburton, Elizabeth	Effects of parasitism on host reproductive investment in a rodent–flea system: Host litter size matters	8

11:30	Jones, Ben	The <i>Schistosoma indicum</i> group: A complex series of species or a series of species complexes	108	Spickett, Andrea	Your address matters: Helminth parasitism in two closely-related but spatially distinct South African rodents	46
11:45	Tkach, Vasyl	Walking with dinosaurs: phylogeography and systematics of proterodiplostomid digeneans parasitic in crocodylians	193	Rodriguez-Pastor, Ruth	Fleas parasitizing common voles: impacts at host population and individual levels	61
12:00	Mokonyane, Morongwa	First report of occurrence of an alien cestode parasite in an alien fish (<i>Cyprinus carpio</i>), Kwena Dam, Mpumalanga Province, South Africa	32	Flatau, Ron	Ecological causes and consequences of endosymbiont abundance in an arthropod vector: <i>Wolbachia</i> and <i>Synosternus cleopatrae</i> fleas	137
12:15	Smit, Nico	Alien freshwater fish parasites from South Africa: Diversity, distribution, status and the way forward	147	Halle, Snir	The impact of <i>Mycoplasma</i> bacteria on three wild coexisting rodent species	131
12:30	Lunch					
	Session 1.1.3			Session 1.2.3		
	Parasites in freshwater systems Chair: Linda Basson			Veterinary parasitology (PARSA) Chair: Banie Penzhorn		
13:30	Bopheka, Luthando	First record of a <i>Trypanosoma</i> species in <i>Austroglanis sclateri</i> (Boulenger, 1901) from Sterkfontein Dam, South Africa	78	Mlangeni, Malitaba	Detection of <i>Trypanosoma equiperdum</i> infections in horses and donkeys in South Africa by PCR and ELISA	95
13:45	Halajian, Ali	Alien parasites alert in South Africa!	41	Lesenyeho, Kenny	Resistance of the African blue tick <i>Rhipicephalus (Boophilus) decoloratus</i> to macrocyclic lactones in the Eastern Cape, South Africa	176
14:00	Van As, Liesl	Ciliophorans collected from a wide variety of hosts from the Okavango system, Botswana	65	Esterhuyze, Marilie	A comparative study of ectoparasite tolerance between purebred Brahman (<i>Bos indicus</i>), Sussex (<i>Bos taurus</i>) and Brahman x Sussex crossbred cattle in the Free State, South Africa	183
14:15	Van As, Jo	The disjunct distribution of branchiuran fish parasites	112	Dvir, Eran	Cystic echinococcosis in the northern Golan Heights: primary findings	179
14:30	Junker, Kerstin	Hooked on crocodiles: Pentastomes of <i>Crocodylus niloticus</i> (Reptilia: Crocodylidae) in the Kruger National Park, South Africa	5	Chaisi, Mamohale	<i>Anaplasma marginale</i> and <i>A. centrale</i> are widespread in cattle in South Africa	199
14:45	Sures, Bernd	Understanding trophic interactions in monogenean-fish associations using stable isotopes of carbon and nitrogen	38	Nyangiwe, Nkululeko	Range expansion of the economically important Asiatic blue tick, <i>Rhipicephalus microplus</i> , in South Africa	122
15:00	End of day					
18:00	Catered Braai @ Cattle Baron Lapa					
Day 3 (26 September 2017)						
07:30-08:00	Registration					
	Venue 1					
08:00	Keynote 2 - Franck Prugnolle - Human and ape malarial: a family business Chair: Conrad Matthee					
	Venue 1			Venue 2		
	Session 2.1.1			Session 2.2.1		
	Molecular ecology & Evolution Chair: Courtney Cook			Diversity & Distribution of parasites in freshwater systems Chair: Jo van As		
08:45	Rougeron, Virginie	Evolutionary relationships of <i>Plasmodium vivax</i> infecting great apes and humans	120	Du Preez, Louis	Madagascar: A parasites' paradise	136

09:00	Matthee, Conrad	The effect of life history and vicariance on the dispersal and evolution of ticks	43	Svitin, Roman	Parasitic nematodes from three species of amphibians in South Africa	81
09:15	Štefka, Jan	Tracing the origins of parasitic invasions using genetics: examples of introduced helminths of fish and deer	171	Kudlai, Olena	Discovering African aquatic parasite diversity: Digeneans of the genus <i>Tylodelphys</i> (Diplostomidae)	105
09:30	Eldridge, Camilla	The evolution of antigenic diversity in vaccine candidates for <i>Schistosoma turkestanicum</i> infecting European populations of wild red deer	94	Basson, Linda	Diversity of fish parasites from a survey in the Phongola floodplain	51
09:45	Dos Santos, Quinton	Benefits and pitfalls of molecular taxonomy: A case study of the Diplozoidae	187	Kmentová, Nikol	Fisheries targets in Lake Tanganyika: Revealing the mystery of their parasite fauna	37
10:00	Blair, David	Host-switching and parasite radiations in herbivorous marine megafauna: turtles and sirenians	208	Avenant-Oldewage, Annemarië	A gyrodactylid on Lake Magadi cichlid fish, <i>Alcolapia grahami</i> : A fish living under extreme environmental and anthropogenic selective pressures	195
10:15	Morand, Serge	Evolution of life history of rodents of Southeast Asia: Role of habitat and parasite diversity	83	Netherlands, Edward	First report and characterisation of eimeriid-type Coccidia (Apicomplexa) from the blood of African anurans using morphological and molecular techniques	97
10:30	Tea & Poster viewing Session II					
	Session 2.1.2			Session 2.2.2		
	Molecular parasitology Chair: Conrad Matthee			Ecology of parasites in marine and terrestrial systems Chair: Annemarië Avenant-Oldewage		
11:00	Wachter, Bettina	First evidence of hemoplasma infection in free-ranging Namibian cheetahs (<i>Acinonyx jubatus</i>)	27	Huston, Daniel	The secret lives of the Eneverteridae: new insights into the evolutionary relationships, biodiversity and ecology of an enigmatic family of digeneans	13
11:15	Ikeda, Priscila	Occurrence and molecular characterization of <i>Mycoplasma</i> spp. in bats sampled in Brazil	63	Mitchell, David	Hexabothriid parasites from Rajidae species of South Africa	162
11:30	Smit, Nico	Molecular identification of leeches from aquatic tetrapods and the haemoparasites they transmit	126	Espinaze, Marcela	Ectoparasite infestations in the nests of African penguins: initial data on the effect of nest type, spatial position of nest and season	96
11:45	Přikrylová, Iva	<i>Gyrodactylus</i> spp. (Monogenea: Gyrodactylidae) of freshwater fishes from South Africa: An unexplored field with new challenges for research	33	Lutermann, Heike	Host-parasite networks in South African small mammals	134
12:00	Mampa, Mogau	Determination of sequence descriptions and predicted functions of selected <i>Theileria parva</i> hypothetical proteins	20	Beveridge, Ian	Complex strongyloid helminth communities in large herbivores: Insights from Australasian macropodid marsupials	155
12:15	Hendrick, Gina	Developing molecular methods for detection of blood meal source in a free-living marine ectoparasite	168	D'Amico, Gianluca	Role of the European wild carnivores in the natural cycle of ticks and tick-borne diseases	68
12:30	Lunch					



Session 2.1.3				Session 2.2.3		
Parasite-host relationships Chair: Marinda Oosthuizen				Parasite diagnostics Chair: Francois Dreyer		
13:30	Barbosa, Andres	Host-parasite interactions in Antarctic penguins	91	Igeh, Patience	The impact of water quality variables and trace elements on the prevalence, mean intensity and seasonal occurrence on the infection rate of <i>Cichlidogyrus philander</i> infesting <i>Pseudocrenilabrus philander</i> in Padda Dam Gauteng, South Africa	135
13:45	Palinauskas, Vaidas	Avian malaria diagnosis in wildlife	201	Gilbert, Beric	Two sides to every story: The case of the infection biology of <i>Lamproglena clariae</i> in relation to water quality and the environment in the Vaal River	152
14:00	Sikkel, Paul	Lethal and sublethal impacts of parasitic gnathiid isopods on post-settlement coral reef fishes	170	Molefe, Mahlogonolo	The decline in parasite diversity along the Vaal River system, the downstream syndrome	182
14:15	Murambiwa, Pretty	Role of cytokines and chemokines in clinical outcomes of helminth and malaria co-infections in Sub-Saharan Africa: A review	110	Juhász, Alexandra	Detection of eggs of <i>Schistosoma turkestanicum</i> in droppings of deer	90
14:30	Umo, Ekuyikeno	Host cytokine responses in Sprague-Dawley rats experimentally co-infected with <i>Trichinella zimbabwensis</i> and <i>Plasmodium berghei</i>	116	Majoros, Gábor	Detection of <i>Schistosoma cercariae</i> from water	107
14:45	Mdleleni, Yanga	Host chemokine responses in Sprague-Dawley rats experimentally co-infected with <i>Trichinella zimbabwensis</i> and <i>Plasmodium berghei</i>	111	-	-	-
15:00	End of day					
	Free evening					
Day 4 (27 September 2017)						
07:30-08:00	Registration					
	Venue 1					
08:00	Keynote 3 - Vanessa Ezenwa - Helminth-tuberculosis coinfection in wildlife Chair: Sonja Matthee					
	Venue 1			Venue 2		
	Session 3.1.1			Session 3.2.1		
	Multi-host/multi-parasite systems Chair: Sonja Matthee			Parasites in terrestrial systems Chair: Liesl van As		
08:45	Hawlana, Hadas	Climbing the ladder of complexity in the study of host-parasite interactions: a case study of rodents, fleas and their bacteria	73	Tkach, Vasyi	Diversity and trends in prevalence of avian malaria in the Brazilian Amazon	192
09:00	Gouy de Bellocq, Joelle	Host-parasite secondary contacts: Barriers and introgression	48	Shamsi, Shokoofeh	A systematic review of <i>Contraecum</i> species (Nematoda: Anisakidae) infecting Australian piscivorous birds	92
09:15	Artzy-Randrup, Yael	Exploring the implications of climate change on epidemiological dynamics of multi-host vector-borne diseases	185	Asakawa, Mitsuhiko	Several topics on parasitic helminthiasis and helminths from free-ranging or captive vertebrates with special reference to recent cases dealt with the Wild Animal Medical Center, Rakuno Gakuen University, Japan	202
09:30	Sweeny, Amy	The consequences of nutrition on parasite community and response to treatment in wild and laboratory wood mouse populations	102	Shamsi, Shokoofeh	Infection with Tongue worms in Australian animals	69

09:45	Allan, Brian	The consequences of livestock-wildlife integration for tick-borne disease risk in central Kenya	145	Sychra, Oldrich	<i>Myrsidea quadrifasciata</i> (Phthiraptera: Amblycera) - unique host generalist among highly host-specific chewing lice	23
10:00	Garrido, Mario	Next generation techniques meet recent challenges: The integration of structural equation models and multimodel inference for the exploration of multihost-multiparasite interactions in natural systems	58	Bakkes, Deon	A 173-year-old unresolved species problem: <i>Ixodes pilosus</i> group (Acari: Ixodida: Ixodidae) systematics with integrative taxonomy	9
10:15	Keegan, Shaun	Parasite-parasite interactions in the wild: beyond the individual host and into the landscape	159	Xiao, Lihua	Molecular characterization of <i>Cryptosporidium</i> spp. and <i>Enterocytozoon bieneusi</i> in straw-colored fruit bats in Nigeria	132
10:30	Tea & Poster viewing Session III					
	Session 3.1.2			Session 3.2.2		
	Parasites in complex landscapes Chair: Kerstin Junker			Medical parasitology (including Zoonoses and One Health) Chair: Oriel Thekisoe		
11:00	Morand, Serge	Fast changing landscapes and wildlife-borne diseases	80	Mukaratirwa, Samson	Prevalence and molecular identification of <i>Trichinella</i> species isolated from wildlife originating from Limpopo and Mpumalanga provinces of South Africa	89
11:15	Mathee, Sonja	Trombiculids parasitising rodents: Their diversity and distribution on and off the host	93	Conrad, Patricia	Perplexing Protozoa: A gateway to wildlife and global One Health	158
11:30	Vineer, Hannah	Gastrointestinal nematode transmission risk at the livestock-wildlife interface in Botswana	75	Xiao, Lihua	Wildlife as a source of <i>Giardia duodenalis</i> in a watershed	133
11:45	Neves, Luis	<i>Ehrlichia ruminantium</i> in Mozambique: A study on prevalence in ticks from cattle and wildlife and isolate genetic diversity	138	Bennett, Annette	Infection studies with the malaria parasite, <i>Plasmodium falciparum</i> , on African malaria vectors, <i>Anopheles arabiensis</i> , <i>An. funestus</i> , <i>An. coluzzii</i> and <i>An. gambiae</i> at the Wits Research Institute for Malaria	66
12:00	Gherman, Calin	Cardiopulmonary nematodes in wild carnivores from Romania	67	Koekemoer, Lizette	Vector incrimination in South Africa: challenges and highlights	39
12:15	Selbach, Christian	Parasites under threat - should we care?	62	Grab, Dennis	Human blood-brain barrier gene expression in response to African trypanosomes and physiologic flow shear stress	194
12:30	Lunch					
	Session 3.1.3			Session 3.2.3		
	Parasites in complex landscapes Chair: Edward Netherlands			Diversity & Distribution of parasites in terrestrial systems Chair: Danny Govender		
13:30	O'Connor, Barry	Ectoparasite communities of small mammals in Madagascar are fundamentally different from those in East Africa	113	González-Acuña, Daniel	Advances in the knowledge of ticks (Acari: Ixodidae, Argasidae) in Chile: New species, host, localities and new reports of ticks borne disease	165
13:45	Welicky, Rachel	Drought and the disappearance of alien invasive anchorworm, <i>Lernaea cyprinacea</i> (Copepoda: Lernaeidae), is linked to changes in fish health	104	Labuschagne, Karien	Report on a <i>Culicoides</i> survey in Mpumalanga, South Africa, during 2015	11
14:00	Hohenadler, Michael	Invasion – lessons learned from Europe	24	Zawada, Jacek	Clade analysis of males in a wild <i>Anopheles funestus</i> swarm in Southern Africa	19

14:15	Waugh-Hall, Cecelia	Assessment of the parasitic helminth fauna of wild rats in Jamaica	169	Cook, Courtney	Haemogregarine biodiversity parasitising snakes of KwaZulu-Natal, South Africa	156
14:30	Pori, Tinotendashe	Avian haemoparasite prevalence in Kruger National Park, South Africa	154	Mortenson, Jack	Spatially modeled surveillance for Deer Hair Loss Syndrome in Columbian black-tailed deer (<i>Odocoileus hemionus columbianus</i>) in the Pacific Northwest United States	207
14:45	End of day					
15:15-16:30	PARSA AGM @ Conference Centre (PARSA members)					
19:00	Gala dinner @ Conference Centre					

Poster Sessions

Day 2 (25 September 2017)

Poster Session I			
Poster no	Presenter	Title	Abstr
S1.1	Smit, Willem	Bioaccumulation of metals and metalloids in the silver catfish and its nematode parasite	42
S1.2	Kasembele, Kapepula	Water quality assessment using monogenean fish parasites as bioindicators in the Lufira upper basin (DR Congo)	160
S1.3	Moema, Esmey	Analysis of digenean trematodes (metacercarial stages) from freshwater fish in the Tshwane Metropolitan Area: Phylogenetic relationships using PCR-techniques	206
S1.4	Luus-Powell, Wilmien	<i>Lernaea</i> infestation at Hardap Dam, Namibia	191
S1.5	Christison, Kevin	The first African record for Anoplodiscidae (Monogenea), and a new <i>Anoplodiscus</i> species from Australia	198
S1.6	Christison, Kevin	The development of a non-lethal diagnostic tool for the diagnosis of <i>Ichthyophonus hoferi</i>	148
S1.7	Canham, Daniel	Morphological and molecular characterization of lymnaeid (Gastropoda: Lymnaeidae) snail populations from Okavango Delta of Botswana	50
S1.8	Prikrylova, Iva	New <i>Gyrodactylus</i> von Nordmann, 1832 (Monogenea: Gyrodactylidae) species of <i>Enteromius paludinosus</i> (Peters, 1852) from South Africa	173
S1.9	De Jager, Gerhard	<i>Trichodina heterodentata</i> Duncan, 1977, (Ciliophora: Peritrichia) species description inferred from 18S rDNA sequences and the evaluation of a possible species complex	87
S1.10	Nicholson, Matthew	Predators and Parasites - Towards a more complete understanding of the trophodynamics of a common coral reef fish	205
S1.11	Strauss, Hester	Using stable isotope analysis to compare the foraging ecology of differently-attaching cymothoid isopods	177
S1.12	Hadfield, Kerry	Diversity of fish parasitic cymothoid isopods from Moreton Bay, Australia, including new distribution and hosts records	178
S1.13	Cook, Courtney	The phylogeny, host-association and distribution of a haemoparasite of <i>Stegastes</i> damselfishes (Pomacentridae) from the eastern Caribbean based on a combination of morphology and 18S rDNA data	184
S1.14	Van der Wal, Serita	Review of the fish parasitic isopod genus <i>Elthusa</i> (Isopoda: Cymothoidae) from southern Africa	172
S1.15	Svavarsson, Jörundur	New species of gnathiids (Crustacea, Isopoda) on the Australian Great Barrier Reef and islands of the Coral Sea	17
S1.16	Georgieva, Simona	<i>Skoulekia</i> spp. (Digenea: Aporocotylidae), blood flukes in Mediterranean porgies	47

Day 3 (26 September 2017)

Poster Session II			
Poster no	Presenter	Title	Abstr
S2.1	Arnathau, Céline	How to get rid of host DNA in <i>Plasmodium</i> -infected blood samples to generate good quality <i>Plasmodium</i> genomes?	143
S2.2	Tsotetsi-Khambule, Ana	qPCR assays to improve the accuracy of bovine and porcine cysticercosis	109
S2.3	Rondón, Silvia	Detection of <i>Plasmodium</i> sp. from faecal samples in non-human neotropical primates in forest fragments in Colombia	118
S2.4	Van As, Michelle	Ticks as possible vectors of a <i>Hepatozoon</i> species (Apicomplexa: Adeleorina: Hepatozoidae) infecting wild African leopards, <i>Panthera pardus pardus</i> (Linnaeus, 1758), in South Africa	86
S2.5	Nkemzi, Achasi	Blood glucose levels in Sprague-Dawley rats experimental co-infected with <i>Trichinella zimbabwensis</i> and <i>Plasmodium berghei</i>	115
S2.6	Casmo, Verónica	Intestinal parasites in children under 5 years of age at Chamanculo Hospital, Maputo, Mozambique	12
S2.7	Casmo, Verónica	Intestinal parasites among army recruits in Munguí, Maputo, Mozambique	34

S2.8	Marco, Ignasi	Prevalence and molecular detection of <i>Cryptosporidium</i> and <i>Giardia</i> spp. at the wildlife, livestock and human interface in and around protected areas in Uganda	100
S2.9	Jacobs, Roanda	Tick-borne haemoparasite occurrence in eastern rock sengi (<i>Elephantulus myurus</i>) of South Africa	163
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Plenary Speakers

Prof. Tom Cribb

Prof. Tom Cribb is an Associate Professor in the Department of Parasitology, University of Queensland, Australia. He completed all his degrees at the University of Queensland. His interests are in parasite biodiversity, mainly that of trematodes, although he has also published significantly on acanthocephalans, cestodes, myxosporeans and nematodes of marine fish. More specifically his work focuses on the biology, taxonomy, distribution and evolution of parasites. He has authored and co-authored more than 280 scientific publications and currently serves on the Editorial Boards of *Systematic Parasitology*, *Folia Parasitologica*, *Acta Parasitologica*, *Parasitology International*, *Parasite* and *Journal of Helminthology*

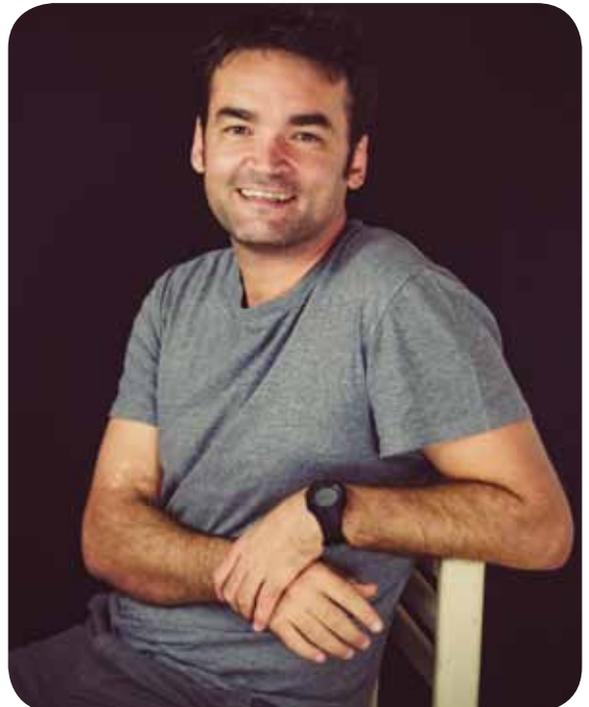


The nature and implications of trematode host-specificity: meaning from the muddle.

The host-specificity of trematodes of fishes presents a broad paradox. At the family level, the host distribution of trematodes is clearly and overwhelmingly driven by the underlying form of the life-cycle. Thus, bucephalids, which have their metacercariae in fishes, infect a multitude of families of piscivorous fishes. Gyliauchenids, which have their metacercariae encysted on algae, infect a wide range of herbivores. This kind of pattern is repeated for almost every family and is termed euryxenous specificity, the infection of hosts united by eco-physiological rather than phylogenetic similarity. In contrast, the overwhelming pattern for individual species is for oioxenous (a single host) or stenoxenous (closely related hosts) host-specificity. How can the contrasting patterns of host-specificity at the family and species be reconciled? Two explanations are possible. Either the host-parasite combinations have arisen by coevolution associated with huge levels of extinction, or there has been a great deal of host-switching. We argue that the evidence supports host-switching as the dominant explanation. How then can host-switching occur between completely unrelated hosts occur when most species are seemingly trapped within a restricted host range. We discuss the evidence and the implications.

Prof. Franck Prugnolle

Prof. Prugnolle is the Head of the Team "Genetics and Adaptation of Pathogens" at the Infectious Diseases and Vectors: Ecology, Genetics, Evolution and Control Laboratory of the Centre National de la Recherche Scientifique (CNRS) in France. He completed his PhD in Integrative Biology at University of Montpellier II, France. His research interest includes amongst others, the evolution of the pathogen-host-parasite system (*Plasmodium falciparum*/Human/Anopheline) and the evolution and diversity of *Plasmodium* species in Great Apes in Africa. He has authored and co-authored more than 70 scientific publications.



Human and ape malaras: a family business

Malaria is a parasitic disease caused by protozoan parasites of the genus *Plasmodium*. For about a decade, the objective of my team has been to understand the origin and evolution of malaria agents in humans and more globally in primates. This work led us to study the diversity of malaria parasites in African primates (especially great-apes) by developing new sampling and new diagnostic methods, to search for the vectors of ape *Plasmodium* and to sequence and compare their genomes to those of human parasites. Our work demonstrated that the diversity of *Plasmodium* parasites infecting wild populations of great apes was historically largely underestimated and that all human *Plasmodium* parasites had a close relative in apes. We demonstrated in particular that the closest species of *P. falciparum*, the most virulent agent of human malaria, was not a chimpanzee parasite (as previously thought), but a gorilla parasite, hence questioning the origin of this deadly parasite. We showed that ape *Plasmodium* are transmitted by three main mosquito vectors in Central Africa, among which some may play a role of bridge between humans and apes and thus explain the historical propensity of primate malaria agents to switch from one host species to another. Finally, the sequencing of the genomes of all chimpanzee and gorilla *Plasmodium* species and their comparison with those of the human parasites allowed us to identify genes that played a role in host adaptations and more globally to better understand the role of introgression, convergence and gene duplication in their evolution

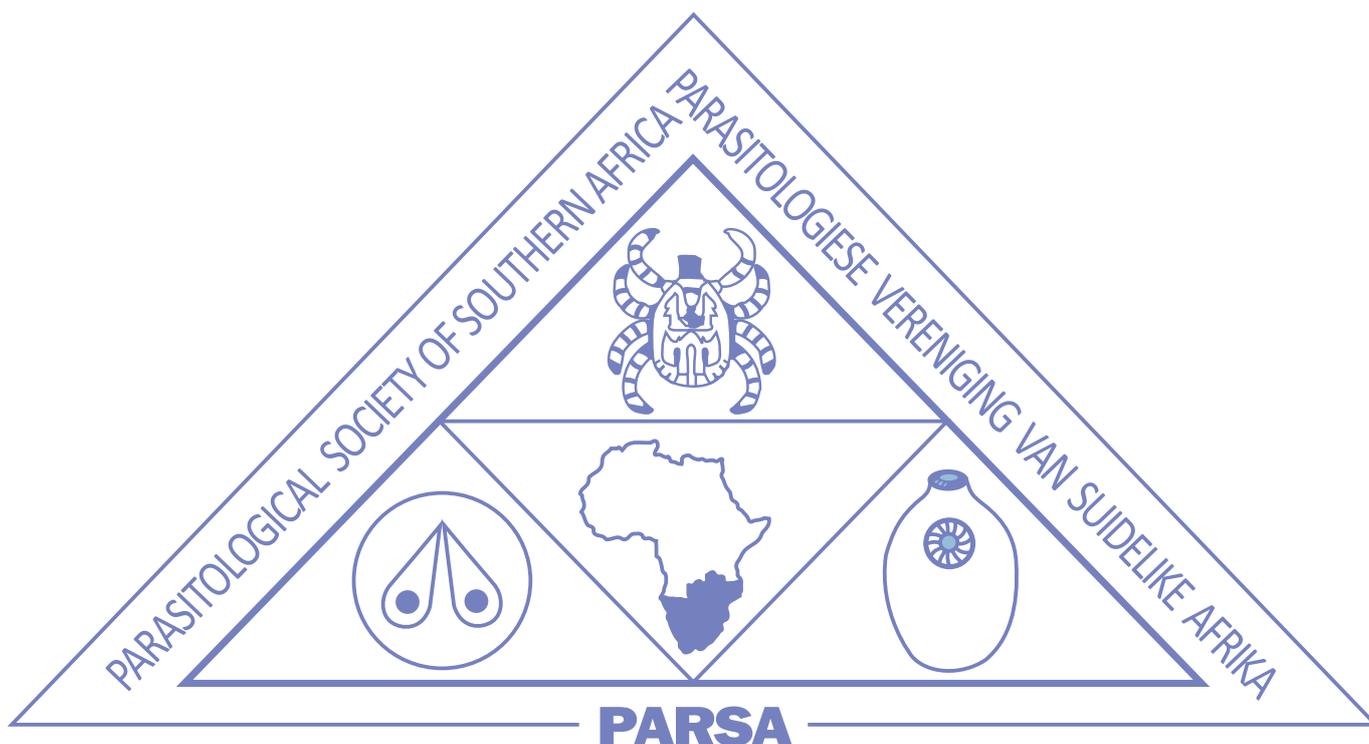
Prof. Vanessa Ezenwa

Prof. Vanessa Ezenwa is a Professor at the University of Georgia, USA, where she holds joint appointments in the Odum School of Ecology and College of Veterinary Medicine. She received a BA in Biology from Rice University, and PhD in Ecology and Evolutionary Biology from Princeton University. Her research focuses on the ecology of infectious diseases in animal populations, with specific attention to helminth infections in wild ruminants. She has more than 60 scientific publications and currently serves on the Editorial Boards of *Ecology Letters*, *Proceedings of the Royal Society of London B*, *EcoHealth*, *Animal Conservation* and *International Journal for Parasitology: Parasites and Wildlife*.



Helminth-tuberculosis coinfection in wildlife

Coinfection with helminths can affect the host response to microbial infections (e.g. viral and bacterial infections), and an increasing number of studies are investigating the consequences of helminth-microbe coinfection in laboratory settings. To better understand the dynamics of helminth coinfection in natural environments, we examined the consequences of helminth infection for bovine tuberculosis (BTB) dynamics in a free-ranging population of African buffalo in Kruger National Park. Using a four-year longitudinal study design, we tested the effects of both anthelmintic treatment and host resistance to helminths on individual and population-level outcomes of BTB infection. Our results indicate that active infection with helminths, and the host's constitutive response to helminth infection, have profound but distinct implications for the outcome of BTB infection.



Oral Abstracts

(0004) Host identity and parasite performance: phylogenetic distance, co-occurrence and implications for evolution and conservation

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Among host species that a parasite is able to exploit, a principal host and auxiliary hosts are distinguished. We report the results of comparative analyses of abundance and laboratory experiments on performance of fleas exploiting different hosts. We found that taxonomic relatedness between the principal and auxiliary hosts determines what abundance a parasite can achieve on auxiliary hosts. Experimental studies supported these findings for energy expenditure of blood digestion and reproductive output of fleas, but only when the analyses were restricted to auxiliary hosts of the same family as the principal host. However, flea performance appeared to be high when they fed on hosts very distant from but co-occurring with their principal hosts. Then, we measured flea performance on hosts that were both distant from to the principal host and inhabit other geographic regions modelling thus host invasions. Flea performance was either high or low on different invasive hosts being thus context-dependent. We conclude that among-host variation in parasite performance may result from interplay of several factors including co-occurrence between hosts, susceptibility of a host to parasite attacks, species-specific level of immunocompetence of a host and the level of host specificity of a parasite. High performance in an unusual but co-occurring host may be one of the reasons for host switching to unrelated lineage such as switch from mammalian to bird hosts that happened during evolutionary history of fleas. From the conservation perspective, we also conclude that the response of a resident parasite to an invasive host is unpredictable.

