

PARSA 2012

The following are abstracts of papers and posters at the 41st Annual Congress of the Parasitological Society of Southern Africa (PARSA) 1-3 October 2012, Department of Zoology & Entomology, University of the Free State, Bloemfontein, South Africa

Invited Lectures:

An overview of parasites and aquaculture in sub-Saharan Africa

Kevin W. Christison¹

¹ *Directorate Aquaculture Research, Department of Agriculture Forestry and Fisheries, Private Bag X2, Roggebaai, 8012, South Africa. E-mail: KevinCH@daff.gov.za*

Despite aquaculture production increasing by 61 % in the latter half of the last decade, sub-Saharan Africa only contributes around 0.13 % to world aquaculture production and 13.6 % to African aquaculture production. FAO have projected that aquaculture production in sub-Saharan Africa will exceed 208 000 tons per annum and may even reach 380 000 tons per annum. Farming technologies in this region range from simple, low input-low output pond systems to high density re-circulating systems in Nigeria and South Africa. Seed and feed supply, quality and distribution remain major constraints to both non-commercial and commercial producers. Diseases are also regarded as a primary constraint to the culture of many aquatic organisms, impeding both economic and social development in many countries internationally. Traditionally, however, parasites and diseases have been regarded as being of little or no consequence in sub-Saharan aquaculture. However, as a consequence of the predicted increase in critical mass of the sector, and the increased intensification and commercialisation, the likelihood of major disease problems occurring also increases. Some of the major concerns posed by aquatic parasites or pathogens in an aquaculture context include parasite translocation and introduction of exotic species, negative interactions between wild and cultured fish populations and production loss through mortalities, reduced growth rates and augmented treatment and veterinary costs. Historically, relatively little research has been conducted on fish and shellfish parasites and diseases in aquaculture in this region. The majority of the published aquatic parasitology manuscripts from the sub-Saharan African region are biased toward species descriptions, which is not surprising for a region with relatively high, yet understudied species diversity.

Beauty and the beast

Ivan G. Horak^{1,2} & Heloise Heyne³

¹Department of Veterinary Tropical Diseases, University of Pretoria, Private Bag X04, Onderstepoort, 0110, South Africa.

²Department of Zoology and Entomology, University of the Free State, P.O. Box 339, Bloemfontein, 9300, South Africa. E-mail: Ivan.horak@up.ac.za

³Parasites, Vectors and Vector-borne Diseases, ARC-Onderstepoort Veterinary Institute, Private Bag X05, Onderstepoort, 0110, South Africa.

In the light of all the negative publicity surrounding the plight of rhinoceroses we decided to create something lasting from the situation, namely a validated host-parasite list. Strange as it may seem these behemoths harbour an array of tick species more beautiful than those infesting any other animal and the objectives of the project were to collect and identify these ticks. Ticks were collected from rhinos in Kenya and Namibia, and from animals in the Eastern Cape, KwaZulu-Natal, Free State, Mpumalanga and Limpopo Provinces, South Africa; approximately 420 animals were examined. A total of 5 830 ticks belonging to 32 species were collected, and 16 of these 32 species are ornate. Three of these ornate species are host-specific to rhinos and of these *Amblyomma personatum* and *Amblyomma rhinocerotis* are possibly critically endangered, and *Dermacentor rhinocerinus* endangered. Rhinos are amongst the preferred hosts of 17 of the remaining 29 tick species, while the other 12 species can be regarded as 'stragglers'. None of the latter 29 species would appear to be in danger of extinction. Only four of the 83 *Rhipicephalus* species (brown ticks) of the world are ornate, and three of these were present on the rhinos. Incidentally, the only *Rhipicephalus* species with reasonably long mouthparts, *R. longiceps*, was also recovered from the rhinos. The disappearance of the two African rhino species will also result in the loss of three African tick species.