(0005) Hooked on crocodiles: Pentastomes of *Crocodylus niloticus* (Reptilia: Crocodylidae) in the Kruger National Park, South Africa

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A total of 32 Nile crocodiles [*Crocodylus niloticus* (Reptilia: Crocodylidae)] were examined for pentastomid parasites in the Kruger National Park (KNP), South Africa and its vicinity during 1995 to 1999 and 2010 to 2011. Pentastomes were spread throughout the study area and occurred year-round. Overall prevalence was 96.9%, with a mean abundance of 23.4 (0-81). Pentastomes collected in the KNP comprised all six species hitherto described from Nile crocodiles: *Alofia nilotici* Riley & Huchzermeyer, 1995, *Alofia simpsoni* Riley, 1994, *Leiperia cincinnalis* Sambon, 1922, *Sebekia cesarisi* Giglioli in Sambon, 1922, *Sebekia minor* (Wedl, 1861) and *Sebekia okavangoensis* Riley & Huchzermeyer, 1995. Crocodiles examined were either adult or subadult. Shared dietary preferences and resulting similar exposure to fish intermediate hosts might account for the observed absence of differences in infection patterns (prevalence, abundance and species richness) between these two age groups, males and females as well as localities. *Sebekia minor* was the dominant species with an overall prevalence of 69% and an overall mean abundance of 11.3 (0-54). *Sebekia cesarisi* and *L. cincinnalis* were equally prevalent (72% and 56%, respectively), but less abundant with a mean of 3.5 (0-22) and 5.3 (0-39), respectively. The prevalence of the remaining species, *A. nilotici*, *A. simpsoni* and *S. okavangoensis*, ranged from 34.4% to 40.6%, and, combined with a relatively low mean abundance (0.9-1.3), they formed the rarer component of pentastome communities. With six species recorded from it, *C. niloticus* has the highest diversity of pentastomes amongst African crocodylians and the second highest world-wide.

(0006) *Crassicauda boopis* in a fin whale (*Balaenoptera physalus*) ship-struck in the eastern North Atlantic Ocean

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On 9 November 2015, a juvenile male fin whale of 11.60 m length was observed on the bulb of a vessel in the Channel Terneuzen - Ghent (The Netherlands - Belgium). Severe parasitosis was present in the right heart ventricle, caudal caval vein and renal vein associated with a thrombus non adherent to the wall. Parasites, identified as *Crassicauda boopis*, were observed macroscopically and microscopically. The sequence of the 18S rRNA gene obtained from the parasite samples was similar to the sequence of the 18S rRNA gene from *C. magna*. While adults of *C. boopis* and *C. magna* are morphologically distinct and found at different locations in the body, the molecular analysis of the 18S rRNA gene seems insufficient for reliable species identification. Although numerous *C. boopis* were found, the cause of death was identified as the collision with the ship, as suggested by the presence of a large haematoma, and the absence of evidence of renal failure. Additionally, while this fin whale was heavily infested, no fibrous masses enclosing the parasites were present. The young age of this whale and the absence of reactive tissue may suggest that the infestation had not yet reached a chronic stage.

(0008) Effects of parasitism on host reproductive investment in a rodent–flea system: host litter size matters

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Parents may alter offspring phenotype depending on the type of environment they encounter. Parasitism is a common stressor; therefore, maternal reproductive investment could change in response to parasitic infection. However, few experiments have investigated the relationship between parasitism and maternal investment, whereas earlier field studies provided contradictory evidence. We investigated number, sex ratio, and growth of offspring in two desert-dwelling rodent species, solitary altricial *Meriones crassus* and social precocial *Acomys cahirinus*, exposed to parasitism by fleas *Xenopsylla ramesis* and *Parapulex chephrenis*. No effect of treatment on litter size or sex ratio of a litter was found in either rodent species. Flea parasitism was found to affect pre-weaning body mass gain in *M. crassus*, but not in *A. cahirinus* pups. Furthermore, it appeared that female *M. crassus* invested resources into their offspring differently in dependence of litter size. In small litters (1–3 offspring), pups from infested females gained more body mass before weaning than pups from uninfested mothers. However, this trend was reversed in females with large litters indicating that parasitized females have a finite amount of resources with which to provision their young. Thus, *M. crassus* mothers parasitized by fleas seemed to receive some sort of external cues (e.g., stress caused by infestation) that prompted them to alter offspring provisioning, depending on species-specific possibilities and constraints. Therefore, parasites could be a mediator of environmentally induced maternal effects and offspring provisioning may have adaptive value against parasitism.

(0009) A 173-year-old unresolved species problem: *Ixodes pilosus* group (Acari: Ixodida: Ixodidae) systematics with integrative taxonomy

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Carl Ludwig Koch described *Ixodes pilosus* in 1844 - 173 years ago. Since that time, the species has come to represent a group of widely variable *Ixodes* ticks that represent more than one species. Many specimens have been subject to misidentification errors involving *Ixodes rubicundus*, the Karoo paralysis tick. Hosts of the *Ixodes pilosus* group include bushbuck, impala, grey rhebok, bontebok, kudu, eland, buffalo, common duiker, mongoose, African clawless otter, scrub hare, jackal and domestic dogs. An initial investigation into the morphology of the type specimens was done to establish *Ixodes pilosus sensu stricto*. In this study, comparative morphology and molecular sequencing methods were employed to delimit previously hidden species and determine their distinguishing traits. Two new species are described based on morphology of adult males and females, as well as immatures and larvae. Interestingly, one new species appears to be implicated in transmission of alpha gal to humans, inducing red meat allergy. Geographic distributions and host utilisation patterns of the three species are revised.

(0011) Report on a *Culicoides* survey in Mpumalanga, South Africa, during 2015

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Agricultural Research Council – Onderstepoort Veterinary Institute, Pretoria, South Africa

A *Culicoides* survey was undertaken in eastern Mpumalanga, South Africa, during October and November 2015. Thirteen farms were visited in the Sabie, Hazyview, White River, Mbombela, Barberton and Kaapschehoop areas. A total of 39 collections were made. Other areas that included Pilgrims Rest, Graskop and Komatipoort were also visited, but no traps could be set because no suitable farms were found. Many farms (horse stables) that were visited 20 years ago, no longer exist, or have undergone a change in farming practices (from livestock to agriculture), or are now urbanised areas. The 'wild' horse herd in the Kaapschehoop area roughly numbers 150 animals. A point of concern is that many of these animals were abandoned along roadsides by people no longer able or wanting to care for them. This may contribute to outbreaks of African horse-sickness and other diseases that affect not just the health of the wild herd, but also that of other domesticated livestock. Weather conditions played a major role in the numbers of *Culicoides* collected; the area was in a period of drought, resulting in lower *Culicoides* numbers at many farms. During this survey 80 510 specimens representing 36 *Culicoides* species were collected. The catch size ranged from 3 – 19 602, with the largest numbers being collected in the Barberton and Mbombela areas.

(0013) The secret lives of the Enenteridae: new insights into the evolutionary relationships, biodiversity and ecology of an enigmatic family of digeneans

Daniel Huston, Scott Cutmore, Tom Cribb

The University of Queensland, St. Lucia, Queensland, Australia

Although the Lepocreadioidea family Enenteridae is morphologically intriguing and unusual, exploration of the biodiversity, ecology and evolutionary relationships of this group remains largely incomplete. The Enenteridae has diversified almost entirely in one host group, herbivorous marine fishes of the family Kyphosidae, and until recently, the family Enenteridae was thought to contain few species with relatively broad geographic ranges and host specificities. However, our recent molecular explorations have begun to reveal a pattern of unrecognized species richness and high host-specificity. Molecular exploration of this group is facilitating new species descriptions and taxonomic revisions within the family. Our increased understanding of the evolutionary relationships and convergent morphologies of the digenean parasites of kyphosids has also begun to provide clues into the ecology of the Enenteridae. While endoparasites have little use for pigmentation, as is seen in nearly all known trematodes, enenterids are brightly orange-coloured in life, suggesting the presence of carotenoids, which cannot be manufactured by animals *de novo*. Furthermore, species of nearly all digenean families have incomplete digestive systems with blind caecae. In contrast, enenterids

have complete digestive systems with a functional anus. The colour of enenterids, their unusual digestive tract morphology and their presence only in herbivorous hosts may suggest that this lineage has adapted to feed on the food of the host, rather than the host itself. Such a lifestyle could be termed 'kleptoherbivory' and appears to be an adaptation which has been adopted by several digenean lineages, each with a distinct expression.

(0014) Parasites lost - lessons learned from a critically endangered Australian marsupial – the woylie

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Approximately one third of the world's mammal species that have become extinct in the contemporary world were indigenous to Australia. This includes 17 marsupial species/subspecies with many others declining in range and/or abundance. What is now also clear, and largely ignored until recently, is the large number of parasite coextinctions that are likely to have occurred. Ongoing surveillance of the sole free-ranging population of brush-tailed bettongs, or woylies (*Bettongia penicillata*) in Western Australia commenced in 2008 with the aim of identifying a possible pathogen(s) associated with the recent decline of over 90% of the woylie population. This has involved a comprehensive investigation of micro- and macro-parasites that has demonstrated the large and diverse parasite fauna of woylies and provided one of the most detailed, unique and complete catalogues of a wild marsupial's parasite assemblage. It has resulted in the description of a new species of nematode, tick, and several haemoproteozoans, with a number of ecto- and endo-parasites still to be described. This ongoing investigation has also yielded critical insights into the life cycles and ecology of these parasites, as well as their potential role as pathogens, which will be discussed. Importantly, the majority of woylie parasites appear to be host-specific and thus clearly in danger of coextinction. It is rare to know the extent of potential parasite loss in a particular species of host because of the lack of sampling data, and our study reinforces the importance of long-term surveillance of native fauna to document parasite diversity.

(0016) Species richness of gnathiids (Crustacea, Isopoda) on the Australian Great Barrier Reef and surrounding habitats – estimates based on adult males

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Gnathiid isopods (Crustacea, Isopoda, Cymothoidea) are among the most common external parasites of marine fish. The larvae are the parasitic life stage, while the adults are non-feeding, occurring in cavities on the bottom, for instance in coral rubble and sponges. The male holds a harem, with female(s) and larvae resting between their feeding migrations in the water column. Despite recent advances, species composition of gnathiids remains poorly documented in most parts of the world. Evaluating species richness is tricky, because of sporadic sampling and difficulties in quantifying the actual sampling effort. Here, we evaluate the species richness of gnathiids on the Great Barrier Reef (GBR) in Australia, and in surrounding waters, and we base this on the presence of adult males. The GBR is comparatively rich in species. Similar numbers of reef species have been recorded from the southern (Heron Island and Wistari Reef) and northern (Lizard Island) part of the GBR, with several species occurring in both locations. The species richness in the outer islands of the Coral Sea is much lower than on the GBR, as would be expected given the isolation of these reefs. Despite under-sampling the GBR has the highest diversity of Gnathiidae of any tropical region in the world.

(0019) Clade analysis of males in a wild *Anopheles funestus* swarm in southern Africa

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The World Malaria Report stated that approximately 438 000 deaths from malaria occurred in 2015, 90% of them in Africa. One of the main African malaria vectors, *Anopheles funestus*, as is the case with many other anophelines, mate while swarming. Newly emerged male mosquitoes need to undergo several physical changes prior to mating. One of these changes is the rotation of the genitalia. The male genitalia consist of the abdominal segments 8 through 10, which include claspers that are tipped with claws that need to rotate between 135° and 180° to enable the male to grasp the female during copulation. The aim of this investigation was to study wild *An. funestus* swarms from Zambia and examine the number of males with fully rotated genitalia. Collections were made in Nchelenge, northern Zambia, during dusk and dawn periods to maximize the collections of specimens from six swarming groups. Genitalia rotation of the males present in the swarms was analysed by viewing the degree of clasper rotation. All the samples were morphologically identified as *An. funestus* group. Molecular analysis revealed that 80% of the males were *An. funestus* s.s. with 83% belonging to clade I compared to 17% clade II. This was similar to the general *An. funestus* population in this part of Zambia. Restriction Fragment Length Polymorphism analysis showed the same profile as those *An. funestus* from southern African (MW-Type). This is the first time that males from *An. funestus* swarms were molecularly characterised and the genitalia rotation classified.

(0020) Determination of sequence descriptions and predicted functions of selected *Theileria parva* hypothetical proteins

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In an effort to understand mechanisms responsible for the variation observed in East Coast fever and Corridor disease, both caused by *Theileria parva*, a transcriptome study was undertaken which detected differentially expressed genes (n=1089) and 867 were hypothetical proteins (HPs). Thus, it became crucial to determine the biological roles of HPs; this was achieved using a combination of in silico methods. A total of 397 HPs with a sequence description from initial analysis with Blast2GO, were investigated. Sequence descriptions of 252 HPs were confirmed by additional sequence similarity search within homologs and conserved domains. Sequence homology analysis identified homologs for 158 HPs while domains detection allowed annotation of 94 HPs. Identified sequence descriptions have shown to possess significant information, which ultimately, in conjunction with gene ontology, metabolic pathways and protein network analyses, allowed prediction of putative functions of 80% of HPs with an assigned sequence description. Functional annotation of *T. parva* HPs revealed a wide variety of proteins ranging from enzymes to members of large protein families conserved in transforming *Theileria* spp. Proposed functions for *T. parva* HPs also revealed that some of the annotated proteins might play critical roles in the parasite development; survival and propagation; parasite-host interaction; host invasion and disruption of the host signaling and immune systems. A search for essential genes identified 104 HPs of which 23% are non-homologous to host. Thus the latter can be considered as potential drug targets. Further experimental investigation is required to confirm the proposed functions of *T. parva* HPs.

(0023) *Myrsidea quadrifasciata* (Phthiraptera: Amblycera) - unique host generalist among highly host-specific chewing lice

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Myrsidea is the most speciose genus of chewing lice and also a good example of highly host-specific lice, with 80 % of species being restricted to one host. The remainders are found on a few hosts, with only a single instance of an overlap between host families: *Myrsidea serini*. Recently we collected *Myrsidea* lice from *Spinus magellanicus* (Fringillidae), a type host of *Myrsidea argentina*, in Peru. After comparison of its morphometric characteristics we found that this species is conspecific with *M. serini*. Our opinion is justified also by molecular data. A portion of COI and EF- α genes were sequenced and divergence among our data and that of *M. serini* from *Agelaioides badius* (Icteridae) from Paraguay is only 6.6%, while in comparison with other species of Neotropical *Myrsidea* with known sequences, p-distance is exceeding 18.2% in all cases. Curiously, the closest to our sequences were that of *M. textoris* ex *Ploceus intermedius* and *Ploceus velatus* (Ploceidae) from South Africa (p-distance 5.3%), followed by *Myrsidea* cf. *viduae* ex *Vidua macroura* (Viduidae) from Cameroon (p-distance 7.7%). Since all aforementioned species of *Myrsidea* belong to the “serini species group” we morphologically revised all 10 species from this species group and we are concluding that all taxa are conspecific. This result led us to a reconsideration of the first-described species from this group, i.e. *Myrsidea quadrifasciata* ex *Passer domesticus* (Passeridae) as its nominate species. We also summarize host spectrum and geographical distribution of this interesting cosmopolitan host generalist.

(0024) Invasion – lessons learned from Europe

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Invasion of non-native species to new environments has become a worldwide problem. Some of these invasions occur naturally, but most are caused by human activities (global trade, weirs, canals, etc.). Invasive species have the potential to cause major effects, both ecologically and economically in their “new” environments. However, possible effects on local parasite communities are largely ignored. Parasites might be introduced to a new environment together with their host species (spill-over) or the arrival of potential host species might cause new conditions for local parasites (spill-back or dilution effect). Either way, invasion has a high potential to change parasite communities in the long term and permanently. A good example for both mentioned instances are invasions from the Ponto-Caspian region (located in Eurasia) to the Rhine River (major European water route) in West and Central Europe. Due to human activities, the amphipod *Dikerogammarus villosus* could spread from the Ponto-Caspian region through the Danube River to the Rhine River, where it outcompeted other native amphipod species, which resulted in an extinction of some of these species. In addition to the change in amphipod composition, parasite communities also changed dramatically at the same time. Acanthocephalans of the genus *Pomphorhynchus* that use different amphipods as their first intermediate hosts, showed a direct effect since native and local acanthocephalans were replaced by the newly introduced species *Pomphorhynchus laevis*. The results of our long-term study are presented and discussed in detail. Overall, our study exemplified effects invasion of free-living species may entail on parasite communities.

(0027) First evidence of hemoplasma infection in free-ranging Namibian cheetahs (*Acinonyx jubatus*)

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Hemotropic mycoplasmas (hemoplasmas) are cell-wall-free bacteria that parasitize red blood cells. *Mycoplasma haemofelis* (Mhf) is the causative agent of feline infectious anemia. Infections with Mhf have been documented in domestic cats and free-ranging feline species with high prevalences in Europe, African lions (*Panthera leo*) in Tanzania and domestic cats in South Africa. The prevalence of hemoplasmas has not yet been investigated in free-ranging felids such as cheetahs in southern Africa. In this study we screened 73 blood samples from 61 cheetahs in central Namibia for the presence of hemoplasmas. Namibia hosts the largest free-ranging cheetah population in the world and it is important to identify the pathogens that might threaten this valuable cheetah population. We used quantitative real-time PCR and demonstrated that one of the cheetahs was PCR-positive. This is the first molecular evidence of a hemoplasma infection in a free-ranging cheetah. Due to the low prevalence, this result suggests that hemoplasma infections might not pose a serious threat to the Namibian cheetah population. Phylogenetic analysis based on partial sequencing of the 16S rRNA and RNase P genes revealed that the isolate belongs to the Mhf/*Mycoplasma haemocanis* (Mhc) group, without clear assignment to either cluster. This is remarkable, because isolates from felids usually can be clearly assigned to the Mhf cluster. Perhaps the Kalahari Desert poses a barrier to infectious agents and thus might have enabled Mhf in Namibia to evolve independently from the *Mycoplasma* previously identified in South Africa or Tanzania into a currently unknown strain.

(0028) Sucker stalk length is not important; it's which fishes you infect with it that matters! Polyphyly among species of *Podocotyloides* Yamaguti, 1934 (Trematoda: Opecoelidae)

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Although the ventral sucker is of little diagnostic value for most genera in the Opecoelidae, several include species which exhibit various specialisations. A pedunculate ventral sucker is a defining feature for *Podocotyloides* Yamaguti, 1934, and all 'plagiopore' opecoelids possessing this character are presently grouped in this genus. We collected specimens from sweetlips (Haemulidae) in Australian waters which we consider to represent two cryptic species congeneric with the type-species, *P. petalophallus* Yamaguti, 1934, also known from a sweetlips, off Japan. By analysing molecular data generated from these specimens, we demonstrated that species of *Podocotyloides* infecting sweetlips are phylogenetically distant from *P. brevis* Andres & Overstreet, 2013, described from a deep-sea eel (Congridae), *P. parupenei* (Manter, 1963) Pritchard, 1966, known only from goatfishes (Mullidae), and *P. stenometra* Pritchard, 1966, a parasite of corallivorous butterflyfishes (Chaetodontidae). These three species are phylogenetically distinct and each warrants recognition of a new genus. We also discovered a third, distinctive species, from sweetlips, with an exceptionally long sucker peduncle. It is consistent with the concept of *Pedunculacetabulum* Yamaguti, 1934, which has been considered a synonym of *Podocotyloides* since 1966. Based on combined evidence from phylogenetic analyses, morphology and host-specificity, we propose resurrection of *Pedunculacetabulum* and revision of *Podocotyloides*. Of 22 nominal species, known from a broad range of fishes, we consider just four infecting sweetlips to genuinely belong in the genus. It seems that for opecoelids, host groups provide a good indication of genus-level distinction, but this has been overlooked historically in favour of arbitrary morphological concepts.

(0029) Advances in understanding of fish blood flukes (Aporocotyliidae) infecting tetraodontiform fishes: taxonomy and systematics

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Since the turn of the century, biodiversity assessments of fish blood flukes (Aporocotyliidae) have greatly expanded our understanding of the faunal richness of this significant trematode family. Despite increased survey effort, however, many groups of fishes are considered undersurveyed for aporocotyliids. The fishes of the order Tetraodontiformes, commonly known as the pufferfishes and their allies, are one such group. My investigations into the aporocotyliid richness of tetraodontiform fishes in Australia have revealed a significant uncharacterised fauna. These include a complex of species infecting pufferfishes of the genus *Arothron*, and new species infecting fishes from the triggerfish (Balistidae), boxfish (Ostraciidae) and tripodfish (Triacanthidae) families, all of which represent the first records of aporocotyliids from these host families. I present a summary of the latest findings of novel taxa, and attempt to contextualise them within our current improved understanding of aporocotyliid phylogeny, host range and biogeography.

(0032) First report of occurrence of an alien cestode parasite in an alien fish (*Cyprinus carpio*), Kwena Dam, Mpumalanga Province, South Africa

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Biological invasions pose global threats to aquatic biodiversity. Introduced species may transfer parasites to native species which may negatively affect their health and eventually alter fish biodiversity. Common carp (*Cyprinus carpio* Linnaeus, 1758), an alien species originally introduced in 1859, is well established in South African waters and is categorised as a fully invasive fish species. Several parasite species, including cestodes, have been reported from carp in South Africa. Cestodes are found in the digestive tract of the host and they lack a digestive system. Kwena Dam is located in the Crocodile River catchment near Mashishing (Lydenburg) in Mpumalanga Province. No parasitological research had previously been done at this dam. The aim of this study was to determine the seasonal occurrence of cestodes of the common carp in Kwena Dam. Fish were collected using gill nets of different mesh sizes in autumn (April 2016), winter (July 2016), spring (October 2016) and summer (February 2017) to determine differences in seasonal mean intensity levels. Fish were euthanised and examined for parasites. Cestodes were fixed in hot water and preserved in ethanol. Based on morphological characters, cestodes recovered from *C. carpio* were identified as *Atractolytocestus* Anthony, 1958 (Cestoda: Caryophyllidae). This study provides a new distribution record of an alien cestode that had previously only been reported from Flag Boshielo and Tzaneen dams in Limpopo Province and Loskop and Witbank dams in Mpumalanga Province.

(0033) *Gyrodactylus* spp. (Monogenea: Gyrodactylidae) of freshwater fishes from South Africa: an unexplored field with new challenges for research

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Viviparous monogeneans of the genus *Gyrodactylus* von Nordmann, 1832 are tiny parasites, predominantly parasitising bony fishes. Nearly 500 *Gyrodactylus* species have been described worldwide, of which only 36 have been identified from African waters. To date, only three *Gyrodactylus* species have been described from South Africa. From March 2012 to February 2017, various fish species from the Cyprinidae, Claridae and Cichlidae were collected during field surveys at 10 localities from four provinces (Limpopo, North-West, Northern Cape and KwaZulu-Natal) of South Africa. Collected hosts were screened for the presence of *Gyrodactylus* species. Gyrodactylids were fixed in glycerin-ammonium picrate for morphometric analyses and selected specimens in ethanol for molecular characterisation. Phylogenetic analyses based on ITS and 18S rDNA were performed to reveal the position of newly found species. *Clarias gariepinus* was collected from nine localities, and hosted eight *Gyrodactylus* species. Four of them are known to the science (*Gyrodactylus alekosi*, *Gyrodactylus gelnari*, *Gyrodactylus rysavyi* and *Gyrodactylus transvaalensis*) and the remaining four represent new species. *Pseudocrenilabrus philander* was parasitised by *Gyrodactylus thlapi* and *Gyrodactylus sturmbaueri*. *Oreochromis mossambicus* was infected by one unknown species. Two new species were collected from *Enteromius paludinosus* and *Labeo cylindricus*; both represent new host records for *Gyrodactylus* species. The present findings show that the knowledge on species richness of *Gyrodactylus* species in South Africa is still very limited.

(0037) Fisheries targets in Lake Tanganyika: revealing the mystery of their parasite fauna

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Lake Tanganyika is the deepest and one of the most species-rich African Great Lakes. While dozens of studies focusing on this lake's cichlids as famous model organisms have been already published, knowledge about economically important species is still poor. The fisheries effort is concentrated mainly in the lake's pelagic zone with two clupeids (*Limnothrissa miodon*, *Stolothrissa tanganyicae*) and four latid species (*Lates angustifrons*, *L. mariae*, *L. microlepis*, *L. stappersii*) as dominant targets. Surprisingly, almost nothing is known about their parasite fauna. We examined the abovementioned hosts for the presence of parasites to answer the following questions: which parasites infect clupeids and latids in Lake Tanganyika? Is there any seasonality or geographical variation in infection parameters? And is the parasite population structure related to host history or geographic origin? Samples originated from many localities in Lake Tanganyika including all three historical subbasins of the lake. Parasite species identification was based on the sclerotised structures. Molecular characterisation was conducted using nuclear and mitochondrial markers with different rates of molecular evolution. In total, three different parasite species belonging to the Monogenea were identified based on morphological as well molecular data. Slight differences in parasite prevalence of clupeids related to geographic origin of *Ancyrocephalus* were observed, but no relation with seasonality was found. The parasite population structure inferred from part of the COI gene shows no north-south gradient. For future studies, the phylogeography of these parasites can reflect historical events that are too recent to be inferred from host genetics.

(0038) Understanding trophic interactions in monogenean-fish associations using stable isotopes of carbon and nitrogen

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Stable isotope signatures of carbon ($\delta^{13}\text{C}$) and nitrogen ($\delta^{15}\text{N}$) are increasingly used to study food web architecture. In ecology, the isotopic discrimination values of $\Delta\delta^{13}\text{C}$ and $\Delta\delta^{15}\text{N}$ are applied as unique fingerprints, which allow for a determination of food sources and trophic interactions between organisms, respectively. For example, investigations of stable isotopes of nitrogen have shown that consumers are enriched in heavy nitrogen ($\Delta\delta^{15}\text{N}$) with an average of 3.4‰ per trophic level. Accordingly, the application of stable isotope analyses might also be helpful to elucidate the trophic relationship between a parasite and its associated hosts. However, the number of studies based on stable isotope analyses of host-parasite interaction remains scarce and no information is available concerning monogeneans and their fish hosts. We have therefore sampled individuals of smallmouth yellowfish (*Labeobarbus aeneus*) and largemouth yellowfish (*Labeobarbus kimberleyensis*) inhabiting the Vaal Dam, both infected with the monogenean parasite *Paradiplozoon ichthyoxanthon*. This system is especially interesting as the fish species occupy different trophic niches and acquire nutrients from different food sources which suggests that these differences might affect the trophic position of the parasite in relation to the respective fish host. Stable isotope analyses were performed for fish muscle and the monogeneans using an elemental analyser coupled with an isotope ratio-mass spectrometer (EA-IRMS). Nitrogen isotope discrimination values indicate that the monogeneans behave like predators when compared to classical food-web interactions. Detailed results for both host species and the deductions drawn are presented and discussed.

(0039) Vector incrimination in South Africa: challenges and highlights

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South Africa has a long and successful history of malaria vector control and is aiming to eliminate malaria within its borders by 2020. However, residual malaria transmission, insecticide resistance and limited cross-border malaria control collaborations remain a challenge. Vector surveillance is key to addressing a majority of these challenges because the information obtained directly informs control efficacy and strategies. Collecting entomological data is costly and faces various obstacles, one of which is budget and human resource limitations. An *Anopheles* mosquito surveillance system was therefore initiated to address these challenges and various mosquito sampling methods were evaluated. Future use of these anopheline collection methods will depend on the need within each province. During the study vectors responsible for outdoor malaria transmission were identified and their susceptibility to insecticides determined. Vector population size at one of the sentinel sites was estimated. Overall, this work provides a potential surveillance system which can be adapted for use by provincial malaria control programmes.

(0041) Alien parasites alert in South Africa!

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Non-native fish introductions have occurred over the last two centuries in South Africa. These alien fishes can act as vectors and introduce a variety of alien fish parasites into the country which may affect hosts in new regions. These parasites can expand their range over the country and even the continent through the importation of infected hosts. A good example is *Bothriocephalus acheilognathi* Yamaguti, 1934, the Asian tapeworm, that was introduced with grass carp from Europe and has since infected a variety of native cyprinid fishes and become widespread. This study expands the distribution area of selected alien parasites of freshwater fishes in South Africa such as *Atractolytocestus huronensis* Anthony, 1958 (Cestoda) from common carp, *Camallanus cotti* Fujita, 1927 (Nematoda) from guppy and *Pseudodactylogyrus anguillae* (Yin & Sproston, 1948) (Monogenea) from longfin eel. Some of these parasites, e.g. *A. huronensis*, are reported for the first time from Africa and elaborate on the distribution of these invasive parasites to include Africa beside Asia, Europe and North America. Considering the lack of ability of native fish to cope with alien parasites, because of weaker immunological responses, and the present development of aquaculture in South Africa, the records of alien and invasive parasites should represent a drive to deal more intensively with the problem of biological invasions.

(0043) The effect of life history and vicariance on the dispersal and evolution of ticks

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With a near global distribution, ticks represent one of the most economically important ectoparasite groups. Due to complex life cycles and their obligate association with vertebrate hosts, the mechanisms that gave rise to the rich biodiversity within the Ixodoidea are enigmatic. It is predicted that host range, abiotic factors affecting the off-host life stages, and vicariance can all contribute towards the diversification of ticks. By making use of dated phylogenetic trees, comparative population genetic analyses, and spatial dispersal vicariance analyses, the present review aims to unravel some of the mechanisms involved in tick speciation. Results indicated that tectonics and / or large-scale climatic changes contributed significantly towards the speciation of *Hyalomma* and *Amblyomma* ticks. In particular, in *Hyalomma*, rifting in east Africa, the collision of the Indian and Eurasian Plates and the closure of the Tethyan seaway all played a role in the earlier diversification of currently recognized species. In addition, vicariance events

that affect multiple vertebrate species resulted in cryptic divergences within *H. truncatum* across the African continent, a pattern also detected within *H. rufipes*. In instances where the entire life cycle can also be completed on a single host species, such as that found in *Amblyomma variegatum*, the effect of similar vicariance effects are less influential. In tick species where multiple hosts are needed to complete the life cycle, factors such as the environment of the host, and in particular the availability of suitable hosts for juvenile stages, are important drivers in tick dispersal.

(0044) Siphonostomatoids collected from White Sharks (*Carcharodon carcharias*) during the OCEARCH project in South Africa

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OCEARCH is a recognized world leader in generating important scientific data about shark species in an attempt to address the globally limited understanding of such species. These species include amongst others the IUCN vulnerable White Sharks. During the expeditions sharks are caught, restrained and supplied with water to assure the flow of oxygen while data is collected within 15 minutes, whereafter the shark is released unharmed. During March to May 2012 such an expedition took place along the south and west coasts of South Africa. As part of this expedition copepods were collected from the external surfaces of the captured sharks. They were fixed and preserved in 70% EtOH and examined using microscopes. The copepods represent seven species with most individuals belonging to the Pandaridae and Dichelestiidae, while only two specimens represent Caligidae.