Freshwater snails, the silent assassins of Africa

Piet H. King¹

¹ Department of Biology, P.O. Box 139, University of Limpopo, Medunsa, 0204, South Africa. E-mail: Piet.King@ul.ac.za

Freshwater snails are known to serve as intermediate hosts in the life cycles of trematode parasites. *Biomphalaria pfeifferi* is well known to serve as intermediate host for *Schistosoma mansoni* in man, but is also the host for *S. rodhaini* in rodents and *S. edwardiense* in hippopotamus. *Bulinus africanus* is known to serve as host for *S. haematobium* in man, but also plays host to *S. bovis* and *S. mattheei* in cattle. *Bulinus tropicus* is mostly known for its role in the life cycle of *Calicophoron microbothrium* in ruminants. This snail also serves as host for *Schistosoma margrebowiei* in antelopes and cattle, and *S. bovis* in cattle. Snails of the genus *Lymnaea* are known to serve as intermediate hosts for fascioliasis. *Fasciola hepatica* in sheep uses *L. truncatula* and *L. columella* as intermediate hosts, whereas *F. gigantica* in cattle uses *L. natalensis* as host. *Lymnaea natalensis* also serves as host for avian schistosome species, especially parasites belonging to the genus *Trichobilharzia*. *Bulinus tropicus* and *L. natalensis* have in the last years emerged as intermediate hosts for a number of lesser-known parasites. Several cercarial types have been identified and described. Echinostomatid cercariae were found to develop into the parasites *Petasiger variouspinosus* in fish-eating birds and *Echinoparyphium elegans* in piscivorous birds, rats and even cats. Many fork-tail cercarial types were identified and described. One of these has been identified as the cercaria responsible for *Tylodelphys xenopi* in piscivorous birds. It is clear that freshwater snails play a major role in the parasite populations of a wide range of invertebrates and vertebrates. Their impact is immense, they survive in many rivers and dams without been noticed, while their cercarial shedding often cause the death of man and many other animals – the silent assassins of Africa.

New adventures in parasite studies of economically important marine fish species in South Africa

Cecile C. Reed¹ & Carl D. van der Lingen^{2,3}

¹ Department of Zoology; University of Cape Town, Private Bag X3, Rondebosch, 7701, South Africa. E-mail: cecile.reed@uct.ac.za

² Marine Research Institute, University of Cape Town, Private Bag X3, Rondebosch, 7701, South Africa

³ Branch Fisheries Management, Department of Agriculture, Forestry and Fisheries, Private Bag X2, Rogge Bay 8012, South Africa

The South African purse-seine fishery for small pelagic species (anchovy - *Engraulis encrasicolus*, sardine *Sardinops sagax*) boasted average landings of 380 000 tons per annum from 1950 - 2005 and over 500 000 tons from 2005 - 2009. Despite its historic existence and long-term economic value, very few studies have focused on parasites and diseases that may influence this fishery, the largest in South Africa. Some 'in house' Fishing Industry Research Institute (FIRI) reports written during the late 1980s and early 1990s concerning the effect of the myxozoan parasite *Kudoa thyrsites* on the quality of sardine fillets used for canning exist, but virtually no work has been conducted since. 2010 saw the initiation of a focused attempt to understand relationships between small pelagic species and their parasites. A survey of parasites infecting sardine was conducted, recording seven different parasite species. Subsequent research includes an assessment of one of those parasites (digenean "tetracotyle" metacercariae in the eyes) as a biological tag for examining sardine stock structure, and how the prevalence and infection intensity of this parasite varies both spatially and seasonally. In addition, the occurrence and physiological effects of another parasite species, the testicular coccidian *Eimeria sardinae*, is also underway, that parasite having been documented as causing "parasitic castration" in another sardine species. Early in 2012 a new study on parasites of Cape horse mackerel (*Trachurus capensis*) was initiated, previous work in the mid-1970s indicated a high prevalence of nematodes (*Ascaris* sp.) infecting horse mackerel gonads. Results of these studies will be described in the presentation. Sardine and horse mackerel are but two of many economically important marine fish species living off South Africa, and we believe that research on parasites of other economically important fish can contribute to the sustainable management of these important natural resources.

Evolution of diagnostic techniques for African trypanosomosis

Oriel M.M. Thekiso¹

¹ *Department of Zoology and Entomology, University of the Free State, Qwaqwa Campus, Private Bag X13, Phuthaditjhaba, 9866, South Africa. E-mail: thekisoemmo@qwa.ufs.ac.za*

Trypanosomosis is a disease of humans and animals caused by protozoan parasites of the genus *Trypanosoma*. Human African Trypanosomosis (HAT) which is commonly known as sleeping sickness, is caused by *T. brucei gambiense* and *T. b. rhodesiense* in the western and eastern parts of the African continent, respectively. Animal African Trypanosomosis (AAT) is caused by *T. b. brucei*, *T. congolense*, *T. vivax*, *T. evansi* and *T. equiperdum* in livestock in the entire continent. The first line of disease diagnosis is by observation of clinical signs, which includes anaemia, fever, fatigue, enlarged lymph nodes, loss of weight, etc. However, clinical signs are not specific for trypanosomosis only. Microscopy was the first technique used for observation of trypanosomes in blood and is still a widely used method for diagnosis of trypanosome infections from blood and cerebrospinal fluid in trypanosomosis endemic countries. Giemsa-stained smears, buffy coat and wet smears are commonly used microscopic techniques for detection of trypanosomes. Serological techniques such as enzyme-linked immunosorbent assay (ELISA) and card agglutination test for trypanosomosis (CATT) have also been developed for detection of antibodies from human and animal serum. The serological techniques are useful in indicating the exposure of patient to infection and are easily applicable for epidemiological studies. Recently, the advent of molecular biological techniques has brought in highly sensitive and specific DNA-based diagnostic techniques, which enables species and subspecies identification. Polymerase chain reaction (PCR) and loop-mediated isothermal amplification (LAMP) are amongst DNA-based techniques adapted for diagnosis of trypanosome infections. This paper reviews the evolution of different diagnostic methods developed for detection of African trypanosomes and seeks to highlight methods with the potential for commercialisation and that can realistically be used at point of care stations, particularly in resource-poor countries where African trypanosomosis is endemic.

Oral presentations:

Molecular detection of tick and tsetse-borne bovine pathogens in Nigeria

Mathew Adamu^{1,2}, Ilse Vorster² & Paul T. Matjila^{2,3}

¹ College of Veterinary Medicine University of Agriculture PMB 2373, Makurdi Benue State, Nigeria. E-mail: admatto30@yahoo.co.uk

² Faculty of Veterinary Science, Department of Veterinary Tropical Diseases, University of Pretoria, Private Bag X04, Pretoria, 0110, South Africa.

³ College of Agriculture and Environmental Sciences, Department of Life and Consumer Sciences, University of South Africa, Private Bag X6, Florida, 1710, South Africa.

A total of 128 blood specimens were collected from apparently healthy cattle from north eastern and central Nigeria. All the specimens were initially screened for the presence of *Babesia* / *Theileria* and *Ehrlichia* / *Anaplasma* genomic DNA using PCR and reverse line blot (RLB) assays. The same specimens were further screened for trypanosome species using a single polymerase chain reaction-restriction fragment length polymorphism (PCR-RFLP) assay, used to characterise all important trypanosome species. The RLB results showed that all 128 (100%) of the cattle were positive for at least one or more parasites. The most common parasites were *Anaplasma marginale*, *Babesia bovis*, *Theileria mutans*, *T. velifera*, *Babesia bigemina* and *T. annulata*. The results of the PCR-RFLP showed that 23% of the cattle were positive for trypanosomes. The only encountered species were *Trypanosoma theileri* 27(90%), *T. brucei* 2 (7%) and *T. vivax* 1(3%). This study reports on the first molecular survey of tick and tsetse-borne bovine haemoparasites in Nigeria. The results also show that the bovine population harbour varied haemoparasites, some of which are reported for the first time in Nigeria.