(0045) A complex of *Macvicaria* Gibson & Bray, 1982 (Digenea: Opecoelidae) in Mediterranean sparids

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Macvicaria Gibson & Gray, 1982, represents one of the most diverse genera within the Opecoelidae Ozaki, 1925 (Digenea), currently comprising 53 species considered valid, parasites of a broad range of marine teleosts worldwide. Due to substantial morphological variation and dubious defining characters, the genus is considered particularly unsatisfactory. During a study of helminth diversity in two sparid fishes, *Sparus aurata* L. and *Diplodus vulgaris* (Geoffroy Saint-Hilaire) from the western Mediterranean off Algeria, we observed frequent infections with species of *Macvicaria*. Detailed morphological examination of the worms was carried out along with molecular characterisation of the isolates. Partial sequences for the 28S rRNA gene and the entire ITS1-5.8S-ITS2 rDNA gene cluster were amplified for representative isolates in order to assess species boundaries in phylogenies inferred from maximum likelihood and Bayesian inference analyses. Phylogenetic analyses confirmed the distinct status of eight species of *Macvicaria* including one new to science. The taxonomic structure of '*Macvicaria crassigula*' species complex is discussed in the light of the new findings. Our results indicate a higher diversity of *Macvicaria* spp. in the Mediterranean and call for further studies to assess the diversity and host-parasite associations of the species.

(0046) Your address matters: Helminth parasitism in two closely-related but spatially distinct South African rodents

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Closely-related host species often share characteristics such as physiology, morphology and diet; however, the habitat and environment they live in can change their behaviour and ultimately their exposure to parasites. Patterns of helminth infection were investigated in two closely-related rodents (solitary *Rhabdomys dilectus* occurring mainly in mesic habitats and social *R. pumilio* occurring mainly in xeric habitats) at 20 localities in different climatic regions in South Africa. We asked whether the differences between the host species were caused mainly by difference in sociality or difference in environmental conditions of their respective habitats. *Rhabdomys dilectus* harboured 19 nematode and 7 cestode species and *R. pumilio* 11 nematode and 5 cestode species. Cestode infection as well as nematode abundance, species richness or prevalence did not differ between the two rodents. However, incidence of nematode infection was significantly higher in *R. dilectus* than in *R. pumilio*. Moreover, nematode numbers and species richness in infracommunities of *R. pumilio* inhabiting the relatively more xeric Karoo region were significantly lower than in those inhabiting the relatively less xeric Fynbos region. Differences in the incidence of nematode infection between *R. dilectus* and *R. pumilio* as well as differences in the number of nematode individuals and species between *R. pumilio* from the Fynbos and the Karoo suggests that the effect of diverse abiotic factors on helminth infection is more important than that of sociality.

(0048) Host-parasite secondary contacts: barriers and introgression

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Hybrid zone studies of host-parasite systems have largely taken a host-centric viewpoint: does parasitism affect the outcome of host hybridization by differentially impacting the fitness of host taxa vs. their hybrid descendants? This viewpoint neglects the possibility that host taxa have distinctive genetic clusters of parasites that may themselves potentially hybridize. Hybridization, bringing together combinations of genes previously untested by natural selection, may affect parasites in similar ways to free-living organisms: revealing a barrier to gene flow, promoting divergence via reinforcement, homogenizing genetic clusters or leading to rapid adaptive diversification via the formation of hybrid parasite species. We compare host-parasite genetic structure across a spectrum of parasites with no intermediate host (from viruses to helminths) and across two rodent secondary contact systems: the multimammate mouse, *Mastomys natalensis*, in Africa and the house mouse, *Mus musculus*, in Europe. Our results show that parasite introgression is correlated with the degree of intimacy with intimate parasites such as arenaviruses strongly structured with the host while generalist parasites such as whipworms showing no host-correlated structure. For those parasites structured by host secondary contact, we predict that advantageous genes such those allowing parasites to overcome the host immune response will preferentially introgress across host secondary contacts. We will test this hypothesis using genomic data on murid betaherpesviruses and pinworms.

(0051) Diversity of fish parasites from a survey in the Phongola Floodplain

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During September 2013, a survey on fish parasites was carried out on the Phongola Floodplains together with scientists from four South African universities. These scientists surveyed fish, birds, amphibians and plankton as part of an umbrella project of the North-West University. The Phongola System forms part of the tropical east coast aquatic ecosystem. Fifty fish species have been recorded from the floodplains, making it the most diverse fish fauna in South Africa. During the survey a total of 140 fish specimens, representing 25 species from 10 families, were examined for parasites. Fishes were mainly collected using sein and fyke nets and kept in aerated holding tanks in a temporary laboratory set up at the Ndumo Rest Camp, whereafter they were examined for endo- and ectoparasites. All parasites collected were fixed and/or stained according the method appropriate for each taxon or group under field conditions. Some groups have been further processed and final identifications made, while other groups are at present in the process of further analysis. A total of 18 parasite taxa were collected. These include several ciliophorans, such as mobiline and sessiline peritrichs (*Trichodina*, *Tripartitella*, *Trichodinella*, *Hemitrichodina*, *Apiosoma*, *Scopulata* and *Epistylis*); suctorians of the subclass Suctorina and the infamous white spot *Ichthyophthirius*. The flagellates *Ichthyobodo necator* and *Trypanosoma* were also found. Several monogeneans and crustaceans (*Lernaea*, *Ergasilus* and *Chonopeltis*) were collected, as well as myxozoans, cestodes and trematodes. A breakdown of host preference, infestation levels and prevalence is provided.

(0053) Taeniid cestodes in African mammals - an unrecognized aspect of biodiversity

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Taeniid cestodes have lifecycles that include only mammals as hosts, predominantly carnivores as definitive hosts and their respective prey as intermediate hosts. Most taeniid species are parasites of wildlife, and even those that are only known from domestic lifecycles must have derived at one stage from sylvatic transmission systems, because their phylogenetic age predates the domestication of livestock by far. Until few years ago, 14 *Taenia* species were known from wild carnivores in sub-Saharan Africa. However, in two recent small-scale molecular studies, conducted in very restricted areas of Ethiopia and Namibia, 13 mitochondrial *Taenia* / *Hydatigera* lineages were identified, of which only two (*T. regis* and *T. crocutae*) could be allocated to described species. In Etosha (Namibia) alone, five such lineages were present in cheetahs, a host from which only two morphological species were formerly in all of Africa. Formerly only one species of *Echinococcus* (*E. felidis*, or "lion strain") was supposed to cycle in wild African mammals. However, recent surveys identified five *Echinococcus* spp. in wild carnivores, some having purely sylvatic transmission and others probably linked with domestic transmission systems. A recent isolate from a human patient in Ethiopia, which cannot be allocated to any described *Echinococcus* sp., is also likely to derive from a wildlife reservoir. Even these preliminary surveys show that taeniid diversity in African wildlife is far higher than previously recognized. Taking into account the "out-of-Africa" hypothesis on the origin of human *Taenia*, Africa appears to be a diversity center for taeniid cestodes.

(0057) Wild carnivores of Europe as reservoirs of vector-borne nematodes

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Several vector-borne nematodes are known to occur in European wild and domestic carnivores. Among the most important are *Dirofilaria immitis*, *D. repens* and *Thelazia callipaeda*, all of them known to infect also humans. Despite a large number of studies in domestic carnivores (mainly dogs), extensive studies on wild carnivores are still scarce. However, wild carnivores play a potentially important role as reservoirs of infections for domestic dogs and cats as well as for humans. During the last 5 years, we have examined extensive sample sets from wild carnivores in Romania, a country known for its large populations of these mammals. Overall, 810 wild carnivores belonging to 14 species were examined. *Dirofilaria immitis*, *D. repens* and *T. callipaeda* were all detected, with variable prevalences according to species and geographical location, including various new parasite-host associations. The results are critically discussed in connection with similar studies in Europe, highlighting the role of wild carnivores in the natural cycles of the vector-borne nematodes and in their territorial spread to and emergence in new territories.

(0058) Next generation techniques meet recent challenges: the integration of structural equation models and multimodel inference for the exploration of multihosts-multiparasite interactions in natural systems

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Traditionally, the study of host-parasite interactions has been approached from its simplest organizational level composed of just one host and one parasite species. However, those simple systems are exceptional cases in nature whereas interactions between multiple host and parasite species are the common rule, creating, thus, a complex network systems, which should also integrate other biotic (e.g., vectors, predators) and abiotic (e.g., substrate, sand humidity) factors in the community. The consideration of multiple hosts or parasites - the present trend in host-parasite studies - challenges the traditional correlation-based analysis, which is limited to one or a few highly-correlated response variables and relies on a limited number of alternative hypotheses. I discuss the great potential of integration between structural equation models (SEM) and multimodel inference (MI) approaches to account for the complexity in natural multihost-multiparasite systems. Specifically, the SEM-MI approach highlights the most likely pathways that may connect a suite of interrelated factors, and explore the strength and direction of both direct and indirect effects. To illustrate the advantages of the integrated analysis over the traditional ones, I review some of our work on rodent-flea-bacterial interactions in which the approach was remarkably insightful. Discussing the possible pitfalls of the integrated approach in concert with some recommendations, I argue that a correct use of the SEM-MI approach is likely to overcome some of the difficulties related to multihost-multiparasite communities.

(0061) Fleas parasitizing common voles: impacts at host population and individual levels

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By experimentally adding or removing parasites, it has been shown that macro-parasites may regulate populations of their hosts. At an individual level, ecto-parasites can affect body condition, growth, life span, energy expenditure, litter size, foraging, and juvenile survival of hosts, which could translate into effects on host population abundances. We investigated the effect of a flea community (*Cenophthalmus apertus*, *Nosopsyllus fasciatus*, *Leptopsylla taschenbergi*) on free-living common vole (*Microtus arvalis*) populations from agricultural landscapes of NW Spain, where voles regularly fluctuate in numbers. We evaluated the numerical response of fleas to vole abundance (direct vs. delayed density-dependence, DD), also considering the abundance of alternative rodent hosts. We tested for negative associations between vole population growth rates (PGR) in spring, summer and winter and species-specific flea abundances. Finally, we investigated whether the body condition of voles (mass relative to size) and the reproductive effort of females (number of embryos) co-varied with flea abundance. We found that: (1) flea abundance had a delayed DD pattern, increasing with previous (8 month before) vole abundance; (2) at population level, a greater flea abundance was associated with a reduced vole PGR in summer and winter; and (3) male body condition in spring and winter and the number of embryos per pregnant female were negatively associated with individual-level flea abundance. These effects varied depending on the flea species, but support the hypothesis that fleas have a regulating influence on common vole populations and have a destabilizing effect in the studied system. Experiments are required to confirm these findings.

(0062) Parasites under threat - should we care?

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Besides their important role as pathogens, parasites have long been considered negligible components of ecosystems. However, recent studies elucidating the patterns of parasite biomass, diversity and their interactions in food-webs have revealed that parasites represent important ecological players in the dynamics of natural systems. Just like their free-living hosts, parasites are susceptible to environmental changes, such as the introduction of invasive species or the global effects of climate change. Due to such changes, we potentially lose parasites, often before we understand what roles they play in ecosystems. Far from making an ecosystem 'healthier', the loss of parasite diversity can have detrimental effects. Based on assessments of molluscs and their trematode communities in Europe and South Africa, we want to highlight (a) the integral role of these parasites in ecosystems and (b) point out the potential diminishing effects of ecosystem changes on such complex host-parasite systems. A study of snail-trematode communities from European freshwaters revealed the presence of 40 trematode species in this habitat, and their substantial contribution to diversity and biotic productivity. The extensive sampling of molluscs from the Phongolo River floodplain in South Africa showed that the invasive snail *Tarebia granifera* outnumbers and potentially displaces native snail species. Since *T. granifera* does not serve as a host for trematodes in Africa, this can have negative effects on trematode diversity and community structure. Parasitologists and conservation ecologists alike should therefore care and consider parasites in the ecological assessment of environmental changes beyond their role as harmful disease agents.

(0063) Occurrence and molecular characterization of *Mycoplasma* spp. in bats sampled in Brazil

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The role of wild animals as reservoirs in the transmission of vector-borne diseases has been investigated. The order Chiroptera, the second-largest group of mammals in the world, hosts important zoonotic virus and bacteria. Hemoplasmas are bacteria that parasitize different mammal species' erythrocytes, causing different clinical manifestations. The present work aimed at investigating the occurrence and assessing the phylogenetic positioning of *Mycoplasma* spp. in bats sampled in Brazil. A total of 325 blood and/or tissue (liver, spleen and heart) samples were collected from 162 bats belonging to 19 species distributed in four different families from five states in Brazil (Mato Grosso, Pará, Paraná, São Paulo and Tocantins). Three samples showed negative results in the conventional PCR based on GAPDH gene and were excluded from analysis. Forty-five out of 322 bats' biological samples (13.97%) were positive to cPCR assays for hemoplasmas based on 16S rRNA gene. In the phylogenetic analysis by Maximum Likelihood and Bayesian Inference, five sequences clustered together as a monophyletic group and closely related to *Mycoplasma coxoides*. The positive biological samples for hemoplasmas were collected from *Artibeus planirostris*, *Eptesicus* sp., *Eumops auripendulus*, *Glossophaga soricina*, *Molossus molossus*, *Molossus rufus*, *Myotis nigricans* and *Sturnira lilium*, representing the first evidence of circulation of this pathogen in these bat species. Therefore, the present work showed the first evidence of circulation of hemoplasmas among bats from Brazil.

(0065) Ciliophorans collected from a wide variety of hosts from the Okavango system, Botswana

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During fish-parasitological surveys conducted in Botswana (1997-2015), representatives of five ciliophoran genera were recorded from 56 fish species. Eighty-six fish species are found in the Okavango drainage basin, 72 of which inhabit the waters of the Okavango River and Delta. Fish were collected using sein, cast, scoop and gills nets, and kept in aerated containers until dissection and examination, that took place in temporary field stations or at the Leseding Research Camp, Samochima. All the symbionts found (protozoans, myxozoa, helminths, roundworms and parasitic crustaceans), were collected, fixed and preserved using standard techniques for each taxon. Ciliophorans collected comprise Phyllopharyngea (*Chilodonella*) and Oligohymenophorea (*Epi-stylis*, *Apiosoma*, *Scopulata* and *Ichthyophthirius*). Numerous trichodinids (mobile ciliates) were also collected, but are excluded from this paper. The ciliates were found on either the skin or gills of the hosts, with low (x) to higher infestations (xxx). Multiple infestations, between two and four genera per host were recorded. It was found that 12 of the 15 fish families were infested. True to their nature, ciliates occur more often on smaller species or juvenile fish and not on larger ones or adults. *Chilodonella* and *Ich* are the best-known culprits that can be detrimental to their hosts, often leading to secondary bacterial or fungal infections. This will most of the time only be found under aquaculture conditions and not occur in natural, pristine habitats such as the Okavango.

(0066) Infection studies with the malaria parasite, *Plasmodium falciparum*, on African malaria vectors *Anopheles arabiensis*, *An. funestus*, *An. coluzzii* and *An. gambiae* at the Wits Research Institute for Malaria

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The malaria parasite life cycle in the adult female *Anopheles* mosquito has received renewed attention in recent years with the development of transmission-blocking strategies. The parasite life-stages in the vector, in particular ookinete formation in the midgut, with subsequent oocyst formation on the midgut wall, and the release of sporozoites and their migration to the salivary glands of the mosquito, are important measurable variables in transmission-blocking strategies. Oocyst prevalence and oocyst intensity are used to evaluate the impact of compounds against the development of the parasite in the vector. Infection studies aimed at artificially infecting African malaria vectors with *Plasmodium falciparum* using the Standard Membrane Feeding Assays (SMFA) were initiated. Recent experiments have been carried out to optimize current protocols best suited for African *Anopheles* species. In successive infection studies done in various mosquito species, progress has been made with regard to the infection rate obtained in these species. The infection rate was determined by the presence of oocysts (prevalence), as well as the mean number of oocysts per specimen (intensity). Successful infection was achieved for four of the main African malaria species. Infection is confirmed by the presence of sporozoites in the salivary glands of these vectors.

(0067) Cardiopulmonary nematodes in wild carnivores from Romania

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Lungworms of wild carnivores belong to the superfamily Metastrongyloidea, two genera, *Angiostrongylus* and *Aelurostrongylus*, being spread worldwide. *Angiostrongylus vasorum* and *Aelurostrongylus abstrusus* parasitize the pulmonary arteries, right ventricle and lung parenchyma of canids and felids in Europe. Our aim was to investigate the presence of these species in Romanian wild carnivores by necropsy, parasitological identification and molecular characterization. Three species of angiostrongylids are described in Romania. The overall prevalence of *A. vasorum* in red foxes (*Vulpes vulpes*) was 3.7% (16/436). The prevalence of *A. chabaudi* in wildcats (*Felis silvestris*) was 6.4%, and *A. daskalovi* was identified in 5 of 10 (50%) Eurasian badgers (*Meles meles*) examined. *Aelurostrongylus abstrusus* was recorded in 3 out of 47 wildcats (6.4%), and a further unidentified *Aelurostrongylus* sp. was found in two badgers. In the case of *A. vasorum*, *A. daskalovi*, *A. chabaudi* and *A. abstrusus*, molecular analysis has shown a high similarity with sequences from GenBank. Further studies are needed to understand the life cycle of *A. chabaudi* and *A. daskalovi* and the role of wild carnivores as reservoirs for domestic dogs and cats.

(0068) Role of the European wild carnivores in the natural cycle of ticks and tick-borne diseases

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Data regarding tick diversity and tick-host associations in wild carnivores in Europe are scarce. Anthropogenic changes and diminished boundaries between wild and domestic animals increase the exposure of domestic species and humans to infective agents, including tick-borne pathogens. Analyzing the role of wild carnivores as tick hosts may lead to understanding the life cycle of ticks in the natural environment and the epidemiology of tick-borne agents. This study aimed to assess the ixodid tick fauna of wild carnivores in Europe, focusing on Romania. We conducted the first large-scale survey of ticks parasitizing wild carnivores in this country. Wild carnivores (n=202; 14 of the 17 species present in Romania) were included in the study and 430 ticks were collected. Of these, 7 tick species were identified: *Dermacentor reticulatus*, *Haemaphysalis concinna*, *H. punctata*, *Ixodes hexagonus*, *I. ricinus*, *Rhipicephalus rossicus* and *R. sanguineus s.l.*. The highest prevalence of infested wild carnivores was recorded in pannonian (66.7%) and steppic (52.7%) ecoregions. Prevalences of 26.7% and 28% were recorded in the continental and pontic ecoregions, respectively. The lowest prevalence was recorded in alpine eco-region (16.7%). Fourteen new tick-host associations were reported. Given that each species of wild carnivores plays an important role in the eco-epidemiology of zoonotic tick-borne diseases, their anthropic incursions may threaten public health. We encourage further studies to be conducted especially in areas where this type of surveillance is limited or absent.

(0069) Infection with tongue worms in Australian animals

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We present our findings on the prevalence, distribution, histopathology and specific identification of an intriguing parasite, the tongue "worm" in Australia. The tongue-worm, *Linguatula serrata* (Pentastomida: Linguatulidae) is an obligate arthropod parasite that may be found in the nostrils of carnivores. Larval stages of the parasite inhabit the lymph nodes, liver and lungs of their intermediate hosts, including various species of livestock and wildlife. Tongue worms are of zoonotic significance, human infection with both adult and larval stages of the parasite having been reported in several countries. In Australia there have been few reports of tongue worms, generally as an accidental finding. In this study we examined wild canids, vulpids and lapids as well as domestic livestock in South-Eastern Australia for infection with these parasites. A combined morphological and molecular approach was used for their specific identification. The prevalence of these parasites in the region was unexpectedly high, with 67% of the wild dogs examined affected. Histopathological examination of the host tissues revealed mechanical damage to the mucosal membranes in the nasal cavity and moderately severe granulomatous lymphadenitis with some intra-lesional parasitic remnants in damaged lymph nodes. Currently tongue worm infection and the human and animal disease impacts arising from infection are not of primary concern to Australian veterinarians and health practitioners. Wildlife is now recognised globally as an important source of emerging human pathogens. The prevalence of these zoonotic parasites in Australian carnivores indicates the importance of increasing public awareness of these zoonotic parasites, particularly health professionals and veterinarians.

(0071) Diversity and host specificity of *Mammomonogamus* in domestic and free-living animals

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Syngamid nematodes of the genus *Mammomonogamus* parasitize the respiratory tracts of felid carnivores, ungulates, elephants and primates including humans in mainly tropical regions of the world. The level of host specificity of the genus is unclear. Some species are described as being host-specific (e.g., *M. okapiae* and *M. ierei*), whereas other species such as *M. laryngeus* or *M. loxodontis* are able to infect phylogenetically distant hosts such as ruminants and humans or elephants and gorillas, respectively. Until recently the DNA of *Mammomonogamus* had not been analyzed. We isolated and amplified DNA of *Mammomonogamus* from (i) eggs isolated from feces of western lowland gorillas (*Gorilla gorilla gorilla*), African forest elephants (*Loxodonta cyclotis*) and African forest buffaloes (*Syncerus caffer nanus*) from different sites in Africa and (ii) adult helminths found in domestic cats and both domestic and wild ruminants in the Caribbean, South America and Northern Mariana Islands. Phylogenetic analysis of fragments of 18S rDNA, 28S rDNA, internal transcribed spacer (ITS) and cytochrome c oxidase subunit 1 showed forming of clades based on geographic distribution and host species. It appears that *Mammomonogamus* is shared by syntopically living elephants and gorillas, but buffaloes are infected by different species.

(0072) The Great American Trichodinid?

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Trichodina heterodentata was first described from fish breeding farms in the Philippines by Bryan Duncan in 1977 as ectoparasites of imported cichlids, more specifically the southern African *Oreochromis mossambicus* from the Limpopo River System. *Trichodina heterodentata* has subsequently been described from Europe, Australia, India, China, South America and Africa, but has not yet been found in North America. This cosmopolitan species, with a seeming preference for cichlid hosts, has unambiguous morphological features, but with distinct variances between and within populations. After reviewing previous descriptions from North American trichodinids, analysing the morphological data (both from literature along with type material obtained from the Smithsonian Museum) and investigating the distribution patterns of the southern African introduced *O. mossambicus* throughout North American water systems, it seems likely that *Trichodina hypsilepis* Wellborn, 1967, *T. funduli* (*T. fultoni* Davis, 1947), *T. salmincola* Wellborn, 1967, and *T. vallata* Wellborn, 1967, are all synonymous to *T. heterodentata*. This not only annihilates several North American trichodinid species, but also probably indicates an insidious African alien introduction sneaking its way into this continent.

(0073) Climbing the ladder of complexity in the study of host-parasite interactions: a case study of rodents, fleas, and their bacteria

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Host-parasite interactions can be studied at three increasing levels of complexity: (1) single host-single parasite; (2) single host-multiparasite (SHMP) or multihost-single parasite (MHSP), and (3) multihost-multiparasite (MHMP), with examination of the latter two levels commonly referred to as the “community approach.” While today it is common wisdom that the simplest level of single host-single parasite is unrealistic, it is uncertain whether climbing the ladder toward the third level of complexity is worth the empirical and theoretical challenges that this level entails. We analyzed the published data on host-parasite interactions and found that most current works deal with the second level of complexity. Quantifying the added value of moving up to the third level of complexity, we then demonstrate that this step is necessary due to the nonlinearity of host-parasite interactions and their interdependence. We suggest that MHMP studies can be accomplished with a sufficient level of simplicity, provided that we choose adequate case studies and complement empirical findings with theoretical work. We review our work on rodent-flea-bacteria communities in the southwestern Negev Dunes, Israel to illustrate that such an approach can indeed bring us closer to achieving the goal of further optimizing the realism-simplicity tradeoff in the study of host-parasite interactions.

(0075) Gastrointestinal nematode transmission risk at the livestock-wildlife interface in Botswana

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Gastrointestinal nematodes (GINs) and the tick-borne disease, heartwater, are cited by Botswanan authorities and farmers as the most problematic animal health issues, along with predation of livestock by wildlife near park boundaries. Grassroots community coexistence projects led by the NGO, Elephants for Africa, in communities bordering the Makgadikgadi Pans National Park include surveys of parasites in wildlife and farmer training to encourage regular monitoring of livestock for parasitism and control of parasitic disease. The community bordering the Makgadikgadi Pans is undergoing a period of flux, whereby the previously dry Boteti River has flooded, damaging fences and allowing significant wildlife and livestock contact. In addition, government plans to move fencing are likely to allow for temporary increases in free-ranging of animals between villages and the National Park, with potential for increasing human-wildlife conflict and transmission of parasites. As the livestock in this region are rarely treated for parasitic disease, and GIN infection dynamics are largely climate-driven, monitoring livestock offers a 'sentinel' system to monitor parasite infection dynamics in less-accessible wildlife populations. Livestock sentinel systems also support mathematical models to simulate GIN disease dynamics and risk of transmission in both livestock and wildlife. Existing knowledge transfer projects in the area are presented, mathematical models of parasite population dynamics introduced, and opportunities for monitoring parasites in both wildlife and livestock in the absence of defined boundaries between communities and conservation areas discussed.

(0076) Biosecurity and treatment of fungal pathogens infecting Loggerhead Sea Turtles (*Caretta caretta*) in South Africa

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Juvenile Loggerhead sea turtle (*Caretta caretta*) strandings are commonly encountered along the South East coast. During the past two years the number of strandings has increased dramatically. Washed up turtles are often dehydrated and immunocompromised, as evidenced by the numerous infections exhibited by these stranded animals. Infections include a wide variety of pathogenic taxa including the filamentous fungi. *Fusarium solani* is a filamentous fungal species showing increased prevalence and severe pathogenic etiology on juvenile Loggerhead sea turtles over the past two years. The different fungal strains isolated from the *F. solani* species complex (FSSC) in this study were characterised as *F. falciforme* and *F. keratoplasticum*. Clinical signs exhibited by infected turtles included excessive epidermal sloughing. *Paecilomyces* sp. is another filamentous fungal species isolated from a stranded turtle. Biosecurity and effective treatment is crucial for the rehabilitation of these animals, firstly to prevent reinfection or spread once in rehabilitation and to ensure effective treatment. The aim of this study therefore was to perform *in vivo* evaluation of Bronopol, Formalin and Chloramine T as potential therapeutants. Cultures were grown and maintained on Potato Dextrose Agar (PDA). A controlled number of spores was inoculated onto PDA supplemented with the respective treatments and incubated at 23 °C. Minimum inhibition concentration (MIC) was determined after 5 days by comparing growth rates to control plates. In a second phase spores were inoculated into RPMI 1460 media supplemented with the respective drugs following incubation. After 24 hours MIC was determined by enumeration of colonies on PDA.

(0077) Diversity and host specificity of strongylid nematodes in primates: lessons learned from a next generation sequencing approach

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Strongylid nematodes tend to occur in their vertebrate hosts in rather complex communities comprised of species of several genera, especially in larger herbivorous hosts. The close phylogenetic relationship between humans and other primates results in partial overlaps of their strongylids. The interface for infectious disease transmission has changed in recent years due to closer and more frequent contact between wild primates and people. Diagnostics of strongylid nematodes is traditionally based on the presence of eggs/larvae in fecal samples, while the taxonomy largely depends on the morphology of adult worms residing in the gut. Broader application of DNA-based techniques is complicated by the absence of reference sequences for the majority of taxa and by mixed infections. We have been studying strongylid nematode diversity and transmission between free ranging African great apes, other primates including humans co-inhabiting tropical forest habitats in model site in Central Africa, using newly developed next generation sequencing (NGS) assays at the Illumina Miseq platform, targeting nuclear and mitochondrial markers and examining ~300 fecal samples and isolated larvae. We briefly describe progress to date, and present results demonstrating the diversity of strongylid communities in lowland gorillas, agile mangabeys and humans, together with host-specificity data of detected haplotypes. In conclusion, the NGS approach provides valuable insight into strongylid host specificity and diversity and is widely applicable to studies addressing vertebrate strongyle communities and their zoonotic potential. However, traditional helminthological studies are urgently needed to expand the range of sequences from well-known nematode taxa.

(0078) First record of a *Trypanosoma* species in *Austroglanis sclateri* (Boulenger, 1901) from Sterkfontein Dam, South Africa

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Trypanosomes, haemoflagellates with a single flagellum, have been documented in the blood plasma of all five vertebrate groups. More than 200 trypanosome species have been globally described in fish and in Africa only a handful have been described in freshwater fish. The aim of this study was to describe the morphology of blood trypomastigotes and to compare these morphometrically to described infections in African fish. The study was conducted at Sterkfontein Dam Nature Reserve in the eastern Free State. From the blood smears made, 50% were found to contain trypanosomes. Standard measurements of the trypanosomes were taken using ImageJ. Blood trypomastigotes observed were long and elongated, with a pointed posterior end and a pointed anterior end. The cytoplasm stained a dark purple colour with dark-stained granules. The nucleus situated centrally or just posterior of the midline, is oval or rounded and stained light pink. The rounded to oval kinetoplast situated at the anterior end of the parasite, stained dark purple. A prominent undulating membrane and long free flagellum were present in all specimens; both remained unstained. This is the first record of a trypanosome species from *A. sclateri* in South Africa. Compared to the known South African freshwater fish trypanosomes, the features of the species encountered in the rock catfish are unique and is most likely a new species.

(0080) Fast changing landscapes and wildlife-borne diseases

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Increasing disease risks and the emergence of novel pathogens appear to result from increased contact between wildlife, domesticated animals and humans. We review the evidence supporting the hypothesis that increasing human domination of habitat favours generalist and synanthropic species and negatively affects the diversity of wildlife-borne pathogens, while favoring those associated with synanthropic species. We investigate this hypothesis for rodent-borne pathogens in Southeast Asia, a hotspot of both biodiversity at threat and emerging infectious diseases. We present analyses at two spatial scales: across localities of Southeast Asia at the broad landscape level, to investigate the effects of land use characteristics on total microparasite species richness; among localities around the location where each individual rodent was trapped, to allow investigation of the effect of the surrounding landscape characteristics on the microparasite infection status. We used extensive pathogen survey data on rodents from seven sites in mainland Southeast Asia alongside with present and past land cover analysis. At low spatial resolution across sites, we found that rodent-borne pathogen richness is negatively linked with increasing urbanisation, characterized by increased habitat fragmentation, agriculture cover and deforestation. At high spatial resolution among sites, we found that some major pathogens are favoured by certain environmental characteristics associated with human domination of landscapes, including irrigation, habitat fragmentation, and increased agricultural land cover.

(0081) Parasitic nematodes from three species of amphibians in South Africa

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Nematodes comprise the biggest component (over 70 %) in helminth communities of African amphibians; however, there are only 24 species reported from fewer than 40 species of amphibians in South Africa. In the helminthological material collected from 103 specimens of *Amietophrynus gutturalis* (Power, 1927), 26 *Amietia delalandii* (Boulenger, 1895) and four *Breviceps adspersus* (Peters, 1882) from different localities in South Africa we found several nematode species. *Rhabdias africanus* Kuzmin, 2001, *Amplichaecum* sp., *Cosmocerca* sp. and *Aplectana* sp. were found in Guttural Toads from Durban (KwaZulu-Natal Province) and from Potchefstroom (North-West Province). In Common River Frogs from Potchefstroom we found *Rhabdias* sp., *Amphibiophilus* sp. and *Aplectana macintoshii* (Stewart, 1914). *Amplichaecum* sp. and *Aplectana* sp. were identified from Bushveld Rain Frogs collected in Polokwane (Limpopo Province). Exact identification of *Aplectana* specimens from *Breviceps* was not possible as only females were present in the sample. In all other cases when nematodes were identified only to the generic level, the studied specimens appeared to be morphologically different from all known species. Taxonomic status of these specimens will be clarified using molecular tools and morphological data on more parasite specimens.

(0083) Evolution of life history of rodents of Southeast Asia: role of habitat and parasite diversity

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We investigated a causal chain of relationships between habitat specialization and parasite species richness in rodent communities in Southeast Asia, and the consequences for variation in immune investment, the degree of sexual competition and sexual size dimorphism. We used data on rodents, their habitat specialization and their parasites in Southeast Asian landscapes. The hypotheses that parasite diversity drives the evolution of host life-traits and sexual selection found some support with: (1) host habitat specialization explained the variation in parasite species richness; (2) high parasite species richness was linked to host immune investment, using the relative spleen size of rodents; (3) according to the potential costs associated with immune investment, the relative spleen size was found to be negatively correlated with the relative size of testes among rodents; (4) a positive

relationship between male-biased sexual size dimorphism and parasite species richness was observed supporting the role of parasitism in sexual selection; (5) the variation in sexual size dimorphism was positively associated with the degree of habitat specialization. These results, also correlative, help to better understand the selective effects of parasites on rodent life-history and behavior.

(0089) Prevalence and molecular identification of *Trichinella* species isolated from wildlife originating from Limpopo and Mpumalanga provinces of South Africa

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Trichinella infections are important food-borne zoonoses which belong to the genus *Trichinella* and family Trichinellidae, phylum Nematoda, consisting of nine species and three genotypes. The spectra of *Trichinella* species in sub-Saharan African countries have not been completely documented. This study was conducted to determine the prevalence of *Trichinella* spp. in wildlife from the Greater Kruger National Park (GKNP) and adjacent areas and to identify the species and/or genotypes of *Trichinella* larvae isolated from muscle tissues. Between 2012 and 2016, a total of 87 samples representing 15 mammalian, two bird and three reptile species were screened for the presence of *Trichinella* larvae using artificial digestion. Isolated larvae were identified by a multiplex PCR amplification of the ITS1, ITS2 and ESV regions of ribosomal DNA followed by molecular analysis of the sequences. Nineteen samples from seven wildlife species were positive for *Trichinella* spp. Larvae. Prevalence was 100% in carnivores and scavengers and 50% in omnivores. Analysis of the sequences of the isolates showed that six of the isolates from two spotted hyenas (*Crocuta crocuta*) (2/5), two lions (*Panthera leo*) (2/8), one spotted genet (*Genetta genetta*) (1/2) and one Nile monitor lizard (*Varanus niloticus*) (1/2) conformed to *T. zimbabwensis*; one isolate from hyena was grouped under the encapsulated species clade comprising *T. nelsoni* and genotype T8 reportedly present in South Africa. This is the first report of natural infection of *T. zimbabwensis* in hyena, genet and Nile monitor lizard.

(0090) Detection of eggs of *Schistosoma turkestanicum* in droppings of deer

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Schistosoma turkestanicum was discovered in red deer in a limited area of Hungary, Central Europe. Formerly this fluke was thought to be a native Asian species only. By investigation of nucleotide sequences of the Hungarian population of this trematode it was revealed that it has been present in this area since the ice age. Because of the close relation of this worm and human schistosomes the research on its natural habitat has a great significance. We could find this worm in no any other animals but in red deer in a swampy area. Adults and eggs were detected mainly in the liver. Because of the strict restriction of hunting, there is no opportunity to examine carcasses of deer throughout the year. Therefore, we tried to investigate the presence of eggs in droppings of animals. Detection of *Schistosoma* eggs in droppings proved extremely difficult since they contain low numbers of eggs and most become desiccated on the ground. Usually 100 g of faeces contained only one or two dead eggs. We have developed a method to concentrate eggs from a large quantity of faeces. After sifting faecal debris through sieves we mix it with neutral fuschin which stains the eggs only. With a repeated flotation of debris in salt solutions with different specific gravity we can concentrate the red-coloured eggs on the top of mixture. This method can probably also be applied to detect blood-fluke eggs in scats of other animals.

(0091) Host-parasite interactions in Antarctic penguins

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Parasitological information in Antarctic wildlife is present from the very beginning of the exploration of this continent. However, such information was limited to the species description and the report of their presence on Antarctic birds or marine mammals. Currently the scenario is very similar and the advance of parasitology in Antarctica has been very scarce during the last century in comparison with other regions in the planet. Although penguins are the most studied organism in Antarctica the information about parasites follows the same pattern being mainly focused on their presence/absence with very few published data on prevalence and intensity. In addition, such information is very limited in spatial and temporal terms. Moreover, published information about the interaction between parasites and the Antarctic penguins is almost absent with very few exceptions on species distributed in the Sub-Antarctic islands. Here we present an overview of our recent findings on the presence of macro- and microparasites and their effects on Chinstrap, Gentoo and Adélie penguin in the Antarctic Peninsula. Parasites present in these bird species are gastrointestinal parasites (nematodes, cestodes and coccidian), ectoparasites (ticks) and tick-borne parasites. We have also information about presence/absence of bacteria and viruses in these bird species. Parasite effects can be summarized as mortality increase, histopathological damage, reduction of body mass, transmission of diseases and increase of the penguin immune response.

(0092) A systematic review of *Contraecum* species (Nematoda: Anisakidae) infecting Australian piscivorous birds

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Parasitic nematodes of the genus *Contraecum* (family: Anisakidae) often occur in large numbers in the stomach of Australian piscivorous birds such as Australian pelican, little penguin or species of cormorants and may cause clinical signs. The population of some piscivorous birds in Australia is declining and, despite the abundance of these parasites, our knowledge about various aspects of the biology and ecology of the *Contraecum* spp in Australia is poor. *Contraecum* spp are also of zoonotic importance and there has been a recent report of human infection with *Contraecum* larvae in the country. In this presentation, diversity of *Contraecum* spp and their life cycle is reviewed followed by a discussion on the importance and potential health impacts of these parasites on Australian piscivorous birds. This study provides some fundamental knowledge which is essential in any conservation studies of birds and aquatic associated animals.

(0093) Trombiculids parasitising rodents: their diversity and distribution on and off the host

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Chigger mites (Trombiculidae) are a group of temporary parasites that are habitat as opposed to host specific. Little is known with regard to the diversity and ecology of these mites in South Africa. The study aims were to record the 1) diversity of chiggers on rodents and 2) effect of habitat type on the chigger species composition. Rodents (n = 184) belonging to eight species were trapped in three habitat types (natural, crop and urban) in the savanna biome during January and September 2015. Eleven chigger species, including four new ones, were recorded from 77 rodents (42%). First record of the genus *Trombicula* s. s. in Africa represents an unexpected faunistic connection of South Africa with the Oriental and Australian Regions, like in some ixodid ticks. *Microtrombicula mastomyia* and *Susa hexasternalaea* were previously known in Central and/or Western Africa; their record in South Africa suggests a probable existence of a faunal complex of chiggers connected with the savanna biome across the continent. Six chigger species were recorded in natural, 10 in crop and four in urban habitats. Four species were shared between the three habitat types, but unique occurrences were also noted. *Microtrombicula mastomyia* dominated crop and urban habitats, but not natural ones. The occurrence of chiggers was also higher in urban habitats compared to the natural and crop ones. Chiggers were often associated with the ear region. Evident from the study is that habitat transformation does not necessarily result in fewer chigger species but rather a change in species composition.

(0094) The evolution of antigenic diversity in vaccine candidates for *Schistosoma turkestanicum* infecting European populations of wild red deer

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Parasites and their hosts are locked in a continuous evolutionary arms race enforcing major selective pressure on the genetic components involved in parasite host interactions. The genetic diversity of genes coding for antigenic proteins at the host-parasite interface has been theorised to be responsible for the current lack in efficacy of certain schistosome antigens as vaccine candidates. Advances in computational methods of sequence annotation and structural prediction from primary DNA and protein sequence data have enabled rapid comparison amongst potential vaccine target antigens with the aim to predict vaccine efficacy before testing *in vivo*. In 2010 an ancient natural focus of *Schistosoma turkestanicum*, a neglected zoonotic parasite, was discovered utilising red deer as definitive hosts in the Gemenc region of Hungary. This discovery has provided a unique opportunity to study the evolution of parasite-host interactions from a molecular to a population level. The current study focuses on the diversity of promising vaccine candidates in a wild and pristine schistosome population that has not been subject to the selective pressures of treatment with praziquantel. Utilising a novel graphing method to aid prediction of antigenic regions at the host-parasite interface from primary sequence data, the antigenic diversity of *S. turkestanicum* populations within and between deer hosts for 3 promising vaccine candidates was measured. Initial results have provided an insight into the natural complexity of parasite antigens with relevance for future vaccine development and further population genetic studies.

(0095) Detection of *Trypanosoma equiperdum* infections in horses and donkeys in South Africa by PCR and ELISA

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Trypanosoma equiperdum, the only trypanosome species transmitted sexually from host to host, causes a disease called dourine in equids. In this study various serological and molecular techniques were used to determine the occurrence of dourine in equids in South Africa. A total of 256 blood and serum samples were collected from donkeys (n=32) and horses (n=224) which were from Free State (FS), Mpumalanga (MP), Northern Cape (NC) and North West (NW) provinces. No samples were collected from donkeys in MP. The overall prevalence of dourine by PCR in horses was 17%, 16%, 12% and 13% in MP, FS, NC and NW respec-

tively, whilst 8.3% and 10% of donkeys were positive in NC and NW, respectively. The sero-prevalence in horses was 14.3% in FS, 12.8% in MP, 17.9% in NC and 29.9% NW by TeGM6-4rELISA whilst TeCA-ELISA detected 8.6% in FS, 20.2% in MP, 7.7% in NC and 22.9% in NW. In donkeys sero-prevalence was 0%, 58.3% and 5% for FS, NC and NW, respectively, by TeGM6-4rELISA whilst TeCA-ELISA detected 0% in FS, 25% in NC and 0% in NW. This study demonstrated that PCR and ELISA with recombinant and crude antigens are capable of detecting *T. equiperdum* infections in equids in South Africa.

(0096) Ectoparasite infestations in the nests of African penguins: initial data on the effect of nest type, spatial position of nest and season

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Ectoparasites are thought to be implicated in the detrimental health status exhibited by the endangered African penguin (*Spheniscus demersus*) and in the current chick and nest abandonment at the Stony Point penguin colony in South Africa. It is suspected that certain habitat characteristics offer a suitable environment for the parasites to thrive, but it is uncertain if the problem is associated with a specific nest type (artificial and natural), nest position (zone) or external factors (season) within the colony. Ticks and fleas were recorded from artificial, natural open and natural covered nests (n=190) and from penguin chicks (n=179) in 4 zones of the colony during winter and spring in 2016. Nest type significantly affected tick and flea abundances with larger parasite loads in artificial compared to natural covered and natural opened nests. Nest position was also important, with nests in zone A recording significantly lower tick and flea abundances compared to the other zones. Nest occupancy had a significant positive effect on parasite abundances in the nest. Tick abundances were significantly higher in nests and on the penguins in spring, though this pattern was less clear for fleas. The body condition of penguin chicks was also significantly lower in spring compared to winter. It is evident that nest characteristics play an important role in ectoparasite infestations in the Stony Point colony. However, the importance of parasites in nest abandonment by adult penguins can only be confirmed with additional research.

(0097) First report and characterisation of eimeriid-type Coccidia (Apicomplexa) from the blood of African anurans using morphological and molecular techniques

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The coccidia are protozoa within the Apicomplexa, and are possibly the most abundant and diverse group of all parasites known. Coccidia infecting amphibians remain the most understudied and neglected group of these organisms. Most classifications of coccidia or their descriptions are based solely on the morphology of the exogenous stages (oocysts). In the present study, we report on the occurrence of an intraerythrocytic-type coccidium, similar to *Lankesterella* but with no ability to assign to a particular genus. Parasites were observed in peripheral blood of 5/33 (15.2%) of the African Bullfrog (*Pyxicephalus edulis*), 1/8 (1.25%) of the Greater Leaf-folding Frog (*Afraxalus fornasinii*), 3/15 (20%) of the Dwarf Puddle Frog (*Phrynobatrachus mababiensis*), and 3/20 (15%) the Plain Grass Frog (*Ptychadena anchietae*). Frogs were collected in the Kruger National Park, the Ndumo Game Reserve, and in Sodwana Bay, South Africa. Molecular characterisation and phylogenetic analysis of a fragment of the nuclear 18S rRNA gene demonstrate how molecular techniques can overcome, to some degree, the limitations of traditional approaches in the systematics of coccidia. However, even though molecular data using the 18S gene are available for some these organisms, it has not yet definitively resolved their phylogenetic affinities.

(0102) The consequences of nutrition on parasite community and response to treatment in wild and lab wood mouse populations

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Nutrition is a key component in determining individual health and fitness. In nature, access to resources is hugely variable and many individuals face challenges from multiple parasites. Host nutrition will, in part, determine the relationship between energetically costly processes like immunity and reproduction. However, much of our understanding of these complex relationships is based on either observational studies in the wild or laboratory studies in sterile conditions. Here we experimentally test the interaction of supplemental resources and drug treatment on the parasite community and host fitness in both a natural and captive population of wood mice (*Apodemus sylvaticus*). Specifically, we used anthelmintics to reduce *Heligmosomoides polygyrus*, a common and well-studied immunomodulatory nematode, but also monitored the non-drug target parasite community (>30 species). I present results from our field experiments, which show that supplemental nutrition can drive parasite infection dynamics and mediate allocation between important life-history processes. Specifically, we found that mice on nutrition supplemented

grids had significantly lower nematode burdens, a more rapid clearance of worms following treatment, and greater investment in reproduction and their immune response. In our laboratory colony, we conducted a controlled *H. polygyrus* infection in nutrition supplemented and control mice, and then treated the mice with anthelmintics to test whether the same dynamics occur in the absence of coinfecting parasites. These parallel studies present unique insights into the role of nutrition on infection dynamics in natural systems, and more broadly, to what degree the stressors of living in the wild mediate life-history.

(0104) Drought and the disappearance of alien invasive anchorworm, *Lernaea cyprinacea* (Copepoda: Lernaeidae), is linked to changes in fish health

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Mozambique tilapia (*Oreochromis mossambicus* Peters, 1852) populations are under threat from hybridisation, pollution, and possibly from infection by the invasive parasitic copepod anchorworm, *Lernaea cyprinacea* Linnaeus, 1758. Given that infection is highly prevalent in some localities, few uninfected fish are typically available to serve as a relative comparison for understanding host health. A severe drought has created hypersaline environments in pans of Phongolo River of northeastern South Africa, such that freshwater parasites cannot survive. To determine how infection influences host health, infected and uninfected *O. mossambicus* were collected before and during drought conditions, from Nyamiti pan of the Phongolo River floodplain. Anchorworms were collected from hosts, and prevalence of infection was determined. Anchorworms were identified to species level using morphological and molecular data of the 18S rRNA gene. For each fish, intensity of anchorworm infection, total length, and weights of the gutted body, liver, spleen, and gonads were recorded. Gutted condition factor, hepato-, spleno-, and gonado-somatic index values per fish were determined. Rapid health assessments were also conducted to obtain a health score for each fish. Molecular analyses confirmed the anchorworm studied was *L. cyprinacea*. Prior to and during drought, prevalence of infection was 100% and 0%, respectively. Before drought, fish had significantly reduced hepato-, spleno-, and gonado-somatic index values, and higher health assessment scores, yet significantly higher gutted condition compared to fish collected during drought. This study demonstrates that host condition and health varies greatly with respect to drought and infection.

(0105) Discovering African aquatic parasite diversity: Digeneans of the genus *Tylodelphys* (Diplostomidae)

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The genus *Tylodelphys* (Diplostomidae) represents a large group of widely distributed trematode parasites with complex life cycles, where fish and amphibians serve as the second intermediate hosts. By infecting the brain (cranial cavity), eyes, body cavity and pericardial sac, metacercariae of *Tylodelphys* spp. can cause diseases and even mortality of their intermediate hosts. To date, only two *Tylodelphys* spp. are known from South Africa, *Tylodelphys mashonensis* from the African sharp-toothed catfish *Clarias gariepinus* and *T. xenopi* from the African clawed frog *Xenopus laevis*. To discover the species diversity of diplostomid digeneans from freshwater fish and frogs in South Africa, samples were collected in the Phongolo River, Ndumo Game Reserve and in the Riet River, Mokala National Park during May and September 2016, respectively. Metacercariae morphologically consistent with the genus *Tylodelphys* were found during examination of the eye vitreous humour and cranial cavity of *C. gariepinus*, *Cyprinus carpio*, *Labeobarbus aeneus*, *Nothobranchius orthonotus* and *Oreochromis mossambicus* and in the pericardial sac of *Xenopus muelleri*. Morphological data and molecular analyses of multiple genetic markers (ITS1-5.8S-ITS2, 28S and *cox1*) of new collections revealed the presence of five species. Metacercariae of two species, one from *C. gariepinus* and one from *X. muelleri*, represented known species, *T. mashonensis* and *T. xenopi*, respectively. Specimens from *O. mossambicus*, *N. orthonotus*, *L. aeneus* and *C. carpio* were infected with undescribed metacercariae of *Tylodelphys*. This study is the first to provide molecular data for *T. xenopi* and describe unknown molecular and taxonomic diversity of the genus *Tylodelphys* in South Africa.

(0107) Detection of *Schistosoma cercariae* from water

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Detection of cercariae of blood-flukes in water is considered an important but very difficult task for researchers. Scattered distribution of temporarily active trematode larvae makes their detection almost impossible in larger lakes and rivers. The mammalian blood-fluke, *Schistosoma tuckeyanicum*, was discovered in an isolated population of red deer (*Cervus elaphus*) in a floodplain of River Danube in Hungary, Central Europe. Formerly this fluke was thought to be native in Asia only, but inspection of nucleotide sequences revealed that the Hungarian population has been present in this area since the ice age; it can therefore also be considered a native species in Europe. We tried to find the swimming cercariae of *S. tuckeyanicum* in lakes and canals in order to detect the habitats where deer can become infected. Since various trapping methods did not give good results, we applied other ways to collect them. Sieving of the water was proved the most effective way for finding cercariae in stagnant waters but this method needs the sieving of a large amount of water through fine mesh, so very few places can be sampled this way in a day. Therefore we developed a floating device which can collect cercariae from surface of water even in virtually inaccessible parts of lakes, among vegetation. I report on experiences gained with this device.

(0108) The *Schistosoma indicum* group: A complex series of species or a series of species complexes

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Despite the extensive studies on the evolution of African *Schistosoma* blood flukes, few studies have addressed the divergence of the Asian species within the *Schistosoma indicum* group. The group contains *Schistosoma indicum* and *Schistosoma spindale*, sympatric parasites of wild ungulates, rodents and carnivores as well as domestic cattle across South East Asia. Based on the analysis of newly sequenced genomes for *S. spindale* and *S. indicum*, distinguishing the boundaries between these two species has become increasingly challenging. Initial comparisons using whole mitochondrial genomes indicated incomplete divergence between *S. spindale* and *S. indicum*, although high levels of positive selection were identified in the genes that regulate the electron transfer chain, a feature which has also been seen in other invertebrate groups where species are closely related. However, a similar level of divergence was also shown between Bangladeshi and Sri Lankan *S. spindale* isolates, which may be a signature of the early stages of a speciation event. This was further supported by the analysis of genetic distance between mitochondrial sequences of *S. indicum* and *S. spindale* from across South East Asia which also failed to define a clear definitive boundary between the species, suggesting that *S. spindale* and *S. indicum* may actually be a series of species complexes with the ability to interbreed and exchange genetic material when sharing the same host. Nevertheless, this study also demonstrates the low capability of traditional molecular markers to distinguish between closely related schistosome species and need for detailed genomic studies on Asian *Schistosoma*.

(0110) Role of cytokines and chemokines in clinical outcomes of helminth and malaria co-infections in sub-Saharan Africa: A review

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Geographical overlap in the endemicity of malaria and soil-transmitted helminth (STH) infections in sub-Saharan Africa (SSA) has made it uncommon for helminth-malaria co-infections to occur. Parasite co-infections reportedly have important but poorly understood consequences for disease development, severity and transmission dynamics. Interestingly, numerous contrasting reports suggest that STHs-malaria co-infection may alter susceptibility to clinical malaria thereby leaving many important questions unanswered pertaining to the exact biological interaction between STHs and malaria during helminth-malaria co-infection. There is also paucity of information on the interaction between malaria and tissue-dwelling helminths such as *Trichinella* and *Toxocara* during co-infection. Comprehension of the competing immune-specific responses associated with each disease is indispensable. Modulation of immune responses to malaria has been reported in various chronic STH infections. Such immune regulation includes the concept of suppression, diversion and conversion of the host immune response to benefit the parasite. Chronic helminth infections such as trichinellosis reportedly induce strong type 2 and regulatory immune responses, which may alter the clinical outcome of malaria. On the other hand, malaria infection induces an acute type 1 immune response. However, the exact effects of concurrent infections on both the development and maintenance of an immune response remain obscure. Therefore, the role of cytokines and chemokines in clinical outcomes of STHs-malaria and tissue-dwelling helminths co-infections in SSA remain divergent and poorly understood to date.

(0111) Host chemokine responses in Sprague-Dawley rats experimentally co-infected with *Trichinella zimbabwensis* and *Plasmodium berghei*

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Trichinellosis is an important parasitic zoonosis caused by nematode species of the genus *Trichinella*. On the other hand, *Plasmodium falciparum* malaria is one of the major causes of mortality and morbidity in sub-Saharan Africa. Co-infection of the two diseases in rural communities is likely to be a common phenomenon. However, there is paucity of information on the consequences of co-infection and outcome of the diseases, especially malaria. Helminths, such as *Trichinella* spp., reportedly induce Th2 immune responses, while malaria induces Th1 immune responses as a survival strategy. Chemokines are chemotactic cytokines produced by host macrophages in order to elicit a protective immune response. Immuno-pathogenesis during co-infection remains obscure. It is against this background that this study aimed to determine host chemokine responses in Sprague-Dawley rats induced during co-infection with *Trichinella zimbabwensis* and *Plasmodium berghei*. A 42-day follow-up study was carried out, where 168 male Sprague-Dawley rats (90-150g) were separated into four groups: control (n=42), malaria infected (n=42), *Trichinella* infected (n=42) and co-infected (n=42). On day 0, Sprague-Dawley rats were infected with *T. zimbabwensis* muscle larvae *per os* followed at day 28 pi with *P. berghei* parasitized RBCs infection. Experimental animals were sacrificed at day 0, 7, 14, 21, 35 and 42 pi, whole blood, sera, brain and spleen were collected. *Plasmodium berghei* parasitaemia, *T. zimbabwensis* larva load, haematological parameters and serum levels of IP-10, RANTES, MDC, MCP-1, EOTAXIN-1 and EOTAXIN-2 were determined. Spleen and brain chemokine expression was determined. Based on current literature, we hypothesize that co-infection may alleviate the clinical outcomes of malaria.

(0112) The disjunct distribution of branchiuran fish parasites

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The global distribution of species of the four genera of freshwater branchiurans provides a classical case study of the geographically discontinuous phenomenon, referred to as a disjunct distribution pattern. The genus *Argulus* comprises 44 marine and 85 freshwater species, of which at least one is found in each of the seven zoogeographical regions of the world. The Afrotropical region hosts 25, Neotropical 21 and Nearctic 18 species. Eleven *Dolops* species are found in South America, of which 10 have been recorded from freshwater fishes in Brazil and one from French Guiana. *Dolops tasmanianus* was described from a galaxiid fish found in Tasmania. A single species, i.e. *D. ranarum*, occurs on a variety of fish hosts in Africa from south of the Sahara to the Limpopo, but is absent from the Orange-Vaal basin and southern coastal rivers. The genus *Chonopeltis* is endemic to Africa with 14 known species, whilst the genus *Dipteropeltis*, with two known species, is endemic to South America. Possible reasons for the disjunct distribution are discussed, considering a marine distribution in the case of species of the genus *Argulus*. The fact that no *Dolops* has been found in the southern tip of Africa as well as South America, well away from the distribution of galaxiid species, makes an oceanic distribution unlikely. It is more likely that *Dolops* dispersed before the Gondwanan vicariance. The question now remains to explain the radiation of *Dolops* in the neotropics, but not in Africa.

(0113) Ectoparasite communities of small mammals in Madagascar are fundamentally different from those in East Africa

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Examination of almost 2,000 specimens of small mammals from 100 sites in Madagascar and almost 3,000 specimens from 97 sites in East Africa (Burundi, Kenya, Malawi, Mozambique, Tanzania, Uganda) over the past 30 years provided details of the communities of ectoparasites Acari (mites and ticks) and Phthiraptera (lice) associated with them. The compound community of terrestrial mammals (all parasites of all hosts) in Madagascar is substantially depauperate in higher level taxonomic diversity compared with that of East Africa, with a number of families completely absent from native hosts. The communities associated with bats (Chiroptera), on the other hand, are relatively similar. Given the small number of founders (one for each order of terrestrial mammals) arriving in Madagascar, stochastic founder effects are the most likely cause for the differences.

(0116) Host cytokine responses in Sprague-Dawley rats experimentally co-infected with *Trichinella zimbabwensis* and *Plasmodium berghei*

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Human co-infections of helminths and malaria parasites are a common phenomenon in areas where malaria is endemic, more so in sub-Saharan Africa where tissue-dwelling helminths, such as *Trichinella* spp., are also endemic. However, the immunopathogenesis of the diseases when there is co-infection remains obscure, hence there is a need to understand the host immune responses induced during co-infection. This study aimed at investigating the host cytokine responses in Sprague-Dawley rats experimentally co-infected with *T. zimbabwensis* and *Plasmodium berghei*. A 42-day study was done, where 168 male Sprague-Dawley rats (90-150g) were divided into four separate experimental groups: control (n=42), malaria infected (n=42), *Trichinella* infected (n=42) and co-infected (n=42). *Trichinella* induction using *T. zimbabwensis* muscle larvae *per os* was done on day 0, while malaria induction using *P. berghei* parasitized red blood cells was done on day 28. Animals were sacrificed at day 0, 7, 14, 21, 35 and 42 post-infection with *T. zimbabwensis* for blood and sera collection, and harvesting of the brain and spleen. *Plasmodium berghei* parasitaemia, *Trichinella* parasite load, haematology parameters and serum levels of TNF- α , IL-10, IL-4 as well as parasite-specific IgM, IgG, IgG1, IgG2a, IgG2b and IgG3 antibody responses were measured. Cytokine expression in the spleen and brain was also determined. Results for parasitaemia, *Trichinella* parasite load, haematology profile, cytokines levels in the serum, brain and spleen are presented. Based on available literature, it can be hypothesized that trichinellosis-malaria co-infection may alleviate outcomes of clinical malaria.

(0120) Evolutionary relationships of *Plasmodium vivax* infecting great apes and humans

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The malaria agent *Plasmodium vivax* is the second most prevalent species in humans, responsible for tens of millions of cases every year all over the world. It is considered to be absent from Central and West Africa because of the protective effect of Duffy negativity. However, there are reports of persons returning from these areas infected with this parasite. The existence of a zoonotic reservoir has been proposed as a possible explanation for this paradox. May great apes be this reservoir? To answer this question, we screened great ape blood samples collected annually during sanitary controls in the La Lékédi Park, Gabon, for the presence of *Plasmodium* parasites by PCR. For each *P. vivax* positive sample, we analyzed the mitochondrial and nuclear genetic diversity and compared it to parasites isolated from travelers returning from these regions of Africa, as well as to human isolates distributed all over the world. We showed that the *P. vivax* sequences from great apes form a clade genetically distinct from the parasites circulating in humans, that we named *P. vivax*-like. We showed that this clade's parasites are infectious to humans by describing

the case of an infected traveler returning from the Central African Republic. Finally, this sampling allowed us to generate genomes of several *P. vivax*-like strains and comparative genomic analysis of these genomes provides foundation for further insights into the genetic basis of human-infectivity with *P. vivax*.

(0122) Range expansion of the economically important Asiatic blue tick, *Rhipicephalus microplus*, in South Africa

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The objective of the study was to record the distribution of the introduced tick, *R. microplus*, and of the related endemic species *R. decoloratus* in the western region of the Eastern Cape, Free State, Northern Cape and Western Cape Provinces of South Africa. Cattle (n=415) were randomly sampled and examined for ticks between October 2013 and September 2015. At each locality, 3 to 6 cattle were examined for ticks. Attention was paid to the predilection sites of ticks such as neck including dewlap, abdomen, and peri-anal region. The ticks from each animal were preserved in separate labelled vials containing 70% ethanol, and subsequently counted and identified to genus and species level using a standard stereomicroscope. A total of 8 408 specimens of *Rhipicephalus* (*Boophilus*) spp. were recovered, of which 28.2% were *R. decoloratus*, the remainder (71.8%) being *R. microplus*. Very low numbers of *R. microplus* were collected in the Northern and Western Cape and it would seem that *R. microplus* is a recent introduction. The tick is now common along the entire coastline in the Eastern Cape, with signs of *R. microplus* displacing *R. decoloratus*. Because of its adaptation to local climatic conditions, *R. microplus* has been reported in habitats in South Africa that were previously considered too cold or too dry for its survival.

(0124) Experimental proof of the ‘Trojan horse’ strategy applied by the swim bladder nematode *Anguillicola crassus*

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The nematode *Anguillicola crassus* is an invasive swim bladder parasite, which has its origin in the Japanese eel (*Anguilla japonica*). It was introduced to the population of European eel (*A. anguilla*) in the 1980s. During the following decades, over 90% of the European eel population was infested with this parasite, which might have been an additional cause for the population's decline. The prevalence of *Anguillicola* infestations in European eels decreased during the last years, but the European eel population is facing a new threat. After opening of the Rhine-Main-Danube Canal in 1992, the invasive goby species *Neogobius melanostomus* conquered the Rhine, introducing another parasite – the acanthocephalan *Pomphorynchus laevis* (Hohenadler *et al.*, not published yet). New research described hidden L3-larvae of *A. crassus* within cysts of *Pomphorynchus* found in gobies from the Rhine river as ‘Trojan horses’ (Emde *et al.*, 2014). It remains to be answered, if gobies are prey of free-living eels and, if so, how the interaction of these species influences the prevalence of *A. crassus* in the European eel population. Our research showed first evidence that *A. crassus* larvae harboured in the acanthocephalan cysts are infectious to eels. Furthermore, we compared stress responses between infestations with ‘Trojan horse’ - *A. crassus* and *A. crassus* directly administered to European eels. Blood samples were taken for measuring cortisol as the main corticosteroid. Additionally, the antibody response was investigated to analyse if the ‘Trojan Horse’ strategy has any advantageous effects for the establishment of *A. crassus* by affecting the eel's immune system.