Distribution of *Giardia duodenalis* genotypes and efficiency of removal in wastewater treatment plants in Vhembe District, South Africa

Samie Amidou¹ & Phindle Ntekele¹

¹ *Molecular Parasitology and Opportunistic Infections Program, Department of Microbiology, University of Venda, Private Bag X5050, Thohoyandou, South Africa. E-mail: samieamidou@yahoo.com*

Over the past decade, *Giardia duodenalis* has increasingly been implicated in diarrhoeal outbreaks, with water and wastewater being recognised as an important vehicle for diseases. Although studies have reported the occurrence of these parasites in developed countries, their occurrence in water and wastewater bodies in developing countries, including South Africa, has not been thoroughly investigated. In the present study, wastewater samples from six different sewage treatment plants in the Vhembe District were collected for a period of six months. The samples were concentrated and tested for the presence of *Giardia duodenalis* using both microscopy and polymerase chain reaction methods targeting the *tpi* gene. Of the 79 wastewater samples tested, 25 (31.65%) were positive. Of these, 15 (60%) were genogroup A, while eight (32%) were genogroup B and two samples (8%) were positive for both genogroups. *Giardia* was more common in samples from Watervaal, occurring in 50% of the samples tested, followed by Malamulele with 41.7% of the samples testing positive. Genogroup A was more common in February 2010 while genogroup B showed two peaks in December-January and March-April and was not detected in May 2010. The general removal rate was 40% for plants using biological filters and 20% for plants using activated sludge. The present study has shown that *Giardia* genogroup A is more common in sewage treatment plants in the district, but the removal efficiency was low. This represents a public-health hazard since these might contaminate drinking water sources. Therefore action needs to be taken for the design of more effective procedures or methods for the removal of this parasite from the environment in order to avoid potential outbreaks.

Site selection in *Dolops ranarum*, a branchiuran fish parasite

Annemarië Avenant-Oldewage¹

¹ Department of Zoology, University of Johannesburg, P.O. Box 524, Auckland Park, Johannesburg, 2006, South Africa. E-mail: aoldewage@uj.ac.za

Previous research by our group confirmed that helminths and Crustacea are site specific. We showed for instance that *Bothriocephalus acheilognathi* prefers the first 20% of the intestine while *Cichlidogyrus philander* attached to gill arch 2 and 3 and occurred dorsally on the distal ends. In the copepods *Lamproglena clariae* parasites occurred predominantly on the fourth gill arch and specifically the median part of the gill arch for attachment; the size of the parasite was directly correlated to the size of the host. However, in *Lamproglena hoi* the parasites attach close to the gill arch. The branchiuran *Dolops ranarum* occurs inside the buccal cavity and gill chamber of *Oreochromis mossambicus* (tilapia), however, it occurs mostly on the skin of *Clarias gariepinus* (African catfish). It was also observed that the parasites are able to move around freely on the host, lay their eggs on the host and is able to relocate to a host after egg depositing. A catfish was placed in a 120mm diameter glass tube at an angle to allow an air space for air breathing. A constant water flow of oxygenated borehole water was pumped in at 300ml/min to force the fish to swim slowly creating water current around the host. Ten *D. ranarum* specimens were inserted into the tube and their movement was monitored for one week at intervals, initially every 30 minutes. It was noted that the parasites initially attach at random but then move around the host to attach selectively and stay in the same position for most of the experimental period. It is deduced that attachment is not a random process but presumably driven by availability of food and shelter in Branchiura but that optimal distribution of eggs additionally influence attachment in copepods.