(0126) Molecular identification of leeches from aquatic tetrapods and the haemoparasites they transmit

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Aquatic leeches are widely distributed haematophagous ectoparasites responsible for transmitting a range of diseases amongst aquatic vertebrates, including blood parasites such as *Hepatozoon* and *Trypanosoma* species. Taxonomic identification of both leeches and blood parasites still relies heavily on morphological descriptions, which is problematic in each case for a number of reasons. With a paucity of information regarding the diversity and taxonomy of these organisms for countless sections of the globe, there is an increased need for molecular identification tools and more robust phylogenetic frameworks to resolve these issues. In the current study, molecular analysis was used to identify leeches from Nile crocodiles (*Crocodylus niloticus*) in the Okavango Delta, Botswana, and additional specimens from redbelly turtles (*Pseudemys nelsoni*), mud turtles (*Kinosternon baurii*) and an alligator (*Alligator mississippiensis*) in Gainesville, Florida, using conventional PCR and sequencing for mitochondrial *cox1* and *nad1*. Using phylogenetic analysis, leeches from Nile crocodiles were identified as *Placobdella fimbriata*, *Placobdelloides multistriatus* and a *Marsupiobdella* sp., while those from the Florida tetrapods were identified as either *Placobdella parasitica* or *Placobdella multilineata*. Samples were also screened for the detection of *Hepatozoon* and *Trypanosoma*, using genera-specific primers for 18S rDNA, with initial analysis indicating that the leeches identified are potentially transmitting these parasites between different tetrapod species. This further highlights the need for molecular approaches to achieve accurate identification of these organisms and to understand the transmission dynamics and incrimination of leeches as vectors of disease.

(0131) From sand stabilization to parasitic communities infecting wild vertebrates

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Emerging infectious diseases have increased dramatically over the past three decades, becoming a major health and economical problem. The common wisdom is that changes in ecological conditions are responsible for this challenge. While many studies have focused on small-scale phenomena (i.e., effect of host traits on parasite community composition) or on large-scale phenomena (i.e., the effect of climate change on parasite distribution), the ecological determinants of parasite community composition across scales are obscure. The psammophilic rodent communities in Israel provide an ideal system to address this goal. These communities, dominated by the three species *Gerbillus andersoni*, *G. gerbillus* and *G. pyramidum*, have been studied intensively in the past decades. Moreover, sand stabilization, an important process in the divergent rodents' habitat preference, was well studied in various contexts. Finally, evidence suggests that the composition of the main rodent blood parasites - *Mycoplasma* and *Bartonella* - is changed seasonally. By combining remote sensing indices, museum records, and long-term field surveys, we have quantified the association between sand stabilization and rodent community composition and found a strong association between these two variables. Then we exploited a natural gradient in sand stabilization and searched for the network of effects of sand dunes stabilization on the probability of rodents to carry *Bartonella* and/or *Mycoplasma*. We found that the bacterial composition was indirectly associated with sand stabilization. Our results suggest that large-scale ecological processes might be indirectly translated to changes in small-scale processes (e.g., bacterial infection). The latter may determine the local disease risk to wild animals and people.

(0132) Molecular characterization of *Cryptosporidium* spp. and *Enterocytozoon bieneusi* in straw-colored fruit bats in Nigeria

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Few data are available on the distribution and human infective potential of *Cryptosporidium* and *Enterocytozoon bieneusi* genotypes in bats. During April-July 2011 we collected 109 fecal specimens from a colony of straw-colored fruit bats (*Eidolon helvum*) in an urban park (Agodi Gardens) of Ibadan, Nigeria, and analyzed for *Cryptosporidium* spp., *Giardia duodenalis* and *E. bieneusi* using PCR targeting the small subunit rRNA gene, triosephosphate isomerase gene, and ribosomal internal transcribed spacer, respectively. Genotypes of these enteric parasites were determined by DNA sequencing of the PCR products. Altogether, 6 (5.5%), 0 and 16 (14.7%) specimens were positive for *Cryptosporidium* spp., *G. duodenalis*, and *E. bieneusi*, respectively. DNA sequence analysis of the PCR products indicated the presence of two novel *Cryptosporidium* genotypes named as bat genotype XIII (in 5 specimens) and bat genotype XIV (in 1 specimen) and one known *E. bieneusi* genotype (Type IV in 1 specimen) and two novel *E. bieneusi* genotypes (Bat1 in 13 specimens and Bat2 in 2 specimens). In phylogenetic analysis of DNA sequences, the two novel *Cryptosporidium* genotypes were genetically related to Bat genotype II previously identified in fruit bats in China and Philippines, whereas the two novel *E. bieneusi* genotypes formed a new genotype group, Group 10. With the exception of Type IV, none of the *Cryptosporidium* and *E. bieneusi* genotypes found in bats in this study are known human pathogens. Thus, straw-colored fruit bats in Nigeria are mainly infected with host-adapted *Cryptosporidium* and *E. bieneusi* genotypes.

(0133) Wildlife as a source of *Giardia duodenalis* in a watershed

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To assess the source of *Giardia duodenalis* in surface water, we compared the distribution of *Giardia* genotypes in wildlife and storm water in a protected watershed in New York, USA. A total of 203 fecal specimens from 23 species of wild mammals and 74 microscopy-positive slides from storm water samples were analyzed for *Giardia* spp. using PCR targeting the triosephosphate isomerase (tpi), β -giardin (bg), and glutamate dehydrogenase (gdh) genes. Twenty-eight, 36, and 13 of the fecal specimens and 40, 27, and 19 of the water samples were PCR-positive for *Giardia* spp. at the tpi, bg, and gdh loci, respectively. DNA sequence analysis indicated the presence of *G. duodenalis* Assemblages A and B and *G. microti* complex in fecal specimens, with Assemblage A being found in a broad range of animals, Assemblage B in only beavers, and *G. microti* complex in cricetid rodents. These *Giardia* genotypes were also found in water samples, with Assemblage B as the dominant one. Differences in the distribution of *Giardia* genotypes were seen among sampling sites for water samples, with Assemblage B especially common at sites with beaver activity. The dominant subtype of Assemblage B in water samples was identical to the subtype found in beavers at all three genetic loci. Data from the study indicate that although host adaptation is present in *Giardia* spp., beavers can be a potential reservoir of human-pathogenic *G. duodenalis* Assemblage B in drinking source water.

(0134) Host-parasite networks in South African small mammals

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High host species diversity is thought to have the potential to reduce the prevalence of parasites and/or pathogens in a host community. Such dilution effects have been shown in several small mammal communities in the northern hemisphere but are rarely addressed in the Afrotropical region. Similarly, the number of systematic studies of host-sharing among parasite species is limited in Africa. Thus, in the current study sampled a small mammal community in Ezemvelo/Telpeper Nature Reserve, Gauteng Province, South Africa over the course of one year. During 9216 trap nights we captured 391 host individuals from 11 small mammal

species (nine rodents, two insectivores). These sustained a total of 23142 ticks (10 species), 1551 fleas (5 species), 8069 mites (14 species) and 448 lice (4 species). Among acari between 2 and 10 host species in interaction networks while it was only up to 5 for fleas and lice. However, the high connectivity among acari hosts was largely attributable to one and three species of mites and ticks, respectively. Bipartite networks furthermore suggest that host sharing may be affected by host phylogeny, habitat choice, body size and diet. For predominantly host-specific parasite taxa, such as mites and lice, host phylogeny and habitat choice were good predictors of module sharing. In contrast, the patterns were less clear-cut for ticks and fleas, which may act as vectors for pathogens including *Rickettsia conorii*, *Yersinia pestis*, *Theileria parva*, *Anaplasma marginale*, *Babesia bigema* and *Ehrlichia bovis*. The implications of these findings are discussed.

(0135) The impact of water quality variables and trace elements on the prevalence, mean intensity and seasonal occurrence on the infection rate of *Cichlidogyrus philander* infesting *Pseudocrenilabrus philander* in Padda Dam, Gauteng, South Africa.

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Increasing awareness of deteriorating aquatic systems due to anthropogenic pollutants that cause sharp changes in water quality has led to the development of fish-parasite relationships as bioindicators of environmental pollution. The direct life cycle of monogeneans makes them good bio-indicators to changes in water quality. Therefore, the aim of this study was to examine the impact of water quality and trace elements on infection variables and seasonal occurrence of *Cichlidogyrus philander* infesting *Pseudocrenilabrus philander* in Padda Dam, Gauteng, South Africa. This dam forms part of the Westdene tributary system, which is one of the origins of the Limpopo River. The dam is known to be polluted with both urban and residential runoff. Records exist of at least two incidents of pollution through oil spills. A total of 189 fishes were collected, sediment and water samples taken and water quality variables measured (*in situ*) between February 2016 and January 2017. *Cichlidogyrus philander* was the only monogenean parasite infecting *P. philander* in Padda Dam. This parasite occurred throughout the year with a seasonal prevalence, abundance and mean intensity reaching maximum values of 98% in both winter and spring, 26.2% in summer and 33.2% in autumn, respectively. These results confirm previous work in the dam. The correlation between environmental parameters, water quality and trace elements on infection variables and the implication these might have on the seasonal occurrence of the parasite is thus presented and the potential of the parasite as a sentinel of pollution are evaluated.

(0136) Madagascar: A parasites' paradise

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The unique biodiversity of Madagascar is well documented, leading to the island being listed as one of the top biodiversity hotspots in the world. This unique biodiversity is not only restricted to the well-known lemurs. In fact, between 60 and 100 new plant and animal species are described from this island per year. In particular, the island has a spectacular diversity of herpetofauna. Of the more than 400 frog species, all but two are endemic to the island. The diversity goes even further: along with their anuran hosts, parasites speciated to the high levels of endemism and diversity we see today. Specifically, a survey of the amphibian polystomatids, a group of species-specific monogenetic trematodes, in Madagascar revealed a unique diversity, albeit with evolutionary links to Africa and India. Currently, the known polystome genera from amphibians from Madagascar include *Metapolystoma*, also found in Africa, and *Madapolystoma* and *Kankana*, endemic to the island but with evolutionary ties to the African and Indian genus *Eupolystoma*. Polystomes are also known to infect freshwater chelonians. The only chelonian polystome known from Madagascar is *Polystomoides chabaudi* from the Helmeted terrapin, *Pelomedusa subrufa*, that also occurs in Africa.

(0137) Ecological causes and consequences of endosymbiont abundance in an arthropod vector: *Wolbachia* and *Synosternus cleopatrae* fleas

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The interaction between arthropods including vectors and their endosymbionts can vary with the ecological conditions. In some cases, the endosymbiont can be beneficial in one situation and harmful in another, affecting the ability of the vector to transmit pathogens. However, at present, in most biological systems, the nature of vector-endosymbiont relationships and the ecological conditions that shape them in nature are unclear. *Wolbachia* is a common endosymbiont of arthropods and is well known in affecting their host life history and ability to transmit pathogens. Despite cumulative evidence for the dominance of *Wolbachia* in various flea species and the role of fleas in pathogen transmission, the dynamic and nature of interaction between them is still obscure. In order to bridge this gap of knowledge, we tested the effect of several ecological factors, namely the parent-flea environment (field versus laboratory), age, and sex on *Wolbachia* presence and abundance within the flea and its effect on the flea reproduction success. Specifically, we sampled two groups of fleas differing in their parental environment. Each group was divided to three subgroups of males and females, which vary in the time allowed for feeding and reproduction. The life of fleas was terminated either before feeding and reproduction or after five, 10 or 15 days of feeding and reproduction. The abundance of *Wolbachia* was quantified by qPCR. I demonstrate the differences among the flea groups in light of their interaction with *Wolbachia* and discuss the possible implications for *Wolbachia*-related manipulations in flea control.

(0138) *Ehrlichia ruminantium* in Mozambique: a study on prevalence in ticks from cattle and wildlife and isolate genetic diversity

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Amblyomma hebraeum and *A. variegatum* ticks are the main vectors of heartwater in Mozambique, an important ruminant disease caused by the bacterium *E. ruminantium*. In order to determine the prevalence of *E. ruminantium* in *A. hebraeum* and *A. variegatum* and to genetically establish the diversity of isolates from different origins, cattle and wildlife were sampled across the south and centre of Mozambique as well as in the Kruger National Park (KNP), South Africa. In total, 1110 ticks were collected from 31 localities and screened for *E. ruminantium*, using a nested *pCS20* PCR and *pCS20 Sol1*TM qPCR. Prevalence of *E. ruminantium* in relation to the tick specie and locality, and correlation with tick abundance was analyzed. Mozambican isolates were typed using MLST and each genotype and corresponding genetic group were linked to their geographical origin. On cattle, *E. ruminantium* tick prevalence varied from 0% to 26.7%. In wildlife the overall prevalence was 8.2 % in the KNP and 6.2% in hunting concessions in Sofala province. However, no significant difference in prevalence was found between sampling sites and tick species. Also, there was no linear correlation between *E. ruminantium* prevalence and tick abundance. Furthermore, genotypes from groups G1 and G2D seems to be associated with adaptation to *A. variegatum* while group G2C seem to be only associated with *A. hebraeum*. These results will contribute to a better understanding of *E. ruminantium* spatial distribution in the studied regions and, therefore, to an improvement of heartwater monitoring and control strategies in Mozambique.

(0139) *Mycoplasma* bacteria in the wild: From patterns to mechanisms

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Understanding the relations between natural patterns of parasite infection and the mechanisms underlying coexistence with their host, will expand our knowledge on the ecology of host-parasite interactions in natural communities. Haemoplasmas are common blood bacteria associated with various hemato-pathologies in vertebrates. They provide an example of a knowledge gap between their extensive prevalence characterization in natural communities and the unknown mechanisms underlying the observed infections. In the Negev dunes (Israel) we have found a *Mycoplasma haemomuris*-like haemoplasma species infecting *Gerbillus andersoni* rodents at high prevalence, while infection of their blood sucking arthropods displayed moderate prevalences. Capture-recapture techniques have revealed that haemoplasma infection remains prevalent in rodent blood, but the infection load decreases from spring, the main reproductive season for rodents, to autumn. In order to investigate haemoplasma transmission and infection strategies, we conducted a series of experiments exploring vector-borne transmission by fleas, direct transmission between hosts and vertical transmission from fleas to their offspring and from host to their offspring. In parallel, we examined the infection dynamics by inoculating naïve hosts with infected blood. In contrast to the hypothesis of vector-borne transmission, we found that the main route of haemoplasma transmission was direct (host-to-host) and that infection persists lifelong, reaching peak loads 25 days after inoculation, corresponding to loads found in field rodents during the reproductive season. These findings suggest that haemoplasmas facilitate direct transmission in a solitary host during periods of maximal intrapopulation interaction, and rely on persistence with low bacterial loads, for long-term coexistence with their hosts.

(0145) The consequences of livestock-wildlife integration for tick-borne disease risk in central Kenya

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Historically, livestock ranching and biodiversity conservation have been considered conflicting uses of African savannas because wildlife and livestock compete for grazing resources and exchange pathogens and parasites. However, recent research demonstrates potential positive interactions between wildlife and livestock from a savanna ecosystem in central Kenya. Our investigations demonstrate at several different spatial scales that cattle dramatically reduce the abundance of host-seeking nymphal and adult ticks, the two stages responsible for transmitting a multitude of tick-borne pathogens. Cattle reduce tick abundance apparently because of the widespread use of acaricides for livestock production. As a result, treated livestock remove ticks from the landscapes in which they graze, thus functioning as “ecological traps” for ticks. This finding, in combination with other recent research from this region, indicates that integrated management of livestock and wildlife has the potential to simultaneously optimize human health and wildlife conservation under some conditions.

(0147) Alien freshwater fish parasites from South Africa: Diversity, distribution, status and the way forward.

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The global translocation and introduction of freshwater fish into non-native regions has created the perfect opportunity for the co-introduction of their parasites. In a recent review on non-native freshwater fish introductions in South Africa 55 fishes were reported as introduced into novel environments, with 27 alien and 28 extralimital. However, the parasites potentially co-introduced by these non-native fishes have received much less attention from researchers than the hosts themselves. Thus far the only attempts at summarising our knowledge on the diversity of introduced freshwater fish parasites in this region dates back to the 1980s when only four parasite species were considered to be alien. In the past 30 years more records were added; this paper aims to provide an up-to-date review of our knowledge on the diversity, distribution, status (co-invasive or co-introduced) and the direction for future studies on introduced freshwater fish parasites in South Africa. Here we consider seven species as confirmed co-invaders and 15 species as co-introduced. In addition, six species previously recorded as invasive are deemed to be of uncertain status and one ciliate is removed from the list of known invasive parasites from this region. It is further proposed that future research should focus on extralimital co-introductions, that all new records of introduced parasites and new distribution records of known invasive parasites should include the deposition of voucher specimens in museums and molecular confirmation of its identification.

(0152) Two sides to every story: the case of the infection biology of *Lamproglena clariae* in relation to water quality and the environment in the Vaal River

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Ectoparasites exposed to the macroenvironment of the host have had to evolve at a similar rate to the host in order to tolerate and survive environmental alterations. Therefore, changes in the infection biology of ectoparasites are a useful indicator of environmental quality and are often more sensitive than changes relating to hosts. In the Vaal River, the usefulness of some parasites as environmental indicators has been explored. *Clarias gariepinus* were collected during mid-summer at six sites along the Vaal River: below Grootdraai Dam (GDVR), Vaal Dam (VD), below the Vaal River Barrage (VRB), Bloemhof Dam (BD), below Vaalharts Weir (VH) and Douglas Weir (DW); these represented both impounded and riverine habitats. *Lamproglena clariae* were removed from the gills following euthanasia of hosts. Physical water quality variables were determined at each site and differed between sites, indicating poorer conditions at VRB, BD, VH and DW in terms of electrical conductivity, total dissolved solids and salinity. Differences in infection variables of *L. clariae* were present with highest prevalence, mean intensity and abundance at GDVR and lowest at DW. Mean intensity and abundance of *L. clariae* are negatively correlated with conductivity, salinity, TDS, oxygen saturation and dissolved oxygen levels. However, prevalence did not show any correlation with these variables but instead was negatively correlated with dissolved and saturated oxygen levels. This therefore serves as a preliminary indication of a relationship between the occurrence of *L. clariae* and water quality and the environment type in the Vaal River.

(0154) Avian haemoparasite prevalence in Kruger National Park, South Africa

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Determinants and impact of avian haemoparasite infection on wild birds is difficult to estimate, especially in areas where infections are endemic and the hosts and parasites have co-evolved. Our study evaluated the prevalence of avian haemoparasites in birds caught within and near the Kruger National Park. We documented the effects of parasite infection on bird immunity and body condition. We also assessed the role of the environment and the bird's life history traits on parasite prevalence. A total of 685 birds from 87 species were sampled and microscopic screening results show an overall haemoparasite infection prevalence of 27.3 %. Infections of *Haemoproteus*, *Microfilaria*, *Hapatozoon*, *Trypanosoma*, *Rickettsia*, *Aegyptianella* and *Leukocytozoon* spp were identified. The was no significant difference on prevalence across different sites and seasons while the highest diversity of parasites was recorded in the southern regions of the park, with minor influences of host life history traits on infection. Location and seasonal prevalence results suggest that parasitaemia is not mediated by, or necessarily coincides with, high mosquito abundance but is more associated with proximity to human habitations. Infected birds had a significantly lower body condition. This study documented parasite prevalence and diversity of infections in areas of southern Africa that have not been sampled before.

(0155) Complex strongyloid helminth communities in large herbivores: insights from Australasian macropodid marsupials

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Complex communities of strongyloid nematodes have been documented in the large intestines of equids, elephants and rhinoceroses as well as in the sacculated fore-stomachs of Australasian kangaroos and wallabies. Currently, the greatest diversity (35 genera and over 250 species) occurs in Australasian macropodid marsupials, with some 50 extant host species, while there are many fewer extant host species among equids, rhinoceroses and elephants. Current studies, both molecular and morphological, on the cloacinine nematodes of macropodid marsupials suggest that the primary mode of evolution of these complex communities has been by host switching, although in one genus (*Cloacina*), there is also some evidence for within-host speciation. Within-host speciation may be allopatric in the case of widely distributed host species, or possibly sympatric in host species with a limited geographical range, situations which require further investigation. The presence of cryptic species, currently being revealed using

genetic data, potentially adds to the complexity of unravelling such evolutionary processes. Equids, rhinoceroses and elephants were once more speciose and their complex helminth communities may have developed from host switching in the distant past. Since the Australasian macropodid marsupials are still represented by numerous extant species, they present a useful model for trying to understand how such complex stronglyloid nematode communities may have developed in large herbivorous mammals.

(0156) Haemogregarine biodiversity parasitising snakes of KwaZulu-Natal, South Africa

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South Africa has a high biodiversity of reptiles and as such much effort has recently been placed in documenting and conserving this diversity. Globally, this diversity is threatened by a range of factors from habitat loss to the illegal international pet trade, the latter allowing for disease dissemination. Reptiles, particularly snakes, host a wide array of endo- and ecto-parasites and as such may serve as 'parasite-taxis'. Protozoan blood parasites of the genus *Hepatozoon* (Apicomplexa: Hepatozoidae) are frequently recorded infecting snakes globally with several of these described from African snakes. Most of those from Africa, however, were described in the early years of the previous century and since then have received little further attention. Over the last four years, an ongoing blood parasite survey of the reptiles of Ndumo Game Reserve, Bonamanzi Game Reserve and surrounds, KwaZulu-Natal, has revealed a high biodiversity of haemogregarines in snakes, including two new species from the genus *Philothamnus* and one new species from the genus *Gonionotophis*. The combination of both traditional morphological (morphometrics) and molecular methods (parasite 18S rDNA sequence analysis) in the description of these parasites is allowing for a better understanding of their distributions, ecology, cytopathic effects and host-parasite relationships.

(0158) Perplexing protozoa: A gateway to wildlife and global One Health

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If not for the discovery of my enduring passion for protozoa, beginning with a fascination for *Theileria* and leading to an appreciation for the intrigues of *Toxoplasma*, I might be practicing veterinary medicine in Colorado rather than promoting a global One Health approach to improve human and animal health in shared environments. In this talk I tell my story of how this love of perplexing protozoa has revealed the important role that wildlife play in disease ecology, from the asymptomatic reservoirs to the victims of the parasites' biology. A special focus will be on how the most recent results of our collaborative studies (VanWormer *et al.* 2016 *Nature Sci Rep*, 6: 29252) demonstrate the impact of both land-use and climate change on the transmission of *Toxoplasma gondii* oocysts from the land to the sea where they infect marine mammals, most notably threatened Southern sea otters. The contribution that wild felids that shed oocysts make to environmental contamination relative to that of domestic cats, and the role of snails and filter feeding bivalves are also discussed.

(0159) Parasite-parasite interactions in the wild: Beyond the individual host and into the landscape

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It is not uncommon for wild animals to be co-infected by multiple parasite species. Furthermore, there is growing realisation that there may be substantial ecological interactions between these parasites within individual hosts. These interactions may be direct, via contact between parasites, or indirect, via immune stimulation or modulation of host defences, thereby resulting in a beneficial or antagonistic interaction for another species of parasite. However, while these interactions undoubtedly often occur in individual hosts, a broader understanding of their impact beyond the individual is not yet fully clear. In particular little is known about how these interactions scale up to drive parasite dynamics at the population or landscape scales. Here, we build on work undertaken on a well-studied, antagonistic parasite-parasite interaction between a protozoan (*Eimeria hungaryensis*) and a nematode (*Heligmosomoides polygyrus*) of the wood mouse *Apodemus sylvaticus*. Our key question: is this antagonistic interaction visible spatially, i.e. do we see total or partial exclusion of one parasite at the landscape scale, in favour of the other, and vice versa? Ultimately, the one-host one-parasite paradigm may yet hold some value, however a full understanding of the scale at which it is relevant is key to inform studies of conservation, public health and agricultural importance.

(0162) Hexabothriid parasites from Rajidae species of South Africa

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Hexabothriid parasites have been described as some of the most host-specific parasites and can be found on the gills of chondrichthyan fish. The study aims to add information to the current scarcity of literature and to provide resolution to the systematics, particularly for South African species. Hexabothriid species already identified from South African Chondrichthyes include the genera *Callorhynchocotyle* and *Branchotenthes*. Both *Callorhynchus capensis* (Cape Elephant fish) and *Rhina ancylostoma* (Bowmouth guitarfish) play host to these two genera. In the current study, hexabothriids were collected from *Rostroraja alba*

(White Skate), *Leucoraja wallacei* (Yellowspotted Skate), and *Raja straeleni* (Biscuit Skate). The monogeneans were stained with alum carmine to aid in the identification process by a closer examination of the reproductive organs. Furthermore, morphometric analysis of the sclerotised haptor armature including the hamuli was measured to assess the sensitivity of these characters to discriminate parasites from closely related host species. Measurements of the hamulus include, among others, circumferential length, shaft width, and aperture angle. These characteristic of the hamulus have the potential to provide species-level information, previously not considered. The monogeneans collected from the Rajidae hosts were identified as *Rajonchocotyle* spp. and *Branchotenthes* spp. The value in resolving an issue of systematics and identification cannot be underestimated due to the high monetary and educational value of aquarium species affected by these parasites. Ethical and responsible captive husbandry of these species may be well served by a targeted treatment for any infestation when correctly identified, thus reducing mortalities.

(0165) Advances in the knowledge of ticks (Acari: Ixodidae, Argasidae) in Chile: new species, host, localities and new reports of tick-borne disease

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Ticks are obligatory hematophagous ectoparasites of vertebrates in some or all postembryonic stages. Several species are vectors of agents that may cause disease and even kill their vertebrate hosts; ticks may also cause dermatoses, and they can inoculate toxins. Globally, the superfamily Ixodoidea contains the families Argasidae (208 species), Ixodidae (723 species) and the African Nuttalliellidae. In the Neotropical region, a total of 200 tick species have been documented. Before 2006, approximately 20 tick species were known to inhabit Chile. In the last 10 years, biogeographic and taxonomic knowledge has increased markedly due to two research projects by our group that allowed us to detect new findings and make new descriptions of ticks in Chile. During 7 years (360 days of field work) we have collected ticks of different hosts and environments in the 14 ecoregions of Chile, including the Antarctic territory. We have developed the biological cycles under laboratory conditions, determined new species and new records of ticks for Chile. Knowledge of Chilean ticks is increasing; we recorded 31 ticks present in Chile, five of them new species. We have elucidated the complete biological cycles of four soft ticks. Recently, we described the new bacteria *Borrelia chilensis* in *Ixodes sigelos* and *Rickettsia* sp. in *Amblyomma parvitarsum* from different localities. The integration of this knowledge will finally allow the implementation of management measures to prevent or anticipate emergent disease transmission between animal and human populations.

(0168) Developing molecular methods for detection of blood meal source in a free-living marine ectoparasite

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Gnathiid isopods, common ectoparasites of fishes, are known to be a driving factor in cleaning symbiosis, and can have multiple impacts on hosts. *Gnathia marleyi*, common in the eastern Caribbean, infests a wide range of host species. However, because most of its life history is spent free-living, the extent to which it feeds on different hosts in the wild is unclear. Sequencing of host blood meals is a promising tool for addressing this. Although established protocols for fish species identification exist, certain challenges must be overcome when samples are subjected to conditions that may contribute to DNA degradation, and efforts to slow DNA degradation during field collection can play an important role in the successful identification of the blood-meal source. Here we develop molecular-based host identification methods for *G. marleyi*, based on the degradation rate of blood meals. To establish blood meal degradation rates, juvenile gnathiids obtained from a colony were allowed to feed on fish overnight. Subsets were then preserved at equal time intervals, over a 24-hour period. The host DNA extracted from gnathiid blood meals was sequenced to validate the integrity of host DNA, at each time interval. This information was then used in host species identification from wild-caught gnathiids, obtained from light traps. Host DNA was extracted from gnathiid blood meals and amplified using COI universal fish primers. DNA sequencing results were entered into BLAST to identify the host species. The data collected in this study will be applied to future, broader scale, studies.

(0169) Assessment of the parasitic helminth fauna of wild rats in Jamaica

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A survey of 437 wild rats (297 black rats, *Rattus rattus*, and 140 brown rats, *R. norvegicus*), for infections with helminth parasites was carried out in the 14 parishes of Jamaica. One hundred and forty (32.0%) were infected with *Angiostrongylus cantonensis* recovered from the pulmonary system and 130 (29.7%) were infected with one or more of nine species of gastrointestinal helminths. The helminths recovered from the gastrointestinal tract were comprised of two cestodes [*Raillietina* sp. (0.2%) and *Hymenolepis diminuta* (3.8%)], six nematodes (*Trichuris* sp. (0.2%), *Rictularia* sp. (0.7%), *Syphacia obvelata* (1.1%), *Strongyloides ratti* (1.4%), *Protospirura muricola* (4.3%) and *Nippostrongylus brasiliensis* (14.2%) and one acanthocephalan (*Moniliformis moniliformis* (11.2%). *Rattus rattus* demonstrated higher prevalence for both *A. cantonensis* and the gastrointestinal helminths than *R. norvegicus* ($P < 0.04$), likewise it had a higher mean intensity of infection ($P < 0.05$). The majority (80.0%) of the 130 infected rats harboured only one species of helminth in their intestines. *Rictularia* sp. represents a new geographic distribution record for the Caribbean region. *Angiostrongylus cantonensis*, *H. diminuta*, *M. moniliformis*, *Raillietina* sp., and *Rictularia* sp. are potentially zoonotic, but only human infection with *A. cantonensis* has been reported from Jamaica. Considering that rats share human habitats and the high prevalence of *A. cantonensis* in rats in Jamaica, these findings have considerable public health implications.