A case-based prediction model aimed at automated sustainable *Haemonchus* spp. Management

Nlingisisi Babayani¹, Jan A. van Wyk¹ & Eric R. Morgan²

¹ *Department of Veterinary Tropical Diseases, Faculty of Veterinary Science, University of Pretoria, Private Bag X04, Onderstepoort, 0110, South Africa. E-mail: jan.vanwyk@up.ac.za*

² *School of Biological Sciences, University of Bristol, Woodland Road, Bristol BS8 1UG.*

Anthelmintic resistance (AR) of small ruminant gastrointestinal parasites in widely disseminated countries of the world has become almost intractable despite the existence of a number of sustainable integrated parasite management (sIPM) systems. For instance FAMACHA[®] clinical evaluation of anaemia is applicable to sustainable *Haemonchus* management through targeted selective treatment (TST) of only those individual animals unable to sustain current worm challenge while leaving the rest untreated. TST is well tested and useful at farm level, but is presently too labour intensive for general application on any but small farming enterprises. This has been attributed to implementation complexity of sIPM, compounded by a global shortage of persons with experience for customised advice to farmers. In reaction a so-called blueprint has been suggested for labour saving through optimal automated on-farm FAMACHA[®] application involving factors such as intervals between evaluation events, and proportion of flock to examine. Most previous mathematical models in parasitology predict parasite burden and are aimed at strategic treatment of animals, an approach that selects severely for drug resistance when there are few parasites in refugia. The novel SEIR transmission model presented here predicts the number of cases of haemonchosis, as detected by FAMACHA[®], as a function of previous FAMACHA[®] scores and intervening infection pressure. This enables farmers to target monitoring and treatment at reducing the chance of disease while also minimising treatment cost and alleviating selection for resistance. The approach is likely to be most helpful to resource-poor farmers, for whom case-based treatment is much more affordable. Haemonchosis has been selected for the initial investigation on application of the mathematical model, since clinical evaluation of severity is readily performed with the aid of FAMACHA[®] as part of the Five Point Check[®] system for identifying overly susceptible animals at an early stage of morbidity, thus making it a safe approach.

Ectoparasites on fish and their suctorian symbionts (Ciliophora: Suctoria)

Linda Basson¹ & Jo G. van As¹

¹ Department of Zoology and Entomology, University of the Free State, P.O. Box 339, Bloemfontein, 9300, South Africa. E-mail: Bassonl@ufs.ac.za

A great variety of parasitic and non-parasitic symbionts occur on the skin and gills of freshwater fish. The most commonly encountered are ciliophorans belonging to two closely related groups, i.e. the mobiline and sessiline peritrichs. Ciliophorans are, however, not restricted to fish, but can be encountered on a wide variety of other substrates and organisms, including other fish parasites, as well as on free-living organisms. It is well recorded in literature that some sessiline ciliophorans sometimes have to deal with their own attached symbionts. These are also ciliophorans and belong to the subclass Suctoria. Adult suctorians are sessile and completely devoid of cilia. Some genera attach directly to the surface of fish, while one genus is an endoparasite of both sessiline and mobiline peritrichs. A number of suctorian genera are found attached to various sessiline genera that themselves are found attached to fish. During fish parasitological surveys in the Okavango River, sessiline ciliophorans were commonly encountered on the skin and gills of several fish. Some of these were found to harbour suctorians. However, during a recent survey at Bloemhof Dam in the Free State, another interesting association was encountered. Huge infestations of the anchor worm, *Lernaea cyprinacea* (Crustacea: Copepoda), were found on one fish species. These pathogenic parasites also showed large infestations of ciliophorans. Whilst sessiline ciliophorans are well known to occur on various crustaceans, both parasitic and free living, it was not the case in this instance. These crustaceans showed infestations of suctorian ciliophorans, both on the adult female *Lernaea*, as well as on the copepodite stages that were also found on the same fish. Very little is known about suctorians. Whilst they are considered to be predatory, the relationship that some species have with their attached host, whether it be ciliophoran or crustacean, has not been studied and still remains a mystery.

Update of the parasitofauna of fishes in the middle Zambezi River and Lake Kariba

Maxwell Barson^{1,2}, Annemarié Avenant-Oldewage² & Iva Přikrylová³

¹ Department of Biological Sciences, University of Zimbabwe, Harare, Zimbabwe. E-mail: barson@science.uz.ac.za

² Department of Zoology, University of Johannesburg, P.O. Box 524, Auckland Park, Johannesburg, 2006, South Africa.

³ Department of Botany and Zoology, Faculty of Science, Masaryk University, Kotlářská 2, 611 37 Brno, Czech Republic.

In an on-going study to update the parasitofauna of Lake Kariba and the Zambezi River, which started in February 2011, 22 fish species belonging to 10 families were sampled and examined for internal and external parasites. Thirty-three parasite groups have so far been isolated from the fishes, of which 27 have been identified at least to genus level. Of these nine new monogeneans belonging to the genus *Gyrodactylus* have been identified on six host species and we are currently working on their specific taxonomy. The African catfish *Clarias gariepinus* hosts the greatest diversity of parasites (17 species), followed by the squeaker *Synodontis zambezensis* (5) and the tigerfish *Hydrocynus vittatus* (4). Could this be an indicator that carnivorous fish are more susceptible to parasitism as a result of trophic transmission? This remains unanswered as more data are being gathered. The possible role of introduced species such as the Nile tilapia *Oreochromis niloticus* and the exotic snail *Melanoides tuberculata* in the transmission of novel parasites to the Zambezi fishes is also being investigated. Current data suggest that the Monogenea (14 species) is the most speciose group, and these have a direct life cycle where parasites actually 'jump' from one fish to the next. Impacts of global environmental change are also hypothesised to affect the distribution of parasites and their host fishes in the middle Zambezi and this study will hopefully provide information that will be vital in unraveling this mystery.

Global diversity of parasitic isopods of the family Cymothoidae

Niel L. Bruce^{1,2}, Kerry A. Hadfield² & Nico J. Smit³

¹ *Museum of Tropical Queensland, and School of Marine and Tropical Biology, James Cook University, 70–102 Flinders St, Townsville, Qld 4810, Australia*

² *Centre for Aquatic Research, Department of Zoology, University of Johannesburg, P.O. Box 524, Auckland Park, Johannesburg, 2006, South Africa. Email: kerryh26@yahoo.com*

³ *School of Biological Sciences, Potchefstroom Campus, North West University, Private Bag X6001, Potchefstroom, 2520, South Africa.*

Of the 95 known families of Isopoda only a few are parasitic, namely Bopyridae, Cryptoniscidae, Cymothoidae, Dajidae, Entoniscidae, Gnathiidae and Tridentellidae. Representatives from the family Cymothoidae are obligate parasites of both marine and freshwater fishes and there are currently 43 recognised cymothoid genera worldwide. These isopods are large (> 6 mm) parasites, thus easy to observe and collect; yet many aspects of their biodiversity and biology are still unknown. They are widely distributed around the world and occur in many different habitats, but mostly in shallow waters in tropical or subtropical areas. A number of adaptations to an obligatory parasitic existence have been observed, such as the body shape, which is influenced by the attachment site on the host. Cymothoids generally have a long, slender body tapering towards the ends and the efficient contour of the body offers minimum resistance to the water flow and can withstand the forces of this particular habitat. Other adaptations to this lifestyle include small sensory antennae and eyes; a very heavily thickened and calcified cuticle for protection; and sharply curved hooks on the ends of the pereopods which allows these parasites to attach to the host. Most cymothoids are highly site and host specific. Some of these parasitic cymothoids have been reported to parasitise the same host fish species for over 100 years, showing this species specificity. The site of attachment on the host (gills, mouth, external surfaces or inside the host flesh) can also be genus or species specific. This paper aims to provide a summary of our current knowledge of cymothoid biodiversity and will highlight their history of discovery, morphology, relationships and classification, taxonomic diversity and ecology.