(0170) Lethal and sublethal impacts of parasitic gnathiid isopods on post-settlement coral reef fishes

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The transition from a planktonic larval stage to a benthic or demersal juvenile stage is a crucial event in the life history of coral reef fishes, and recruitment success has a strong influence on reef-fish population size. Post-settlement predation is thought to limit recruitment success. Most studies on post-settlement predation have focused on piscivorous reef fishes. However, recent studies suggest that blood-feeding ectoparasites may also be an important source of predation and may further have significant sublethal effects on post-settlement reef fishes. In this study, we quantified the relationship between levels of infestation by gnathiid isopods and mortality rates among juvenile reef fishes as a function of body mass both within and among species. We found that a single gnathiid could kill individuals of all species shortly after settlement, up to .116g (18mm FL) in French grunt (*Haemulon flavolineatum*), .01g (9mm FL) in beaugregory damselfish (*Stegastes leucostictus*) and .027g (15mm FL) in masked goby (*Coryphopterus personatus*). For *S. leucostictus*, we also compared the ability of fish infested with a sublethal number of gnathiids versus uninfested individuals to hold a territory. Uninfested fish were significantly more likely to win pairwise contest versus infested fish. These findings suggest that gnathiids can significantly impact juvenile coral reef fishes well past the settlement stage and have significant effects on population dynamics.

(0171) Tracing the origins of parasitic invasions using genetics: examples of introduced helminths of fish and deer

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Invasive species are affecting ecosystems all over the planet. Facilitated by the movement of humans and their commodities, the results have been disastrous for global biodiversity. Parasites, either introduced with their native hosts or independently, often become invasive after switching to a new non-adapted host. Tracing the origins of parasitic invasions to their source can help prevent recurrent mishaps in the future. Population genetic analysis of multilocus markers (e.g., based on coalescent methods) provides a powerful tool in tracing these introductions. Here I provide one example of a cryptic introduction, where a non-native lineage of a freshwater fish cestode, *Ligula intestinalis*, was introduced to N. Africa. The introduction was revealed and traced back to its origin in S. Europe using microsatellite analysis. Second example involves populations of the giant liver fluke, *Fascioloides magna*, originally parasitizing ruminants in N. America and now spreading across Europe. Whilst single-locus analyses allowed distinguishing two independent introductions, multilocus analysis enabled tracing these two events back to original localities within the N. American continent. Future analyses, when extended with immunogenetic and population genomic data, will allow characterization of the processes affecting populations of the parasites and their wildlife hosts during the invasion process.

(0176) Resistance of the African blue tick (*Rhipicephalus (Boophilus) decoloratus*) to macrocyclic lactones in the Eastern Cape, South Africa.

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Ticks are obligate hematophagous ectoparasites of vertebrates causing serious problems worldwide by transmitting a variety of pathogenic microorganisms to their hosts. Tick infestations have been a big problem for cattle farmers for many years and acaricides such as pyrethroid, amidines and organophosphates are mostly used to control ticks such as blue ticks, *Rhipicephalus (Boophilus) microplus* and *R. (B.) decoloratus*. Due to over-use of these chemicals, resistance to acaricides in these species has been reported in Brazil, Australia, and South Africa. More recently it was discovered that macrocyclic lactones (MLs), originally used to control endoparasites, are also able to control blue ticks. Use for this purpose became a more frequent alternative for blue tick control to the extent that incidences of *R. microplus* resistant to ML have been found in Brazil. In SA, pharmaceutical companies also increasingly receive complaints of insufficient control of blue ticks by MLs from farmers, especially in the Eastern Cape. To investigate this problem, a method to determine *R. decoloratus* resistance as well as the South African strain of *R. microplus* needs to be developed. For this purpose susceptible strains of both ticks species were used to determine the method best-suited for ML-resistance testing against South African strains of the blue tick. Based on the Shaw Larval Immersion Test, the Test-tube and Pie-plate methods were compared, also taking different post-evaluation periods into consideration. Preliminary testing showed the Pie-plate method produced the best results under 72 hours larval incubation.

(0179) Cystic echinococcosis in the northern Golan Heights: primary findings

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Cystic echinococcosis (CE), a major health problem in the Middle East, is endemic in several areas of Israel. The Druze in the Golan Heights are an isolated community that has a high standard of medical care, but practises home and religious slaughter and family farming with pasture grazing. They live close to the border between Israel and Syria through which some domestic and wild animal migration takes place. These settings constitute a unique opportunity to study the epidemiology of CE. A preliminary abattoir survey which included the inspection of bovine and ovine carcasses over 3 months was carried out. Cysts suspected as hydatid were examined microscopically and further tested by PCR for *Echinococcus granulosus*. Faecal samples from 1 wolf and 34 dogs were examined by microscopy and copro-PCR. DNA was extracted using a commercial kit (QIAamp-DNA-FFPE, Qiagen, Germany) and molecular identification was based on detection of the EgG1 Hae III repetitive DNA sequence (133 and 269 bp) of *E. granulosus*. The survey revealed CE infection in 2/181 cows, 4/37 sheep and 8/34 dogs. The wolf sample was negative. The difference in prevalence of infection between herd and home dogs was 5/19 vs. 1/13, respectively, and was not significant ($p=0.2$). The bovine cysts were sterile; however, the 3/4 ovine cysts contained protoscolices. These findings confirmed that the northern Golan Heights is a CE hot spot and warrants investigation of risk factors for infection and further potential hosts including wild canines and herbivores.

(0182) The decline in parasite diversity along the Vaal River system, the downstream syndrome

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Environmental changes are often due to human-related activities and pose serious impacts on other living organisms. Considering the aquatic environment, biomonitoring is a popular method to measure change or at least distinguish between good and bad water quality. One way of achieving this is by using the parasites as bioindicators. The project aims to assess the quality of water along the Vaal River. A minimum of 10 fish (*Labeo capensis*) and a maximum of 20 fish were collected along the Vaal River. Beginning upstream and ending downstream, sites include: Vaal River below Grootdraai Dam (VRGD), Vaal Dam (VD), Vaal River Barrage (VRB), Bloemhof Dam (BD), Vaal-Harts Dam (VHD) and Douglas Weir (DW). The fish were examined for parasites. Water quality parameters including temperature, pH, conductivity, salinity, total dissolved solids (TDS) and dissolved oxygen were measured per site. Prevalence, abundance and mean intensity were calculated. *Chonopeltis* sp. were only found in the VRGD, with a high prevalence. The second highest prevalence was observed for philometrids in the VRGD. A single *Argulus* sp. specimen was found in VD, which is the site closest to the VRGD. Only one larva of *Contracaecum* sp. was found in VHD. Beginning at the VRB site, there is an increase in conductivity, salinity and TDS which might be attributed to a spike in the anthropogenic activities in this area. These activities seem to have a ripple effect which may be the main driver that causes the decline in the parasite diversity.

(0183) A comparative study of ectoparasite tolerance between purebred Brahman (*Bos indicus*), Sussex (*Bos taurus*) and Brahman X Sussex crossbred cattle in the Free State, South Africa

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The focus of sustainable profitability on any cattle farm falls on monetary gain but also on production of a quality product while being environmentally conscious. Crossbreeding *Bos indicus* with *Bos taurus* cattle was explored as a measure to manage tick infestation, specifically comparing tick and mite resistance between Brahman, Sussex and Brahman x Sussex crossbreds. The study area was located in the central Free State. Cattle breeds were followed over different camps and closely located farms to monitor ectoparasite presence and abundance and to compare these results to possible ectoparasite-repelling characteristics (hair and skin features, tail length, animal weight and rectal temperatures) of the different breeds. Ticks and mites were collected on a monthly basis from March 2014 to March 2015 from the on-host and off-host environment. It was found that other than the host characteristics, rainfall and temperature greatly influenced the viability of the on-host and off-host microhabitat conditions and were associated with an overall tick presence and abundance on all the breeds, that peaked during the hottest and most humid months of the year. When comparing tick load on the three cattle breeds studied, Sussex cattle was the most affected over the entire test period.

(0185) Exploring the implications of climate change on epidemiological dynamics of multi-host vector-borne diseases

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Understanding how pathogen dynamics are affected by modes of transmission is critical for predicting disease emergence, pathogen persistence, and potential impacts of climate change. Here we study a model of two vector borne pathogen species in a multi-host community. We investigate their patterns of competitive exclusion and co-existence, where we also identify in- and out-of phase transient dynamics. We then discuss implications of these findings in climate change scenarios.

(0187) Benefits and pitfalls of molecular taxonomy: A case study of the Diplozoidae

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The use of molecular applications in taxonomy has recently grown to a substantial and crucial component of parasite studies. This addition to the arsenal of taxonomists has mostly produced useful and often more objective conclusions. However, relying on molecular data, especially from lesser known publications and direct submissions on online databases, can be tricky and even unreliable. The Diplozoidae are a group of monogeneans parasitizing mainly freshwater cyprinids. This group has only recently been studied from a molecular aspect and as such the limitations and variables concerning the use of such techniques for the taxonomic study of diplozoids has not been clearly defined. In this study, an attempt is made to critically assess the history and information available for molecular study of the Diplozoidae. All literature and available molecular information, mostly from online databases such as GenBank, were compiled and scrupulously analysed. Based on this, three molecular markers were identified and their phylogenies and relations studied. Additionally, these three markers, cytochrome oxidase 1 (COI), large subunit rDNA (28S) and internal transcribed spacer 2 (ITS2), were amplified and sequenced for five diplozoid taxa. The resultant phylogenies indicated that the use of a single marker for the accurate study of this group is sub optimal, especially for determining evolutionary history. The accuracy and validity of some records are also questioned and may highlight some of the pitfalls that should be avoided in future research.

(0192) Diversity and trends in prevalence of avian malaria in the Brazilian Amazon

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Avian haemosporidians are a highly diverse group of blood parasites that includes representatives of three apicomplexan genera, *Plasmodium*, *Haemoproteus* and *Leucocytozoon*. Brazilian Amazon supports world's highest avian diversity (1300 species) and expected equally rich yet undescribed diversity of avian haemosporidians. This study is the first large-scale survey of avian haemosporidians in the Amazon, with 3381 blood samples collected from 372 bird species, from 17 orders and 46 families; 527 samples (15.6% prevalence) were infected, with *Plasmodium* accounting for 466 (88.4%) of infections. *Plasmodium* prevalence (13.8%) was significantly higher than *Haemoproteus* prevalence (2.1%). A total of 303 haemosporidian genetic lineages were described, with *Plasmodium* accounting for 246 of them. More than 90% of discovered genetic lineages were new. A subset of the samples from 6 out of 9 recognized Amazonian areas of endemism (Belém, Guiana, Imeri, Inambari, Rondônia, and Tapajós) provided significant data to reveal trends in distribution and ecology of these parasites in Amazonia. Data on parasite distribution related to various bird ecological traits (e.g., nest height, nest type, foraging height and flocking) were analyzed. Relative importance of particular ecological traits as predictors varied in different areas of endemism. For *Haemoproteus*, nest height (Guiana, Rondônia), foraging height (Rondônia), and flocking (Belém) were found to be significant, whereas for *Plasmodium* nest type (Inambari), foraging height (Guiana, Imeri) and flocking (Belém) were significant predictors. However, area of endemism had an overall overriding effect which indicated that both host and parasites community structure and diversity follow the biogeographical patterns in Amazonia.

(0193) Walking with dinosaurs: phylogeography and systematics of proterodiplostomid digeneans parasitic in crocodylians

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Crocodylians are an ancient group of reptiles that evolved at least 225 million years ago. The ancestors of today's crocodylians already inhabited the supercontinent Pangea prior to its breakup. The geographic range of crocodylians was fragmented and the descendants of early crocodylians were separated from each other by continental drift. Associated speciation and extinction events ultimately shaped today's fauna and distribution of crocodylians. The same likely happened to their parasites. Although parasites of crocodylians have not been studied sufficiently, it has been demonstrated that they possess a relatively rich and highly distinct helminth fauna. One of the most characteristic groups of helminths found in crocodylians is the digenean family Proterodiplostomidae. At least some proterodiplostomids have been found in every region of the planet inhabited by crocodylians. No prior molecular phylogenetic work has been done on proterodiplostomids and sequence data on this group were completely lacking. The goal of our study was to infer phylogenetic relationships of proterodiplostomids and test the monophyly of some of its constituent genera using sequences of nuclear ribosomal DNA. The results based on specimens from 3 continents have provided evidence that at least some of today's proterodiplostomid lineages are very ancient and likely evolved before the break-up of supercontinents, thus reflecting long co-evolutionary history between these parasites and crocodylians. In addition, molecular phylogeny has permitted a reassessment of the taxonomic value of some morphological and biological characteristics of proterodiplostomids, resulting in amended systematics.

(0194) Human blood-brain barrier gene expression in response to African trypanosomes and physiologic flow shear stress

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How African trypanosomes that cause human African trypanosomiasis (HAT) compromise the human blood-brain-barrier (BBB) to cause central nervous system disease is not fully understood. Using parallel plate flow chambers, we investigated gene expression in human brain microvascular endothelial cells (hBMEC) exposed 4h (when maximal transcriptional changes were anticipated) to *Trypanosoma brucei rhodesiense* (Tbr) using static and SS conditions (PCV and capillary pulsatile flow). We identified 333 to 491 genes differentially expressed at more than ± 3 SD for each of the three comparisons. Pathway-enrichment of 405 significant canonical pathways altered by infection showed that 60-77% of those associated with SS were largely metabolic vs. 16% for static conditions. The data also highlight potential pitfalls associated with interpretation of BMEC-derived transcriptome data based solely on static BBB models. While many pathways were shared between Low SS, High SS and static conditions, almost all pathways under static conditions show changes in PI3KR gene expression, but this was mostly absent under SS conditions. However, a role for PI3KR in trypanosome transmigration in areas of blockage where static flow exists is possible. Interestingly, based on the published literature there was a high level of agreement regarding the gene expression with metabolites identified in plasma of Tbr HAT patients versus controls. How the metabolites impact or affect the enriched pathways or vice versa to ultimately cause disease is not clear. Considering the importance of metabolic pathways in maintaining brain capillary homeostasis, one could argue that some neurological consequences associated with HAT may be due to flow-induced changes.

(0195) A gyrodactylid on Lake Magadi cichlid fish, *Alcolapia grahami*: A fish living under extreme environmental and anthropogenic selective pressures

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Alcolapia grahami is a small cichlid fish which subsists in the scattered lagoons of the Greater Lake Magadi and the Little Lake Magadi, which are located in a highly tectonically active part of the eastern arm of the Great Rift Valley of Kenya. To enable the fish to tolerate severe environmental conditions which include high water temperature (42°C), large diurnal shifts in oxygen availability in the water and high alkalinity (pH ~10), exceptional physiological, morphological and behavioral adaptations have developed. Among others, these include highly specialized gills for gas exchange and osmoregulation and, uncharacteristic of fish, excretion of products of nitrogen metabolism entirely in the form of urea. It was therefore very unexpected to find the gills infected with a gyrodactylid parasite. The morphology of the parasite has been compared to species from the environment and it was concluded that the shape and size of the attachment structures differs enough to make this parasite a distinct taxon. Urgent conservation measures of a unique fish which offers rare glimpse into the astounding degree to which animals can adapt to harsh environmental conditions and one which an appropriate model of the effects of global warming on animal life are urgently required.

(0199) *Anaplasma marginale* and *A. centrale* are widespread in cattle in South Africa

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Bovine anaplasmosis, caused by *Anaplasma marginale*, is one of the most economically important tick-borne diseases of ruminants. *Anaplasma centrale* causes a milder form of the disease, and is used as a live vaccine against bovine anaplasmosis. A duplex quantitative real-time polymerase chain reaction (qPCR) assay was recently shown to be more sensitive than the nested PCR and reverse line blot hybridization assays in detecting *A. marginale* in cattle samples. In this study, the level of variation in the qPCR target regions of the *msp1b* (*A. marginale*) and *groEL* (*A. centrale*) genes from cattle field samples was assessed by amplicon sequencing. The *A. centrale groEL* was conserved and different from *A. marginale*. A total of 186 *msp1b* sequences were obtained from 40 samples, yielding 11 variants within the qPCR target region. Evaluation of the most diverse variants indicated that the polymorphisms had no significant effect on the efficiency of the assay. The duplex qPCR assay was then used to screen 517 cattle samples from all nine provinces of South Africa for the presence of these organisms. *A. marginale* and *A. centrale* were detected in 56.8% and 17.2% of the samples, respectively; 81 (15.3%) samples had mixed infections. *A. marginale* is widespread in cattle in eight of the nine provinces of South Africa, confirming that the organism is endemic in the distribution area of the vector ticks. The presence of *A. centrale* in many unvaccinated cattle suggests that there is a natural transmission cycle of this organism in South Africa.

(0201) Avian malaria diagnosis in wildlife

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Plasmodium parasites are prevalent worldwide. These haemosporidians cause malaria in domestic and wild birds. Over 50 avian *Plasmodium* species have been described based on morphology and more than 700 unique mitochondrial cytochrome b gene lineages were recorded in various avian species. Although accumulated huge data about diversity of avian *Plasmodium* parasites, their development in vectors and vertebrate hosts, especially during primary infections, and impact on host fitness is insufficiently investigated. To understand host-parasite interactions, specificity and development of disease in different bird species, field and experimental studies on vertebrate hosts and blood sucking insects should be performed in different areas. I present recent data

about worldwide prevalent malaria parasites, their impact on host fitness and peculiarities of diagnosis. The talk illustrates that light infections (previously considered as benign) in blood samples, which are commonly observed in wild birds, are not always a measure of birds' health. Current applications of different methodologies, e.g. traditional (microscopy) and molecular methods for investigation of avian malaria and other haemosporidian parasites, are discussed, showing their strengths and weaknesses together with recommendations for field studies. Information provided is important for better understanding the epidemiology of avian malaria infections, patterns of transmission and precise diagnostic methods in wild and domestic birds.

(0202) Several topics on parasitic helminthiasis and helminths from free-ranging or captive vertebrates with special reference to recent cases dealt with the Wild Animal Medical Center, Rakuno Gakuen University, Japan

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In 2004, to provide facilities for conservation medical research and education, the Wild Animal Medical Center (WAMC) was established in the Teaching Animal Hospital of the School of Veterinary Medicine. Principally, the main research activities of WAMC are veterinary medicine for wild and zoo animal medical practice, epidemiology on infectious pathogens of both human and (captive and wild) animals, bio/chemical toxic agents, positive diagnosis of parasitic diseases, etc., with zoo vets, university staff, NGOs and students who are interested in ecotourism. Because the present WAMC manager, namely the present author, has been a wildlife helminthologist, most scientific papers belong to the scientific field of helminthology. The Japanese Society of Zoo and Wildlife Medicine designated the WAMC as the Wildlife Helminthiasis Center in 2006. The designation is accelerating to make stronger relationships between zoos/aquariums /wildlife officers/researchers/exotic vets etc. and the WAMC. In this presentation, the author shows several topics on parasitic helminthiasis and helminths from free-ranging or captive vertebrates with special reference to recent cases supported by the Ministry of the Education, Science and Culture, Japan.

(0207) Spatially modeled surveillance for Deer Hair-Loss Syndrome in Columbian black-tailed deer (*Odocoileus hemionus columbianus*) in the Pacific Northwest, United States

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Hair-loss syndrome (HLS), which has affected Columbian black-tailed deer (*Odocoileus hemionus columbianus*) in western Oregon and Washington, is the first documented example of a transcontinental cervid chewing louse invasion. The presence of exotic lice *Damalinia (Cervicola)*, a normal ectoparasite of native deer in Asia, has been implicated as a causative factor in affecting population densities. Surveying black-tailed deer is inherently difficult due to dense coastal forests. The goals of this analysis were twofold: first, using ectoparasite collections identify environmental and ecological variables that might be associated with the presence of lice; second, use these variables to identify areas where surveillance for the lice should be focused. The geographic location of ectoparasite collections from deer (n=199) were merged with environmental and climatic data to look for associations between the presence of the lice and HLS sightings. These data were then used as spatial constraints to identify areas important for risk-based targeted surveillance of HLS and the lice. The area resulting from application of the spatial constraints was compared with reported sightings of HLS by biologists (n=1 973). The presence of lice increased significantly in areas with an average minimum temperature above 5.0°C (odds ratio=2.5; P<0.000). Elevations below 300 meters were also significantly associated with presence of the lice (odds ratio=2.7; P<0.000). This spatial analysis indicates that a correlation may exist between the presence of lice, elevation, and temperature. These analyses serve as a foundation for identifying areas important for targeted surveillance and management implications.

(0208) Host-switching and parasite radiations in herbivorous marine megafauna: turtles and sirenians

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Host-switching leading to establishment of new lineages of trematodes is probably rare, but is most likely where unrelated groups of host species share a common diet. Green turtles (*Chelonia mydas*) belong to an ancient lineage of marine reptiles (> 150 million years old) and host an extraordinary array of trematodes. One group of these (Pronocephaloidea) is morphologically like trematodes found in sirenians (especially dugongs), a group that became marine around 50 million years ago. Dugongs and green turtles have overlapping diets (e.g., seagrasses), offering opportunities for trematodes, that often exploit the food chain for transmission, to host-switch from turtles to sirenians. I present molecular evidence that this has indeed happened. Having established in the new sirenian hosts, pronocephaloids then radiated into at least a dozen species occupying different organs and exhibiting remarkable specialisations and morphologies in each. There are other likely examples of parasites host-switching into sirenians. One of these is especially noteworthy: a blood fluke occurs in Australian dugongs, but it is not a schistosome, as originally assumed. It is an aporocotylid, a group that otherwise is only found in the circulatory systems of fish. There has been a host switch across a great phylogenetic gap, from fish to mammals. Blood flukes penetrate the skin of their vertebrate hosts directly and are not transmitted via the food chain. In light of that, it is interesting that spirorchiids, the highly pathogenic blood flukes of turtles, have not yet been found in sirenians.

Poster Abstracts

(0010) Gertrud Theiler Tick Museum - Standing on the shoulders of giants

Deon Bakkes

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The Gertrud Theiler Tick Museum was started with specimens collected by Gerald Bedford in 1912. Since that time, several prominent scientists have made contributions to the collection in both specimen depositions and scientific study. This has elevated the collection to stand as the largest to house African ticks globally, containing 55 type specimens and 375 identified species amongst more than 2 500 specimens. The collection moved to its current holdings at the ARC-OVI in 2005. The value of museums in 21st century biology is a topic of important discussion in light of the biodiversity crisis and impending climate change. Moreover, museums may come of age once they acquire an adequate number of specimens and species that capture a considerable degree of natural variation. Study of this variation may be used to answer important questions regarding public health, agriculture, biodiversity and evolutionary processes. Of course, these are all underpinned by the relentless pursuit of the main function of museum collections - systematics. The Gertrud Theiler Tick Museum is poised to realise this vision, having come of age to represent the most complete collection of hard-earned African ticks. The raw data preserved in each specimen, comprising its species designation, morphology and collection data, in combination with modern methods of data capturing, analysis and dissemination will serve to elevate the Tick Museum further, toward a crucial position in a developing continent.

(0012) Intestinal parasites in children under 5 years of age at Chamanculo Hospital, Maputo, Mozambique

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Intestinal parasites (IP) are distributed globally mainly in tropical and subtropical regions, which includes Mozambique. They are more prominent in children because of their vulnerability to the risks. The purpose of this work was to determine the frequency of IP in children under 5 years of age seeking health-care at this hospital. Stool samples (n=70) were collected for analysis. Ethics approval been obtained. We used Ritchie techniques, modified Ziehl-Neelsen staining and fast immunofluorescent test. Overall, 36/70 children (54.4%) were infected by IP. *Trichiuris trichura* (28.6 %) and *Ascaris lumbricoides* (22.9%) were the most frequent parasites. The most frequent protozoa were non-pathogenic *Entamoeba coli* (11.4%), and pathogenic *Cryptosporidium* sp. and *Giardia lamblia* (10%). The proportion of IP in children whose family drank untreated water was much higher than in families that drank treated water: 61.1% and 5.6%, respectively. The proportion of IP infection was higher in children whose families used traditional latrines compared to families using self-care: 52.8% and 30.6%, respectively. The proportion of IP in children whose mothers had low schooling level was higher (33.3%), compared to children of mother with a high schooling level (2.5%). Our study demonstrates that the studied area was infected by IP, associated with low sanitary conditions. These findings suggest the involvement of other sectors than ministry of health to avoid cases of reinfection by IP in the country.

(0017) New species of gnathiids (Crustacea, Isopoda) on the Australian Great Barrier Reef and islands of the Coral Sea

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Gnathiid isopods (Crustacea, Isopoda, Cymothoidea) are peculiar crustaceans both in morphology as well as lifestyle being parasitic on fish during their larval stages, while during the non-feeding adult stage these occur in cavities on the bottom, within sponges or in coral rubble. Recent studies of gnathiids on the Great Barrier Reef and islands of the Coral Sea have revealed a number of species previously unknown to science, indicating hitherto unexpected species richness. To date Gnathiidae are known from the Great Barrier Reef, but based on the limited sites and depths investigated, that is considered to be less than 50% of the potential total. Several of those species are presented here. Most of these belong to the genus *Gnathia*, while two species of the genus *Elaphognathia* have recently been discovered.

(0018) Tick-transmitted protozoal and rickettsial parasites of free-ranging black-backed jackals (*Canis mesomelas*) in South Africa

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Black-backed jackals, which are common and widespread in Southern Africa, have recently been shown to be natural hosts of *Babesia rossi*, the causative agent of virulent canine babesiosis in domestic dogs in sub-Saharan Africa. A large set (n = 91) of blood specimens from free-ranging jackals from Mogale's Gate, on the border between Gauteng and North West Province, was available for screening for occurrence of other tick-borne protozoa and rickettsias. On reverse line blot, 77 (84.6%) of the 91 specimens were positive for the *Babesia*1-probe, of which 27 (29.7%) were confirmed positive for *B. rossi*. Forty-six (50.5%) specimens reacted with the *Ehrlichia/Anaplasma* genera-specific probe. Using Haemogregarine-specific PCR primer sets, 20 (21.9%) specimens reacted positively. From these 14 (15.4%) were confirmed positive for *Hepatozoon* species from within the *Hepatozoon canis* species complex. Two (2.2%) specimens were found positive for two different *Hepatozoon* species.

(0030) Literature overview on parasite infections in cheetahs (*Acinonyx jubatus*)

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Little is known on parasite infections in free-ranging cheetahs. Cheetahs are listed as vulnerable in the Red List of the IUCN (International Union for Conservation of Nature), thus it is important to know with which pathogens cheetahs are infected and what the prevalence of these pathogens in the different cheetah populations in Africa is. Many publications describe case studies in captive cheetahs, however, captive cheetahs are known to have a higher susceptibility to pathogens than free-ranging cheetahs. This study presents an overview of the literature on parasite infections in free-ranging cheetahs and compares the results with the ones of captive cheetahs and conspecific carnivore species. Investigated parasites were *Neospora caninum*, *Theileria*-like Piroplasms, *Hepatozoon* sp., *Babesia* spp., *Toxoplasma gondii* and *Mycoplasma* sp. Most studies were conducted in Namibia, South Africa and Tanzania. Prevalence in free-ranging cheetahs varied from 0% to 100% depending on the parasite, with 1 to 40 investigated individuals. The large range of prevalence might depend on contact rate amongst cheetahs, i.e. their densities, the presence and number of other large carnivore species and/or the presence of humans in the range of cheetahs. The study also identified study areas in which free-ranging cheetahs have not yet been tested for the above mentioned parasites. This map might be useful to plan further parasite studies in this species and to allow for comparisons of parasite prevalence between cheetah populations in Africa.

(0034) Intestinal parasites among army recruits in Munguúe, Maputo, Mozambique

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Intestinal parasites include a range of worms and protozoa highly prevalent in low-income countries such as Mozambique. The infestations impact negatively on the quality life of affected persons. Its occurrence reflects insufficiencies in standards of hygiene and sanitation: infestation are propagated in context of lack of basic safe sanitation and unfavorable socioenvironmental factors. Agglomeration of people increases the chance of transmission of parasites. The study aimed to determine the frequency of intestinal parasites in recruits from the Munguine Army Practical School (MAPS). A survey was conducted during July and August 2016 in which urine and stool samples were collected as per standard protocols. We used filtration method for examine the urine, and formalin-ether and Kato-Katz techniques for stool samples. Recruits infested were offered treatment as per Mozambican protocols. The study involved 362 participants (75% male and 25% female), between 20 and 27 years of age. Eighty-five (23.5%) were infected; 68 (18.8%) had multiple infections. Ten (2.8%) were infected with *Schistosoma haematobium*. The most prevalent helminths were *Trichuris trichiura*, detected in 6.9%, and *Ancylostoma duodenale*, detected in 3.6% of recruits. *Entamoeba coli* (10.2%), *Endolimax nana* (3.3%) were the most prevalent non-pathogenic protozoa. The prevalence of intestinal infestation among Army recruits was high. The findings show that intestinal parasites also affect young adults in Mozambique, suggesting a need to extend the mass treatment policies to cover all ages.

(0040) *Schistosoma mansoni* in western lowland gorillas and chimpanzees in Loango National Park, Gabon

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Schistosomiasis is a widespread zoonosis in sub-Saharan Africa and can have severe socioeconomic and public health impacts. Most of the human schistosome species can produce patent infection in other mammals including nonhuman primates, hosts that can in turn serve as reservoirs of the infection. Almost all information we have comes from experimental conditions which

confirmed that the course and morbidity of *Schistosoma mansoni* infection in chimpanzees strongly resembles that reported for humans, including severe liver fibrosis, and may lead to death. We detected eggs of *S. mansoni* in western lowland gorilla and central chimpanzee fecal samples in Loango National Park, Gabon. We analyzed internal transcribed spacer (ITS) and cytochrome c oxidase subunit 1 (cox 1) fragments using maximum likelihood phylogenetic analysis and haplotype network respectively which showed the position of our samples from gorillas and chimpanzees within the *S. mansoni* clade. This is the first record of any schistosome species in gorilla and first confirmed record of *S. mansoni* in Gabon which urges surveillance in the area and prompts questions regarding the extent of zoonotic transmission and clinical impact.

(0042) Bioaccumulation of metals and metalloids in the silver catfish and its nematode parasite

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Heavy metals from mining, domestic and agriculture sources have impacted a number of South Africa's rivers. As a consequence, fish and their parasites, which are known to accumulate metals from the surrounding environment, are adversely impacted. Therefore, the aim of this study was to compare the accumulation of metal and metalloids in larvae nematode parasites (*Contra-caecum* spp.) and the muscle and liver tissues of their host; the silver catfish *Schilbe intermedius* collected from different localities with varying pollution levels. Twenty *Schilbe intermedius* were captured using gill nets from three impoundments (n = 60) within the Limpopo River System. Water samples were taken from each locality and analysed to determine the water quality. The morphometrics of specimens collected was recorded to correlate host size with the accumulation of metals and metalloids. We found higher concentrations of metals in older fish and in fish sourced from the most impacted sites. Most metals and metalloids occurred in greater concentrations in the liver than in the muscle and parasites. Preliminary results indicate that due to the abundance, prevalence and distribution of *Contra-caecum* spp. and its high metal uptake, this parasite could serve as a bioindicator to detect the impact of metal pollution in aquatic environments.