First reports of epizootic ulcerative syndrome from South Africa

Kevin W. Christison¹, Brett Macey¹ & Anna Mouton²

¹ Directorate Aquaculture Research, Department of Agriculture Forestry and Fisheries, Private Bag X2, Roggebaai, 8012, South Africa. E-mail: KevinCH@daff.gov.za

² Amanzi Biosecurity, Private Bag X15, Suite 190, Hermanus, 7200, South Africa.

Epizootic ulcerative syndrome (EUS), caused by the water mould *Aphanomyces invadans* (Oomycetes: Saprolegniales), is listed by the World Organisation for Animal Health (OIE) as an internationally significant and notifiable disease. More than 76 species of both farmed and wild freshwater fish have been documented as being susceptible to EUS and include members of the Cyprinidae, Clariidae, Cichlidae, Mormyridae and Centrarchidae. *Aphanomyces invadans* has a direct life cycle and is transmitted horizontally from one host to another through the release of motile flagellated secondary zoospores, which infect the new host. A successful transmission usually requires skin damage, susceptible fish and favourable environmental conditions. In the early stages of the infection, infected fish develop small pinpoint red spots with localised swelling and raised areas of the body surface which progress to the loss of scales and skin erosion. These areas eventually develop into large ulcerative lesions with a necrotic centre exposing the underlying muscle tissue. These lesions are most commonly observed on the lateral surfaces of the affected fish. In December 2010, the first suspected case presented itself in South Africa. Juvenile bluegill sunfish (*Lepomis*) and largemouth bass (*Micropterus salmoides*) with fungal infections were sampled from the Palmiet River System near Grabouw, Western Cape. EUS was confirmed from these fish by skin scrapes showing typical *Aphanomyces*-like secondary zoosporangia and histopathology showing typical deeply penetrating fungal hyphae with a characteristic granulomatous tissue reaction. Definitive confirmation was obtained through the amplification of the internal transcribed spacer (ITS) region of the ribosomal DNA by PCR according to the specifications of the OIE and comparison of sequence data to existing sequences on the Genbank database. In October 2011, a second positive case presented itself in the lower Eerste River drainage system near Stellenbosch, Western Cape. Large-scale mortalities of sharptooth catfish (*Clarias gariepinus*) were reported and the EUS diagnosis was again confirmed by histology and PCR.

The variability of mHC IIB class genes in two congeneric cyprinids and its influence on the composition of metazoan parasite communities

Kristína Civaňová¹, Andrea Šimková¹, Caroline Costedoat² & André Gilles²

¹ Department of Botany and Zoology, Faculty of Science, Masaryk University, Brno, Kotlářská 2, 611 30 Brno, Czech Republic. E-mail: kristin@sci.muni.cz

² Evolution Genome and Environment, UMR-CNRS 6116-IMEP, University of Provence, Marseille, France.

To characterise the immune system of vertebrates, genes of major histocompatibility complex (MHC) are tested. The most variable sites of MHCII B molecules in fish (ABS-antigen binding sites) are determined by exons 2 of DAB1 and DAB3 genes. The individuals differ in DAB genes expression, some of them express only DAB1 or DAB3 genes, and others express the genes of both loci. Two cyprinid species, the introduced *Chondrostoma nasus* and the native, protected and endemic *Chondrostoma toxostoma*, live in sympatry and form a hybrid zone in the Durance River (South France, Mediterranean Sea drainage). Our studies in the family Cyprinidae are aimed to analyse life processes and the genetic diversity of fish populations. The potential influence on the level of perception to parasite infections in relation with diversity and evolution of hosts' MHC genes is also tested. The aims of this study were to investigate the composition of metazoan parasite communities in two pure species and their respective hybrids. Based on the hypothesis of parasite-mediated selection maintaining MHC polymorphism it could suggest the difference in parasite load between chondrostomes living in allopatric areas and those living in hybrid zones. All individuals were genotyped for mtDNA (cyt b), 41 microsatellite loci and DAB1 and DAB3 genes (MHC IIB class). Two allopatric and four sympatric populations were analysed. A total of seven Monogenea, eight Trematoda, three Crustacea, one *Acanthocephala* species and larval stages of Mollusca were found on *Chondrostoma* species. Monogenea and Trematoda were the most abundant parasite groups. Among them, *Dactylogyrus* was the most abundant parasite genus. When comparing two allopatric localities, low similarity in the presence of parasite species was observed. Higher similarity in parasite species richness was observed between sympatric localities. This study was funded by the Czech Science Foundation, projects Nos. P505/12/G112 (ECIP) and P505/10/1138.