(0047) *Skoulekia* spp. (Digenea: Aporocotylidae), blood flukes in Mediterranean porgies

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The sparids (porgies) are a group of teleosts of great economic importance in fisheries and aquaculture. Aporocotylid blood flukes often remain unnoticed as they live in the intricate circulatory system of fishes, inhabiting several microhabitats such as the gill blood vessels, heart, sinus venosus or kidney blood vessels. Aporocotylids have occasionally been found in blood vessels of girdles (*Paradeontacylix* spp.) or brain (*Skoulekia meningialis*). Blood fluke infections are often associated with large mortalities in aquaculture: adults release eggs to the blood stream which get trapped in gill vessels where the miracidia hatch through gill epithelium causing severe damage leading to asphyxia. During a parasitological study of Mediterranean sparids, including *Pagellus erythrinus*, *Diplodus vulgaris* and *D. puntazzo*, aporocotylid blood flukes were detected. In this study, a species of *Skoulekia* is reported from the blood vessels of the kidney, heart and gills of *P. erythrinus* (adult prevalence, 14%). Morphological and molecular data are provided, supporting the validity of the genus *Skoulekia*. New specimens of the type-species, *S. meningialis*, collected from *D. vulgaris* (type-host) and *D. puntazzo* (new host) are redescribed.

(0050) Morphological and molecular characterization of lymnaeid (Gastropoda: Lymnaeidae) snail populations from Okavango Delta of Botswana

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Freshwater snails of the Family Lymnaeidae play a major role in the transmission of *Fasciola* worldwide. In most areas, lymnaeid populations tend to share the same habitat. Due to their great intraspecific variability and diversity in their shell morphology, classifying the *Lymnaea* snails based on their shell morphology has always been problematic. Since reliable taxonomic classification of this genera is required for adequate the control and understanding of trematode epidemiology, this study aimed to use both molecular (PCR) and morphological techniques to characterize lymnaeid snails from Okavango Delta, Botswana. Five shell morphological characters were measured and parameters analysed with SPSS. The snail's DNA was amplified using the ITS-2 and 18S genes. Morphometric analysis showed that there is variability within and between populations, which may have been contributed by environmental conditions of their origin. Preliminary molecular analysis further confirmed the variation. The results also showed that the snail populations collected from the Okavango Delta of Botswana belong to the *Radix natalensis* and *Pseudosuccinea columella*.

(0052) Avian malaria on Madagascar

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The island of Madagascar is located in the Indian Ocean approximately 400 km east of Africa. Due to its isolation from mainland India and Africa it has many endemic species and is classified as an important biodiversity hotspot. Avian malaria is caused by haemosporidian parasites including the genera *Plasmodium*, *Haemoproteus* and *Leucocytozoon*. To date, few studies exist on blood parasites of Malagasy birds. Either blood samples were examined microscopically or just a small number was analyzed by PCR. In our study over 1000 Malagasy birds of over 50 different species (mainly Passeriformes), sampled in the years 2003-2016 were analyzed using molecular techniques. We found an extremely high variety of blood parasites. Over 80 different lineages of haemosporidian parasites could be identified. Due to the high number of investigated birds we could determine if the parasite lineage is a specialist or a generalist, highlight multiple infections and which ecological and life history factors might influence their prevalence in the birds.

(0054) Ticks and tick-borne diseases associated to cattle transhumance in West Africa

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Livestock production is one of the most important pillars of the economy of West African countries. It contributes up to 44 % of agricultural gross domestic product. In this region, however, cattle production is hampered by ticks and protozoan parasites they transmit, namely *Babesia* spp., *Theileria* spp. and *Ehrlichia ruminantium*. The purpose of this study is to assess the impact of the transhumance on the spread of ticks, especially *Rhipicephalus (Boophilus) microplus*, and associated diseases transmitted to cattle between Burkina Faso and Benin. In 2016-2017, ticks and blood were collected from 490 cattle in three border provinces of Burkina Faso which represent the transhumance departure zone to Benin. Additionally, 456 cattle were sampled in four border departments of Benin. Presence of tick species and associated blood parasites were therefore evaluated in the departure and arrival zone of transhumance. Furthermore, locality names, GPS coordinates and climate data were recorded. The on-going analyses are focused on tick species identification and DNA extraction for parasite screening. Blood smears and DNA extracted from cattle blood will also be analyzed for blood parasites. Analyses will reveal cattle tick species and related transmitted diseases circulating in study area. Furthermore, the presence of the invasive tick, *Rhipicephalus (Boophilus) microplus*, and the impact of transhumance on its further spread will also be determined. Such results will be useful for tick and tick-borne disease control programs within areas between Burkina Faso and Benin.

(0064) The biological role of Akirin in *Anopheles arabiensis*, at both a phenotypic and a transcriptional level

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Anopheles arabiensis is the main malaria vector in Southern Africa. Selection pressure on the vector has resulted in increased insecticide resistance despite vector management efforts. In addition to insecticide resistance, this species is found resting and feeding both indoors and outdoors. Current control methods are not targeting the outdoors portion of the population, and thus additional novel methods of vector control are needed. Population suppression using gene knockdown is a promising alternative for vector control. Inhibition of the transcription of *Akirin* has been shown to be able to reduce vector fecundity, and hence contribute to population suppression in ticks. The biological function of *Akirin* in *An. arabiensis* is not fully characterized, and will, therefore, be investigated in this study. The role of *Akirin* in *An. arabiensis* will be determined, using CRISPR interference, where the knock-down effect will be assessed at both a phenotypic and a transcriptional level, in order to evaluate the use of *Akirin* knockdown as a tool in vector control and to clarify its biological function. The results of these experiments could aid in the future production of an *Akirin* knockdown vaccine, which would be administered to *An. arabiensis* via livestock, as *An. arabiensis* is both zoophilic and anthropophilic, ultimately leading towards population suppression.

(0074) Occurrence of *Babesia rossi* in black-backed jackals, African wild dogs and domestic dogs in South Africa

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Numerous studies have reported on the occurrence of *Babesia rossi* in domestic dogs in South Africa, but information on occurrence of *B. rossi* in free-ranging indigenous canids, e.g. African wild dogs and black-backed jackals, is sparse. This study aimed at investigating the occurrence of *B. rossi* in black-backed jackals (n = 104) from Mogale's Gate Biodiversity Centre (Gauteng province) and S.A. Lombard Nature Reserve (North West Province), African wild dogs (n=36) from De Wildt Cheetah and Wildlife Centre (North West Province) and also in domestic dogs (n=75) presented as patients at the Onderstepoort Veterinary Academic Hospital, South Africa. Preliminary results of Reverse Line Blot hybridization assay revealed an overall *B. rossi* occurrence of 53.07%, with the highest occurrence (88%) detected in domestic dogs. Mixed infection of *B. rossi* sensu stricto and *Hepatozoon* sp were observed in the wild canine specimens. The sequencing results of the 18S rRNA gene confirmed the presence of *B. rossi* sensu stricto in black-backed jackals, African wild dogs and domestic dogs. Future studies will focus on investigating the genetic

diversity of *B. rossi* in domestic dogs, African wild dogs and black-backed jackals, with emphasis on the relatedness of the strains occurring in the three canine hosts.

(0082) High diversity of *Echinococcus* spp. in wild mammals of Namibia

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There is intense involvement of wild mammals in the transmission of *Echinococcus* taxa in Namibia; some lifecycles (*E. felidis* and *E. equinus*) appear to be entirely or predominantly sylvatic. The presence of the five *Echinococcus* spp. is correlated both to regions and host species. Lions are known to be suitable definitive hosts for *E. felidis*, *E. granulosus* and *E. equinus*. Lions were also found shedding eggs of *E. canadensis* G6/7, which renders lions clearly good hosts for most, if not all, agents of cystic echinococcosis (CE), in clear contrast to leopards, which seem to be a very poor host of *Echinococcus* spp. Negative results for 16 animals in this study support the lack of an important definitive host role for this species. Finding *E. canadensis* in cheetahs constitute a new definitive host record for any *Echinococcus* spp. Spotted hyenas had on several occasions been reported as hosts of *Echinococcus*. Findings of *E. felidis* and *E. granulosus* s.s. eggs in faecal samples could hypothetically be the result of coprophagy of lion faeces, but adult worms of *Echinococcus* sp. had also been found at necropsy in 3 of 19 spotted hyenas in Kenya. Considering the increasing value of the game industry and the translocation of wildlife, as well as the increasing livestock densities and human density, more attention needs to be paid to the interface of wildlife, domestic animals and humans, analyzing and managing the risk of potential diseases including CE.

(0085) Ticks of domestic animals in Lesotho

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Ticks are notorious haematophagous pests of domestic animals, including companion animals and livestock. This is an on-going study which is aimed at documenting ticks infesting domestic animals in various districts of Lesotho. A total of 719 ticks were collected from three districts: Leribe (n=123) with cattle (n=54), horses (n=3) dogs (n=3) and sheep (n=63); Maseru (n=57) with cattle (n=57); and Qacha's Nek (n=539) with cattle (n=331), horses (n=88), dogs (n=69), sheep (n = 50) and one cat. Tick species identified included *Rhipicephalus decoloratus* (n=2 from cattle); *R. microplus* (n= 81) with 75 and 6 from cattle and dogs, respectively; *Haemaphysalis elliptica* (n= 2) from dogs); *Hyalomma truncatum* (n=23) with 8, 4, 2 and 9 from cattle, dogs, horses and sheep, respectively); *Hy. rufipes* (n=21) with 21 from cattle; *Otobius megnini* (n=244) with 169, 24, 1, 1 and 49 from cattle, dogs, horses, cat and sheep, respectively); *R. appendiculatus* (n=50) with 2, 2, 3, 4 and 41 from cattle, horses, dogs and sheep, respectively); *R. evertsi evertsi* (n=247) with 149, 85 and 13 from cattle, horses and sheep, respectively); *R. sanguineus* (n=34) with 32 and 2 from dogs and cattle, respectively) and *R. simus* (n=15) with 14 and 1 from cattle and sheep, respectively). We continue to collect ticks from other districts and molecular characterization as well as detection of tick-borne pathogens will be conducted.

(0086) Ticks as possible vectors of a *Hepatozoon* species (Apicomplexa: Adeleorina: Hepatozoidae) infecting wild African leopards, *Panthera pardus pardus* (Linnaeus, 1758), in South Africa.

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The African Leopard, *Panthera pardus pardus* (Linnaeus, 1758), has been a popular research subject since the late 1960s, especially in the fields of behavioural and ecological science. However, research on the health aspects of leopards in Africa is scanty, leaving gaps in knowledge of especially their haemoparasites. Intracellular apicomplexan haemoparasites from the genus *Hepatozoon* Miller, 1908 have been widely reported from wild carnivores in Africa, including some non-specific reports from leopards. Yet, reports on the mode of transmission and life cycle stages in infected vectors remains relatively uncommon. The aim of this study was to investigate the role of ticks as possible vectors of a *Hepatozoon* sp. found in African leopards. Blood samples and engorged ticks were collected from five wild leopards, three females and two males, while under sedation. Giemsa-stained smears from leopards were immediately screened for *Hepatozoon* parasites. Engorged ticks from infected leopards were kept alive in a fasting state for seven days before being squashed on clean microscope slides, stained with Giemsa solution, and screened for possible life cycle stages. Sporogonic stages, including microgametes, immature and mature oocysts and infective sporozoites, were observed in a tick (*Ixodes* sp.) collected from a male leopard infected with mature and immature intraleucocytic gamont stages of a *Hepatozoon* sp. Stages were photographed, differentiated and measured with ImageJ software. This is the first report on the characteristics of different developmental stages of a feline *Hepatozoon* sp. in both its potential tick vector and African leopard host.

(0087) *Trichodina heterodontata* Duncan, 1977, (Ciliophora: Peritrichia) species description inferred from 18S rDNA sequences and the evaluation of a possible species complex

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Trichodina heterodontata Duncan, 1977 shows little host specificity (found on various fish and tadpoles), a wide range of morphological variation as well as a wide distribution worldwide. Taxonomic work to date has primarily focused on morphological characteristics together with host and distribution records of these mobile ciliophorans. With the advent of modern biochemical laboratory procedures, more and more emphasis is placed on molecular techniques in all fields of taxonomy, especially in parasitology. However, little molecular taxonomy work has been done on trichodinids. Morphological analysis of *T. heterodontata*, shows that this species is highly variable in regards to its denticle structure, which leads one to wonder if it might be a species complex, or indeed a single species. *Trichodina heterodontata* specimens were obtained from six different isolated host tadpole (*Schlerophrys* spp.) populations on the Nxamasere flood plains, Okavango Panhandle, Botswana. Genomic DNA was isolated from *T. heterodontata* and selected regions of the 18S rDNA coding sequence amplified by PCR. The amplicons were sequenced by Sanger sequencing, and compared to detect genetic variability. The 18S rDNA is also used to determine the evolutionary relationship between *T. heterodontata* and other closely related trichodinid species already sequenced on the NCBI database.

(0098) Estimating Apicomplexan parasite exposure in Icelandic Arctic foxes (*Vulpes lagopus*)

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The Arctic fox (*Vulpes lagopus*) is the only native terrestrial mammal in Iceland. The population comprises both “coastal” and “inland” fox ecotypes, with regard to food resources. While coastal ecotype foxes mainly feed on seabirds and eggs, invertebrates and marine mammal carcasses, the inland foxes feed on ptarmigans, migrating waterfowl, eggs and wood mice. Because of the relatively low biodiversity within arctic ecosystems and the involvement of the species in both marine and terrestrial ecosystems, Icelandic Arctic fox populations could serve as sentinels for overall ecosystem health of Iceland. We tested serum samples from 37 Arctic foxes for the presence of antibodies to *Toxoplasma gondii*, *Neospora caninum* and *Besnoitia besnoiti*. A seroprevalence of 72.9% to *Toxoplasma gondii* antigens was found, whereas no antibodies were detected against the other two Apicomplexan parasites. There was no difference in exposure between gender and ecotype groups; however, adult foxes had a significantly higher seroprevalence than juveniles (90.9% and 46.6%, respectively). Compared to previous studies from Svalbard and from Medny Island (51.7% and 5%, respectively), the seroprevalence in Icelandic arctic foxes is the highest. Since the seroprevalence in the human population is low (10%), further studies on the ecology and epidemiology of *T. gondii* in Iceland are warranted.

(0100) Prevalence and molecular detection of *Cryptosporidium* and *Giardia* spp. at the wildlife, livestock and human interface in and around protected areas in Uganda

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The objective of this study was to determine the prevalence of *Cryptosporidium* and *Giardia* spp. and their molecular detection and characterization in wildlife, livestock and humans in and around Mgahinga Gorilla, Queen Elizabeth and Murchison Falls National Parks in Uganda. A total of 708 fecal samples (157 from buffaloes, 63 from Uganda kob, 214 from cattle, 105 from goats, 64 from sheep and 105 from humans) were randomly collected from 2015 to 2016. A modified Ziehl-Neelsen carbol fuchsin staining method was used for detection of *Cryptosporidium* spp. and zinc sulphate flotation technique for *Giardia* spp. The prevalence of *Cryptosporidium* spp. in buffalo was 32%, in Uganda kob 27%, in cattle 35%, in goats 20%, in sheep 23%, and in humans 15%. The prevalence of *Giardia* spp. in cattle was 15%, in goats 7%, in sheep 14%, in buffalo 19%, in Uganda kob 24% and in humans 8%. DNA extractions obtained were analyzed by polymerase chain reaction (PCR) using sets of specific primers.

(0101) Gastrointestinal parasites at the wildlife, livestock and human interface in and around protected areas in Uganda

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Gastrointestinal parasites were investigated in wildlife, livestock and humans in and around Mgahinga Gorilla, Queen Elizabeth and Murchison Falls National Parks in Uganda. A total of 1357 fecal samples (333 from buffaloes, 197 from Uganda kob, 420 from cattle, 189 from goats, 131 from sheep and 105 from humans) were randomly collected in February and July 2014, and February and July 2015. Flotation, sedimentation and faecal culturing for larvae identification were used. Overall, there was a high prevalence of parasite infections in cattle (cestodes 7.4%, trematodes 10.4%, nematodes 23.7%, protozoa 8.1%), goats (cestodes 5.9%, trematodes 5.8%, nematodes 21.7%, protozoa 9.5%), sheep (cestodes 10.2%, trematodes 10.3%, nematodes 25.7%, protozoa 21.4%), buffaloes (cestodes 6.1%, trematodes 11.1%, nematodes 17.1%, protozoa 36.4%), Uganda kob (cestodes 10.5%,

trematodes 4.8%, nematodes 16.8%, protozoa 8.6%) and humans (cestodes 28.6%, trematodes 10.5%, nematodes 46.3%). In general, most of the animals had high intensity of infection, with a wide range of nematode, cestode, trematodes egg and protozoa oocyst counts. Gastrointestinal parasites are widely distributed in these areas and may lead to disease or sub-optimal performance in livestock. In addition, cross-transmission among livestock, wildlife and humans may occur. Therefore farmers and local people need to be informed on the impact of gastrointestinal parasites on animal productivity, wildlife and human health. For effective control strategies the diversity of parasites would have to be considered.

(0103) Detection of helminth parasites from faecal samples in the wildlife-livestock interface at Golden Gate Highlands National Park

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Helminths are gastro-intestinal parasites that infect and cause disease in humans and animals. Dynamics of helminth infections in livestock and animals differ, whereby the former are reported to be more susceptible whilst the latter are mostly reported and regarded as carriers or reservoirs. Golden Gate Highlands National Park (GGHNP) is unique in that it houses both wildlife and domestic livestock. There is no information on the occurrence of helminth parasites in both livestock and wild animals in GGHNP. This study documented the occurrence of helminth parasites in both livestock and wildlife within the park. Fresh faecal samples of livestock, viz. cattle, sheep and horses, as well as wildlife, viz. blesbok, impala, black wildebeest and zebra, were collected in different seasons of 2014 and 2015 and screened for presence of helminth eggs by McMaster technique. Data expressed in eggs per gram (EPG) showed the presence of *Strongylus equinus* eggs in horses (mean = 151) and zebras (mean = 199), whilst we also detected *Haemonchus* spp in cattle (mean = 220), wilde beest (mean = 173), sheep (mean = 274) and blesbok (mean = 120), *Bunostomum* spp in cattle (mean = 109) and wildebeest (mean = 133), and *Trichostrongylus* spp. in cattle (mean = 139) and blesbok (mean = 94). It is well known that wild animals are resistant to most parasitic infections and mainly remain carriers. It will be important to assess the impact of the helminth parasite infections in livestock within the GGHNP.

(0109) qPCR assays to improve the accuracy of bovine and porcine cysticercosis detection

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Consumer protection from bovine and porcine cysticercosis relies on meat inspection, although this method has been questioned in terms of accuracy and efficiency. The aim of the study was therefore to develop real-time PCR (qPCR) assays for diagnosis of *Taenia saginata* and *T. solium* cysticerci. Mitochondrial *cox 1* gene-specific primers and probes were designed from the gene of each species. Control DNA samples were serially diluted to determine the sensitivity of the assays and DNA extracted from closely related *Taenia* species were tested to determine specificity of each assay. *Taenia saginata* (n=71) and *T. solium* (n=2) "cysticerci" were collected from positive carcasses in abattoirs and used as field samples. The standard curves generated and linear regression calculations made showed that both qPCR assays were successfully optimised. The *T. saginata* and *T. solium* assays showed detection limits of 0.013 ng/μl and 0.0034 ng/μl, respectively, and both specifically amplified their target gene. The qPCR assays confirmed 63% (n = 71) *T. saginata* and 100% (n = 2) *T. solium* cysticerci, respectively. Analytical sensitivity of the newly developed *T. saginata* qPCR was 37% lower than that of conventional PCR; this could be due to factors including DNA degradation and PCR inhibitory factors. Further experiments are therefore recommended to improve on the analytical sensitivity of this assay. Meat inspection records in South Africa show that cysticercosis, especially porcine cysticercosis is frequently observed at very low levels, and hence only two *T. solium* cysticerci were collected.

(0114) Genetic variability of *Anaplasma phagocytophilum* strains circulating in wild rodents in Bushbuckridge, Mpumalanga, South Africa

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Anaplasma phagocytophilum is a zoonotic, tick-borne, obligate intracellular bacterium capable of causing disease in diverse hosts, including humans, dogs, cattle and horses. It has not often been detected in Africa but recent research suggests its presence in the Mnisi community, a rural community nestled in the heart of a human/livestock/wildlife interface in Bushbuckridge Municipality, Mpumalanga Province, South Africa. It is documented that wild rodents are reservoir hosts for many tick-borne pathogens, however it is not known if wild rodents play a role in the transmission of tick-borne zoonoses in the community. Recent research in the area indicated 76% of households sampled reported seeing rodents in and around their homes, hence the aim of this study was to explore the genetic diversity of *A. phagocytophilum* in wild rodents in order to better understand its circulation in the study community. To achieve this, DNA extracted from blood samples from 282 wild rodents collected from five different habitat areas, were screened for *A. phagocytophilum* using a quantitative real-time polymerase chain reaction (qPCR) assay that targets the *msh2* gene. Results revealed that 59% of wild rodents sampled were positive for *A. phagocytophilum*. Characterization of different strains by targeted sequencing of the 16S rRNA, and *msh2* genes from positive samples revealed the presence of different and unique genotypes of *A. phagocytophilum* circulating within the community. This is the first detailed report of *A. phagocytophilum* in wild rodents in South Africa and highlights its possible importance as a cause of acute febrile illness in the country.

(0115) Blood glucose levels in Sprague-Dawley rats experimental co-infected with *Trichinella zimbabwensis* and *Plasmodium berghei*

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Trichinellosis is a zoonotic disease which is endemic in sub-Saharan Africa where malaria is endemic. Although no human cases of trichinellosis have been reported, there is likely to be an overlap of transmission of both parasites on a single host, resulting in co-infection. Infection caused by these parasites has presented a series of pathophysiological derangements in metabolic complications, emanating from disturbances in glucose homeostasis. However, alterations in blood glucose metabolism during malaria and trichinellosis co-infection are still controversial and remain obscure. It is against this background that a laboratory-based study was conducted to investigate the effects malaria and trichinellosis co-infection using *Trichinella zimbabwensis* and *Plasmodium berghei* on blood glucose levels using male Sprague Dawley rats as the animal model. A 42-day follow-up experimental study was done, where 168 male Sprague Dawley rats of body weight 90–150g were used. The animals were sub-divided into 4 groups (control, malaria, *Trichinella* and co-infection group; n=42 in each group). *Trichinella* induction was done using *T. zimbabwensis* muscle larvae *per os* on day 0, while malaria induction was done via intraperitoneal injection of 1×10^5 *P. berghei* parasitized red blood cells on day 28 post-infection with *Trichinella*. Results of parasitaemia, *Trichinella* muscle larvae parasite load, haematology profile, plasma blood glucose concentration, serum insulin, liver and muscle glycogen concentration, histopathological analysis of the liver and spleen results are presented. It is hypothesized that co-infection alleviates malaria and trichinellosis associated hypoglycaemic complications.

(0117) Sporogonic biology of *Plasmodium intabazwe* Van As, Cook, Netherlands and Smit 2016 in scale mites *Ixodiderma inverta* Lawrence, 1935 and *Zonurobia semilunaris* Lawrence, 1935 infesting crag lizards.

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The life cycle biology of naturally occurring *Plasmodium* infections in lizard hosts has been poorly documented. Some studies show that Ceratopogonid, Phlebotomine and Culicine flies can harbour sporogony, although only in experimental conditions. Therefore this study aimed to elucidate the sporogonic stages of saurian malaria in naturally infected lizards and to identify the natural vector for *Plasmodium intabazwe* Van As, Cook, Netherlands and Smit 2016 in crag lizards. Scale mites *Ixodiderma inverta* Lawrence, 1935 were collected from the skin of infected *Pseudocordylus melanotus*, as well as *Ixodiderma pilosa* Lawrence, 1935 and *Zonurobia semilunaris* Lawrence, 1935 from infected *P. subviridis*. Mite squashes were prepared immediately following removal from host, Giemsa stained and examined for the presence of the developmental stages of *P. intabazwe*. Additional infected mites were also collected for molecular analysis, targeting fragments of the cytochrome-*b* gene, to genetically confirm the presence of this *Plasmodium* species. Intraerythrocytic gametocytes were observed in the midgut of mites after a blood meal. Other life stages observed included further development such as elongated flagellated male gametes in the process of fertilising female gametes. Mobile nucleated ookinetes with azurophilic granules were also identified in the mite midgut. Furthermore, various stages of developing oocysts were identified, some of which contained numerous sporozoites. Mature infective sporozoites were found in the haemolymph. This is the first report of sporogony in the naturally occurring prositigmatic mites infesting eastern Free State crag lizards, supporting previous suggestions that these mites might act as natural vectors of *P. intabazwe*.

(0118) Detection of *Plasmodium* spp. from faecal samples in non-human neotropical primates in forest fragments in Colombia

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Plasmodium parasites are present in non-human primates (NHP) living in tropical regions around the world. In Latin America, NHP are considered as potential reservoirs of *Plasmodium brasilianum* / *Plasmodium malariae*, and some species have been found infected with *Plasmodium falciparum* and *Plasmodium simium*, which is closely related to *Plasmodium vivax*; but in spite of their importance in malaria transmission cycle, relatively little attention has been given to them. This study aimed to determine the circulating species of *Plasmodium* in three NHP species living in fragmented forest areas. The study site was located in a forest fragment in Santander, Colombia (06°43'N, 74°09'W). Primates were followed from dawn to dusk. Faecal samples were collected from the soil immediately after defecation, and placed in falcon tubes with 96% ethanol. Samples from 24 brown spider monkeys (*Ateles hybridus*), 32 capuchin monkeys (*Cebus versicolor*) and 30 red howler monkeys (*Alouatta seniculus*) were collected. DNA was extracted using a ZR faecal DNA MiniPrep Zymo Kit, *Plasmodium* sp. detection was performed through PCR, and second reactions were conducted for *Plasmodium falciparum* and *Plasmodium vivax* detection. All PCR products were visualized on agarose gel and positive samples were sequenced. *Plasmodium falciparum* was identified by sequencing in one faecal sample of *A. seniculus*, while *P. vivax* was identified by sequencing in one faecal sample of *C. versicolor*.

(0119) Ecological factors affecting the quantity and diversity of bacteriocins in the rodent gut and their implication for disease risk

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Bacteriocins - extracellular toxins produced by almost all bacteria - are the most abundant and diverse group of bacterial defence systems. Bacteriocins differ from low molecular antibiotics, as they have a relatively narrow killing spectrum, which is restricted to closely related species. The current view is that due to their unique activity spectrum bacteriocins play a major role in mediating intra- and inter- species interactions among coexisting bacteria in nature, but their role in disease protection of wild vertebrates is unclear. We present a newly developed molecular, culture-free method that can detect and describe bacteriocin diversity in faeces collected from wild rodents and show with our data how it can be employed to test associations between bacterial diversity, bacteriocin diversity, and disease risk of rodents by *Salmonella*.

(0127) Morphological and molecular insights into the diversity of filarial nematodes infecting rupicolous lizards in South Africa

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Filarial nematodes are of considerable medical and socioeconomic importance because of their devastating impacts on the health of people and domestic livestock. However, little is known of the diversity of filarial nematodes infecting reptiles which are becoming of increasing concern in the pet trade and for conservation efforts. South African lizards are one such group which have been harvested from the wild for the pet trade and yet little is known about their infections. Blood films from three wild caught species of lizards, which included *Agama atra*, *Cordylus polyzonus* and *Pseudocordylus melanotus*, were examined for microfilaria. Three host-specific morpho types of microfilaria were identified which, based on morphometric analysis using principle component, multivariate and discriminant analysis, were estimated to different species. Molecular phylogenetic analysis confirmed the filarial nematodes infecting *A. atra* to be within the genus *Foleyella*, a parasite of chameleons and frogs, and those infecting *C. polyzonus* to be in the genus *Setaria*, a parasite more normally associated with large domestic ungulates. Although it was not possible to sequence microfilaria from *P. melanotus*, owing to its distinct morphological features it is considered to be a separate species. This current study represents one of the most detailed accounts of filarial nematodes in lizards, illustrating the requirement for further study not only to provide insights into reptile health but also the potential role that reptiles may play as reservoirs of socioeconomically important diseases.

(0130) Interactions among two bacteria and one host wild species at large and small spatial scales

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Most organisms are co-infected by different species of parasites. Multiple parasite infections have been intensively studied in various systems; however, the studies' focus is usually either on the effect of parasite interaction on their population dynamics or its effect on the host's behavioral and health changes. Moreover, the parasite's interactions are usually studied in a single community and location, and thus the spatial variability in the nature of the interactions is overlooked. In practice, each organism has its own interests, they all respond simultaneously to each other, and the nature of interaction can change depending on the local conditions. We explored the causes and consequences of the interactions between *Mycoplasma* and *Bartonella* bacteria within the *Gerbillus andersoni* rodents by combining large-scale field survey and a long-term laboratory manipulation. Gerbil blood and flea samples were collected throughout the Northwest and Southeast Negev sand dunes of Israel and their bacterial co-infection status was assessed. The field correlations suggest that the interactions between the bacteria can range between neutral to negative associations and highlight three possible factors shaping bacterial interactions: (i) the host species, (ii) the host's body condition, and (iii) the timing of infection. The survey was complemented by a long-term laboratory manipulation in the co-infection status of forty gerbils during which we quantified simultaneously the dynamics of the bacteria and their separate or combined effects on the body temperature, body mass, stress levels, and behavior of the rodents. The experimental results will be discussed in light of the field data.

(0143) How to get rid of host DNA in *Plasmodium*-infected blood samples to generate good quality *Plasmodium* genomes

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A major challenge when sequencing blood samples infected by malaria parasites is the abundance of "contaminating" host DNA. Indeed, if the amount of host DNA is important, this will ultimately greatly reduce the sequence coverage of the *Plasmodium* genome and increase the cost as well as the difficulty to get a good whole genome sequence. Therefore, reducing host DNA in infected blood samples or increasing the amount of parasite DNA is very important, even in the case of high parasitaemia. To address this issue, we took advantage of two different techniques according to the nature of the samples (frozen, fresh blood samples), describing specifically one that we developed ourselves in our laboratory: (i) When working on fresh blood samples, a reference technique is to deplete leucocytes by using CF11 columns. (ii) When working on frozen samples, flow-cytometry and cell

sorting were implemented by our team to separate trophozoites from host cells. Through these different technical strategies, we successfully reduced the contaminating host DNA in our studied samples, which resulted in obtaining good quality whole genomes of different aye *Plasmodium* species.

(0148) Development of a non-lethal diagnostic tool for the diagnosis of *Ichthyophonus hoferi*

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Ichthyophonus hoferi has been diagnosed at the Two Oceans Aquarium. *Ichthyophonus* is a mesomycetozoon parasite that multiplies in blood rich organs in the fish host causing a wide range of clinical signs relating to organ dysfunction. *Ichthyophonus* can be diagnosed from microscopic examination of tissue squash prep, culture or PCR. In the literature only lethal methods of diagnosis are described. The development of a non-lethal diagnostic tool for disease monitoring is vital for collections where sacrifice of specimens is not possible. Liver biopsies were obtained from (n=30) White Stumpnose (*Rhabdosargus globiceps*) comparing two surgical methods, coeliotomy (n=15) and coelioscopy, (n=15), 10 fish used in a control group. Biopsy material for each fish was divided into three pieces for squash preparation examination, PCR and culture. All fish were monitored for 43 days post-surgery and blood samples drawn at two week intervals. After 43 days fish were euthanized for full examination of the liver, kidney, spleen and heart allowing correct assignment to one of two groups; *Ichthyophonus*-infected fish and non-infected fish. PCR and culture of liver tissue was also performed. Preliminary results show a 64% sensitivity of the wet mount biopsy and a 38% sensitivity of biopsy in culture with a 100% specificity for both. Wet mount and culture of the biopsy showed a sensitivity of 81%. Final post mortem on all organs showed 25 fish to be positive for *Ichthyophonus*. 5 fish were negative for *Ichthyophonus* in all diagnoses. Coelioscopy was less invasive and caused fewer organ adhesions than coeliotomy.

(0160) Water quality assessment using monogenean fish parasites as bioindicators in the Lufira Upper Basin (DR Congo)

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Parasites receive particular attention because they induce diseases, reduction of growth, mortality and so on. However, they can also be useful as an interesting scientific tool (biological tag), for example as indicator of the biology of the host: the host's diet, phylogeny, biogeography, systematics, or even as bioindicator of pollution. Regarding water pollution, the accumulation of heavy metals in surface water is a major environmental concern worldwide, limiting the supply of drinking water and presenting a risk of contamination for the aquatic environment. As an illustration, in the DR Congo, mining is done without taking into account the standards of environmental protection (discharge of the mining effluents in the rivers, without preliminary treatment). Classical monitoring methods include mainly measurements of the physicochemical parameters of the water and analysis of pollutants in the water, sediments and fish. Within an ongoing study of which I am a co-author, we are using monogenean fish parasites as bioindicators to assess the water pollution in the Upper Lufira Basin, near an important mining region in DRC. We explore the possibility that monogeneans show different occurrence patterns according to environmental conditions (sensitivity to physicochemical changes), to evaluate water pollution, by analyzing the structures of their communities in polluted and unpolluted areas (from the point of view of diversity, prevalence, abundance...). That is our parasitological research and, to learn more about parasites, I would like to take part in this interesting meeting of established parasitologists.

(0161) PacBio circular consensus sequencing uncovers the haemoparasite microbiome in South African wild and domestic felids

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In a preliminary study using universal primers that amplify nearly full-length 16S or 18S rRNA genes, samples were sequenced using a circular consensus proofreading approach on a PacBio instrument, opening a window to the microbiome in wild and domestic felids. Samples collected from domestic cats and various wild felid species (lion, cheetah, African wild cat, caracal and tigers bred in captivity in South Africa) were sequenced at the Genomics Core Laboratory at Washington State University, Pullman, USA. Altogether 21 data sets were obtained: nine from samples amplified with the 16S rDNA universal primer set and twelve from samples amplified with the 18S rDNA primer set. These data revealed a number of previously described haemoparasites in felids and a number of blood-borne bacteria and parasites not previously reported in felids. We detected sequences with similarity to *Rickettsia* spp., *Babesia odocoilei*, *B. rodhaini* and *Hepatozoon* spp., but which couldn't be definitively assigned. In addition, sequences were detected that were assigned as *Hepatozoon felis*, *Anaplasma phagocytophilum* and *Babesia microti*. These latter three species have been reported in felids before, but little is known about the occurrence and pathogenicity of these parasites in domestic and wild felids. This is the first report on the blood microbiome, including both bacteria and protozoa, in felids.

(0163) Tick-borne haemoparasite occurrence in eastern rock sengi (*Elephantulus myurus*) of South Africa

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Sengis, or elephant shrews, of the order Macroscelidea, are small insectivorous mammals endemic to Africa. Several studies have shown that sengis are parasitised by large numbers of ixodid ticks. Previous studies also provided strong evidence that the eastern rock sengi (*Elephantulus myurus*) may be a natural reservoir host of *Anaplasma bovis*, a rickettsial pathogen of cattle. Despite the importance of sengis as hosts of immature ticks and the association of these tick species to known pathogens, limited information is available on the role of *E. myurus* as a reservoir of tick-borne pathogens. The aim of the study was, therefore, to determine the tick-borne haemoparasite diversity in eastern rock sengi of South Africa by screening blood samples for the presence of *Theileria*, *Babesia*, *Ehrlichia* and *Anaplasma* spp. using the Reverse Line Blot (RLB) hybridization assay. A total of 47% of the blood sample extracts tested negative or below the level of detection of the assay. PCR products hybridized with the *Theileria/Babesia* catch-all probe in 1.5% of the samples and 33.3% hybridized with the *Ehrlichia/Anaplasma* catch-all probe. The PCR products failed to hybridize with any Anaplasmataceae species-specific probes. This could suggest the presence of a novel species or variant of a species. The parasite 16S rDNA of selected positive samples was subsequently amplified and sequenced. The results confirmed the presence of *A. bovis*-like DNA and enable design of an RLB probe specific for the detection of the sengi *A. bovis*-like strain.

(0164) Patterns of infestation of lice (Insecta: Phthiraptera) in rodents in Big North of Chile

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In order to assess seasonal spatial variations (ecoregions) and the prevalence (P), mean intensity (MI) and mean abundance (MA) of communities of lice associated with rodents, 13 locations in four ecoregions in northern Chile were visited seasonally for one year: Coast desertic (DC); Interior desertic (DI); Height tropical (TA) and Marginal tropical (TM). For removal of lice, rodents were captured by Sherman traps and sedated with Ketamine-Xylazine 2%. For each ecoregion and season, P%, IM and AM of each louse species collected was calculated; Fisher Tests by Bootstrap and related regressions were applied for comparisons. The species with the highest P% (15.7) and AM (0.47), *Hoplopleura aitkeni*, was isolated from 11 species of rodents. Seasonal variation in ecoregions was observed. *Hoplopleura reducta* was isolated from 9 species of rodents; seasonal variation in ecoregions was observed. *Hoplopleura andina* was collected in 9 species of rodents; no seasonal variation in ecoregions was observed. Finally, *P. spinulosa* was isolated from the DI ecoregion in two species of introduced rodents, with no differences between stations. Significant differences were found when occurrence of lice on males and females of the same rodent species was compared. A positive regression between prevalence and abundance of lice with density of rodents was found in one case. There was a seasonal variation in two ecoregions and two species of lice; sex was not a determining factor in the changes of P%, IM and AM, nor could a positive association between density, P% and abundance be established.

(0166) Parasitism gastrointestinal and external in Common Tenca *Mimus thenca* in central and southern Chile

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Parasites provide information on population structure, evolutionary hypotheses, environmental stress, trophic interactions, climate and biodiversity. In Chile, parasites of endemic vertebrate species have been poorly studied; the aim of this study was to characterize the parasitic fauna of the tenca (*Mimus thenca*), endemic to central-south Chile. Parasitological necropsy on 15 tenca collected between the years 2004-2014 was performed, all from the Bio Bio Region. This study was complemented with 6 tenca caught alive in central Chile. Each parasite was mounted and classified according to the corresponding key. 57.1% of the birds was positive for some kind of parasite: *Myrsidea* sp. 38.1% (Amblycera: Menenoponidae); 23.8% *Brueelia rotundifrons* (Ischnocera: Philopteridae); 19.1% *Philopterus* sp. (Ischnocera: Philopteridae); 9.5% *Analgas* sp. (Acariforme: Analgidae); 4.8% *Proctophyllodes* sp. (Acariformes: Analgoidea); 4.8% *Capillaria* sp. (Nematoda: Trichinellidae); 4.8% *Dispharynx nasuta* (Nematoda: Acuariidae). Except for *Brueelia rotundifrons*, all species of ectoparasites collected are new host-parasite associations.

(0167) Haemoparasite infections and relationship with adaptive immune responses in Afromontane lizards of the eastern Free State Province, South Africa

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The reptile immune responses to haemoparasite infections remains to be poorly understood in comparison to the mammalian immune system as it is very complex and there are still unidentified areas regarding the structure and functions of reptilian immune system. This study is aimed at profiling the relationship between haemoparasite infections and the measure of adaptive immune responses in the Afromontane lizard hosts by indirect ELISA and cytokine expression by RT-qPCR. Adult *Pseudocordylus melanotus* (A. Smith, 1838) and *Pseudocordylus subviridis* (A. Smith, 1838) and *Agama atra* Daudin, 1802 lizards were collected from Metsi-Matsho, Masaleng and Sentinel trail areas in the eastern Free State Province. Haemoparasites detected from Giemsa-stained blood smears from all sampled *P. subviridis*, *P. melanotus* and *A. atra* included *Plasmodiumintabazwe* Van As, Davies, Netherlands & Smith, 2016, *Hepatozoon affluomaloti* Van As, Davies & Smit, 2015, unknown *Sauroplasma* sp. and filarial nematodes. Indirect ELISA has shown increased serum IgY levels in haemoparasite infected *P. melanotus* (mean O.D. = 5.53, SD± 0.98, n=12); *P. subviridis* (mean O.D. =4.94, SD± 1.02, n=14) and *A. atra* (mean O.D. =4.38, SD ± 0.59, n= 6) as compared to the control (mean O.D. = 2.85, SD ± 0.39). The mean IgY levels of individual lizards were relatively higher than the uninfected control serum. This is the first report on immunological properties of *Pseudocordylus* lizards in South Africa. This on-going study will ultimately shed a light on how Afromontane lizards cope with multiple haemoparasite infections.

(0172) Review of the fish parasitic isopod genus *Elthusa* (Isopoda: Cymothoidae) from southern Africa

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Cymothoidae isopods are well known parasites of marine and freshwater fishes, most often attaching to the external surface, branchial chamber or buccal cavity of their hosts. Within this family, the branchial attaching genus *Elthusa* Schioedte & Meinert, 1884 is considered to be among the most morphological varied and species-rich genera. Currently there are 30 known *Elthusa* species. *Elthusa raynaudii* Milne Edwards, 1840 is the only species that has been described from southern Africa. As part of a larger project on the global diversity, systematics and functional ecology of fish parasitic isopods, all material previously collected by NWU-Water Research Group members with general *Elthusa* characteristics, were examined. This included specimens collected during 1993 in the intertidal zone of Alexander Bay, as well as from deep sea trawlers during April 2003 off the south coast, and during February 2010 off the west coast of South Africa. From morphological analyses, three distinct species were identified. Several specimens conformed to the description of *Elthusa raynaudii*. However, three specimens obtained from the *Africana* research vessel fish sorting table during April 2003, represent a new species. Similarly, the specimens collected from Alexander Bay also represent an undescribed species. Some of the prominent differences among these three species include the shape of the rostrum, the anterior margin of pereonite 1, the shape and size of the uropods as well as the number of setae on mouthparts. To supplement the morphological analysis of this study, molecular characterisation using the COI gene of each specimen will also be completed.

(0173) New *Gyrodactylus* von Nordmann, 1832 (Monogenea: Gyrodactylidae) species of *Enteromius paludinosus* (Peters, 1852) from South Africa

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Viviparous monogeneans of the genus *Gyrodactylus* are tiny parasites mostly parasitising bony fish. Nearly 500 *Gyrodactylus* species have been described worldwide, of which only 36 is known from the African continent. Parasitological survey of *E. paludinosus* at the Barberspan Ramsar site in South Africa in October 2015, recorded the presence of a new *Gyrodactylus* species. Sixty percent of the hosts were infected on the fins with up to three of these specimens. This new species of *Gyrodactylus* constitutes the first description of this parasite from *E. paludinosus* and, the 37th species described from the African continent. The morphologically new species represents a typical gyrodactylid specimen with noted similarities in the shape of haptor sclerites. This specimen closely resembles to *Gyrodactylus kyogae* (Paperna, 1973) from *Enteromius neumayeri* (Fischer, 1884). Dissimilarities from *G. kyogae* are however evident in the overall larger size of the hamuli, ventral bar and marginal hooks. The elongate root of the hamuli and presence of a prominent membrane on the ventral bar also justify this as a new species. Furthermore, larger marginal hooks and definite disparity in the shape of the sickle is evident. The proposed name for this new species is *Gyrodactylus paludinosi*.

(0174) Invasion of *Rhipicephalus (Boophilus) microplus* (Acari: Ixodidae) on a farm in the Eastern Cape Province, South Africa

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The Asian blue tick, *Rhipicephalus microplus*, is an invasive tick species which was introduced to South Africa in 1896. Reports dating back to the early 1900s state that the displacement of the African blue tick, *Rhipicephalus decoloratus* had occurred within the Cape region. The ability of *R. microplus* to outcompete *R. decoloratus*, its role as a vector for diseases as well as the reported cases of resistance towards available acaricides, pose a great problem to cattle farmers. The Eastern Cape Province accounts for the highest percentage of communal livestock production in the entire country. This study provides information regarding the blue cattle tick composition on a commercial cattle farm near Grahamstown in the Eastern Cape. Engorged adult females were collected directly from the cattle and questing larvae was collected from the vegetation via drag sampling. All ticks were identified up to species level with the aid of morphological characteristics. The Shaw Larval Immersion test (SLIT), was conducted to establish resistance profiles for the various camps on the farm where the ticks were collected. The chemicals which were tested included: Amitraz (Amidine), Chlorfenvinphos (Organophosphate) and Cypermethrin (Pyrethroid). The study showed that *R. decoloratus* was still the dominant blue tick species present on the farm, however, *R. microplus* was also found in low numbers. The results of this study provide a foundation for future tracking of the invasion of *R. microplus* on this commercial farm as well as the management of resistance on the farm.

(0175) Identification of tick-borne *Babesia bovis* and *Babesia bigemina* on a farm in the Eastern Cape

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Redwater is caused by the protozoans *Babesia bovis* and *Babesia bigemina*, transmitted by the tick vectors *Rhipicephalus (Boophilus) decoloratus* and *Rhipicephalus (Boophilus) microplus*. Due to increasing reports of *R. microplus* displacing *R. decoloratus* in the Eastern Cape and cattle producers being confronted with outbreaks of the more serious *B. bovis* type of redwater on commercial farms not previously known to harbour its vector *R. microplus*, this study was conducted to confirm both the presence of the vector *R. microplus* and the protozoan *B. bovis* on a farm in the Eastern Cape Province. Ticks collected were identified up to species level. For the tick transmitted diseases, morphological identification was done by making use of cattle blood smears. On molecular level, Polymerase chain reactions (PCR), using primers devised for amplifying protozoan pathogens when present in whole blood samples, were used. DNA was extracted by means of the Cetyl Trimethyl Ammonium Bromide (CTAB) extraction method, its presence confirmed by Nanodrop spectrophotometry and after PCR, visualised on a 1% agarose gel by means of UV-Trans illumination and the E-Box E-Capt software. It was found that both parasites and associated tick species were present within the area of collection. This project confirm claims of redwater outbreaks caused by *B. bovis* presence due to the invasion of the Asiatic redwater parasite into this area.

(0177) Using stable isotope analysis to compare the foraging ecology of differently-attaching cymothoid isopods

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Cymothoid isopods are among the most conspicuous ectoparasites of marine fishes. They infest the flesh, buccal, and gill cavity of hosts, and have been reported to alter the condition, behavior, and foraging patterns of some hosts. Anecdotal reports have suggested these parasites feed on fish tissues, but limited data on the foraging ecology of cymothoids are available. The foraging patterns of cymothoids likely vary by attachment site, as the attachment site influences the parasite's access to host tissue and other possible prey items. Whereas *Anilocra* spp. infest the flesh and have more access to host muscle tissue and zooplankton in the water column, *Mothocya* spp. infest the gill chamber and potentially have different access to host muscle tissue and zooplankton, as they are covered by the opercula. Moreover, *Cinusa* spp. and *Ceratathoa* spp. infest the buccal cavity and tongue, respectively, which may influence if and how they obtain nutrition from their hosts and/or the external environment. To describe the foraging patterns of differently-attaching cymothoids we collected infested fish in the northeastern Caribbean and the southeastern Cape of South Africa. Thus far 33 *Anilocra haemuli* and 23 *Anilocra chromis* from the Caribbean, 4 *Ceratathoa famosa* and 4 *Cinusa tetradontis* from South Africa, and their respective hosts have been sampled. Tissue from the cymothoids' marsupium and scale, heart, gill, and muscle tissue from each fish were extracted for stable carbon and nitrogen isotope analysis. Isotopic comparisons between each host and parasite, and by attachment site are underway. Preliminary results are reported.

(0178) Diversity of fish parasitic cymothoid isopods from Moreton Bay, Australia, including new distribution and hosts records

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Moreton Bay, situated on the east coast of Australia, is an important coastal resource frequented by recreational and commercial fisherman. This bay is listed as a Ramsar site due to its important role in migrating and resident shore birds as well as several threatened plant and animal species. As part of a larger project on the marine fish parasites from Moreton Bay, and one on the global diversity, systematics and functional ecology of fish parasitic isopods, eight species of cymothoid isopods were collected from ten commercially important fish species during the summer and winter of 2016. All isopods collected were identified using available literature and, where possible, through comparison with type material. Species identified include: *Ceratothoa banksii* collected from *Selenotoca multifasciata*; *Ceratothoa imbricata* from *Trachurus novozealandicus*; *Cymothoa indica* from *Sillago ciliata* and *Sphyaena obtusata*; *Cymothoa vicina* from *Mugil cephalus*; *Elthusa sigani* from *Siganus fuscescens*; *Mothocya karobran* from *Tylosurus gavioloides*; *Nerocila monodi* from *Acanthopagrus australis* and *Rhabdosargus sarba*. A species collected from *Arrhamphus sclerolepis* does not conform to other known species and could be new to science. New host and locality records for Moreton Bay are presented here, as well as the seasonal prevalence for each species collected during 2016. This is the first comprehensive review of cymothoid parasites from Moreton Bay.

(0180) Evaluation of the attenuated heartwater vaccine in the field

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Heartwater is an infectious, non-contagious, and often fatal disease of domestic and some wild species of ruminants affecting the sub-Saharan livestock sector, threatening the livelihoods of small and emerging farmers. Currently, the disease can only be controlled through immunization with the commercial blood vaccine infection and treatment regimen, which has a number of drawbacks. A live attenuated tissue-culture-derived heartwater vaccine was developed and demonstrated to be safe and efficacious in Merino sheep, Angora goats and cattle under laboratory-controlled trials. The aim of this study was to further evaluate the safety and efficacy of the attenuated heartwater vaccine under natural field challenge conditions. Field trials were conducted on three farms in the Eastern Cape environs. A total of 345 animals were vaccinated on the 3 farms: 157 adult goats, 33 pregnant ewes, 55 adult sheep, and 100 one- to 6-week-old kids. There were no adverse vaccine reactions in all vaccinated sheep and Angora goats and no abortions. However, the observed data are insufficient to gauge vaccine efficacy at this stage due to low mortality rate experienced in the unvaccinated animals. It is concluded that the attenuated heartwater vaccine meets vaccine requirements as it is safe to use, requires no antibiotic treatment, easy to administer by intra-muscular route, and requires no monitoring following vaccination. Once registered, it will increase vaccine usage in animals at risk, thereby improving economic benefits for farmers and ultimately on food security.

(0184) The phylogeny, host-association and distribution of a haemoparasite of *Stegastes* damselfishes (Pomacentridae) from the eastern Caribbean based on a combination of morphology and 18S rDNA data.

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Apicomplexan parasites are obligate parasites of many species of vertebrates, however to date, there is very limited understanding of these parasites in the most diverse group of vertebrates, actinopterygian fishes. While many of these parasites from amphibians, reptiles and mammals have been characterised molecularly using the 18S rRNA gene, identification of apicomplexans infecting fishes has relied solely on morphological identification by microscopy. A recent study that developed a DNA barcoding method, targeting the 18S rRNA gene primers for identifying apicomplexans parasitizing certain actinopterygian fishes, has made molecular characterisation of some of these parasites possible. During a haemoparasite biodiversity survey of reef-associated fishes of the eastern Caribbean, a newly discovered *Haemohormidium*-like parasite was identified microscopically infecting *Stegastes* damselfishes (Pomacentridae). Species of the genus *Haemohormidium* have been assigned to the order Piroplasmida (Phylum: Apicomplexa), along with species of the genera *Theileria* and *Babesia*. However, this placement remains uncertain. This study aimed at identifying this parasite using a combination of morphology and molecular data, a first in apicomplexans of fishes, along with determining the host associations and distribution of this parasite in the Caribbean. Based on 18S rDNA, it was found that this parasite does not fall among the Piroplasmida, nor does it fall with other known genera of apicomplexans. Furthermore, the parasite has a wide distribution in the eastern Caribbean, infecting five species of *Stegastes*. This study highlights the importance of identifying haemoparasites of fishes using a combined method to support the review of their present taxonomy.

(0191) *Lernaea* infestation at Hardap Dam, Namibia

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Lernaea species, commonly known as anchor worms, are copepod parasites found externally on fish and amphibians. The female attaches during the last copepodid stage, mate and transform into an adult with the abdomen and egg-sacs hanging from the host's body. Several lernaids have been described with *Lernaea cyprinacea* being invasive and reported worldwide. Very few parasitological studies have been done on freshwater fish in Namibia. A survey was done during June 2016 at Hardap Dam (24°29'58"S, 17°51'31"E), Fish River System. The dam has a surface area of 25 km² with a 40 m high dam wall forming the largest reservoir in Namibia. This dam is of strategic importance because of the size and location in Hardap Nature Reserve and it joins the Orange River in South Africa and thus any changes in this system can indirectly affect the aquatic health of South Africa. Eight fish species were examined: *Barbus paludinosus* (n=92), *Cyprinus carpio* (n=1), *Labeo capensis* (n=11), *Labeo umbratus* (n=1), *Labeobarbus kimberlyensis* (n=9), *Oreochromis mossambicus* (n=6) and *Clarias gariepinus* (n=5). Numerous ecto- and endoparasites were recorded from these fish species including monogeneans, digenean larvae, adult and larval cestodes, nematodes and copepods. However, high prevalence and mean intensity levels were recorded for *Lernaea* sp. from some of the fish species. Focal inflammation and haemorrhage occurred at the attachment site of the imbedded parasites, making the area appear red and ulcerated. These lesions may lead to secondary infections and have detrimental effects on the health of the host.

(0198) The first African record for Anoplodiscidae (Monogenea), and a new *Anoplodiscus* species from Australia

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Anoplodiscidae is a monotypic monogenean family represented by six *Anoplodiscus* species. Until now, all *Anoplodiscus* species were considered ectoparasites of sparid fishes, and no *Anoplodiscus* species has been formally recorded from Africa. We encountered *Anoplodiscus cirrusspiralis* on captive *Chrysoblephus gibbiceps*, *Chrysoblephus laticeps* and *Cymatoceps nasutus* in South Africa. *Anoplodiscus cirrusspiralis*, considered by us as the senior synonym of *Anoplodiscus tai*, has previously been reported from Australia, Japan, South Korea and New Zealand. The synonymy is based on a lack of morphological differentiation between these two species after extensive comparative measurements of the type material. Recently, we also discovered an undescribed *Anoplodiscus* species in the collections of the Australian Museum, Sydney, Australia, and the South Australian Museum, Adelaide, Australia. The species is easily differentiated from other *Anoplodiscus* species by the morphology of the vagina, and the sclerotised accessory piece associated with the male copulatory organ. Permission was granted to process the material and to describe the new species. The new species is unique in that it parasitises the host members of Nemipteridae, *Scolopsis bilineata*, *Scolopsis marginifera* and *Scolopsis monogramma*. Members of *Anoplodiscus* are known to cause chronic disease in sparid aquaculture. These monogeneans also demonstrate low host-specificity and should therefore be considered of potential concern for future sparid aquaculture in Africa.

(0204) Seasonal variations in sheep roundworms population infesting communal grazing at Amatole Montane Grassland in the Eastern Cape, South Africa

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The objectives of the study were to establish seasonal changes of roundworms in communal sheep and to develop health management guide for controlling roundworms infestations. The study was conducted at Warburg community which is situated in Stutterheim under Amahlathi Local Municipality. Three farmers were randomly selected to contribute with 10 female sheep (2-tooth); animals were tagged for identification. Samples were collected monthly for four years (January 2012- December 2015) with a total number of 1 188 faecal samples. Prior the start of the trial, the experimental animals were drenched with a broad-spectrum remedy to standardize the egg count for internal parasites. During the experiment all animals were only dosed when the roundworms egg per gram (e.p.g) counts exceeded the levels above 3000 e.p.g. Significantly higher levels of roundworms during winter (2347.1±3543.5) than spring (980.9±1405.8) for the study period. Summer roundworms levels were significantly higher (1226.1±701.3) compared to winter (597±628.4). Significantly higher levels of roundworms were observed in spring (1467.61±1308.9) than in autumn (951.23±1376). The study highlights that autumn and winter have lower roundworms infestations than summer and spring.

(0205) Predators and parasites - Towards a more complete understanding of the trophodynamics of a common coral reef fish

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Compared with predation, the role of parasites in coral reef food webs remains poorly known, and no studies in marine reef systems have compared biomass consumed by predators with that consumed by parasites. Gnathiid isopods, the most commonly occurring parasite in reef ecosystems, infect a myriad of host species. Thus, they are likely significant contributors to coral reef tro-

phodynamics. This study aimed to compare nutrient/energy flow from consumption of damselfish biomass by predators with that consumed by gnathiids from damselfish hosts. This was accomplished by catching, tagging, and monitoring individual fish in their territories over a 1–2-month period to estimate mortality due to predation, and by quantifying gnathiid infestation of fish over a 24-hr period and then extrapolating to one month. To accomplish the latter, caged fish were placed on the reef at equally spaced time intervals. After 45 minutes on site, cages were retrieved and gnathiids were counted and sorted by developmental stage. While we did find variability across sites with respect to parasite infestation (ranging from 17.6 parasites/24h to 108.2 parasites/24h), predation pressure over a one-month period was consistently low (88% survival, n=131). Thus, from adult damselfish, the estimated biomass removed by gnathiid isopods via micropredation during a one-month period appears to exceed the biomass lost to predation by carnivorous fishes. Thus, we believe results of this study should serve as further impetus for the inclusion of parasites in studies on coral reef trophic dynamics.

(0206) Analysis of digenean trematodes (metacercarial stages) from freshwater fish in the Tshwane Metropolitan Area: Phylogenetic relationships using PCR-techniques.

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Most digenean trematodes have a similar life cycle with their first intermediate hosts being molluscs, second intermediate hosts of fish or other vertebrates and higher vertebrates as their final hosts. The identification of these parasitic organisms using morphology is usually difficult during the larval stages as they are not fully developed. This project was therefore aimed at applying molecular techniques to classify metacercarial stages of the genera *Clinostomum* and *Euclinostomum* and of the family and Diplostomatidae collected from freshwater fish species from two dams in the Tshwane Metropolitan Area according to their DNA composition using four sets of primers (ITS-1, ITS-2, Isr-DNA and ssr-DNA). Gel electrophoresis was done to check the size of the DNA that was amplified using the 1kb Generuler DNA ladder. The DNA was then sequenced for characterization. For the ITS-1 primers, the DNA bands were ~ 700bp; The ITS-2 primers amplified genes that were ~ 500bp. The Isr-DNA primers were able to amplify genes that were ~1300bp – 1500bp. ssr-DNA primers amplified genes that were ~1800pb – 2000bp. All four sets of primers were able to amplify certain regions on the whole genome of the *Clinostomum* spp., *Euclinostomum* spp. and diplostomatids. Molecular techniques may be used as guidelines for the identification of trematode metacercarial stages phylogenetically.



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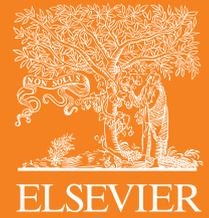
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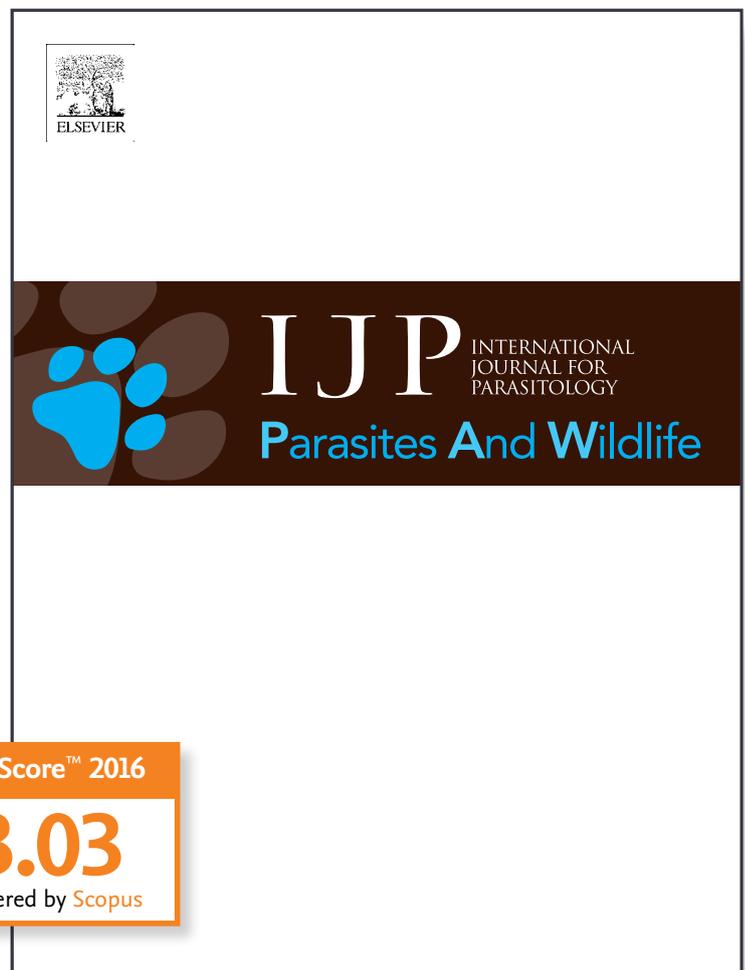
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