Tsetse flies (Diptera, Glossinidae) in the conservation areas of North- Eastern KwaZulu-natal, South Africa

Chantel J. de Beer¹ & Gert J. Venter¹

¹ Parasites, Vectors and Vector-borne Diseases, Agricultural Research Council-Onderstepoort Veterinary Institute, Private Bag X5, Onderstepoort, 0110, South Africa. E-mail: DeBeerC@arc.agric.za

Distribution surveys of *Glossina brevipalpis* and *Glossina austeni* were conducted in northeastern KwaZulu-Natal from 1993 to 1999. Additional surveys, focusing on areas of uncertain tsetse distribution, were conducted from 2002 to 2012. In addition permanently active odour-bated H-traps were erected in seven conservation areas and monitored monthly from 2006 to 2009. Results were expressed as Apparent Density (AD) of each species in terms of flies/trap/day. The distribution maps, elaborating on the 1993 to 1999 data, show tsetse flies to be widely distributed and AD to be higher in the conservation areas. Significant differences in AD were found between conservation areas. Tsetse AD seems to be linked to vegetation, with *G. austeni* prevalent in denser vegetated areas and *G. brevipalpis* more tolerant to open areas. For both species AD varied significantly between years. These variations were not linked to specific years and differ between areas. In the north the highest AD, for *G. austeni*, was in summer (December to February) and in the south in autumn (March to May). For *G. brevipalpis* the seasonal peak was not as pronounced. Overall no significant growth or decline in populations was observed throughout the four years. Although an initial drop in the AD of *G. austeni* was found at four sites after the commencement of trapping there was an increase at three. Natural variation between sites and years make it unadvisable to ascribe this to trapping. It can be concluded that permanent trapping did not influence tsetse numbers in the conservation areas. The data show that the conservation areas maintain stable populations of tsetse flies. Although tsetse flies can also be abundant outside these areas, they provide a stable environment for long term monitoring and population studies regarding these flies. Studies on these populations will be fundamental for the development of integrated disease management practices.

An alternative approach to sustainable tick control

Christa du Rand¹ & Ellie M.S.P. van Dalen¹

¹ *Department of Zoology and Entomology, University of the Free State, P.O. Box 339, Bloemfontein, 9301, South Africa. E-mail: durandc@ufs.ac.za*

Ticks have a major economic impact on cattle farming through diseases they transmit, direct losses due to their detrimental effect on the animals and the efforts invested in prevention measures directed against them. The appearance of tick resistance to many acaricides available in the marketplace is becoming a fast-increasing problem in tick control. This study focuses on an alternative, more natural approach in controlling ticks on cattle in a sustainable way. The study was performed on a farm outside Grahamstown in the Eastern Cape Province, a major problem area concerning tick resistance. The test product, in the form of a dissolvable tablet, was added to the cattle's drinking water. The product was tested against a negative control, chemical treatment and a combination of chemical treatment and the test product itself. Blue tick counts were monitored at regular intervals over a 35-day period by taking photographs from selected body areas of each test animal to monitor changes in the tick burden amongst the different treatment groups during the course of the study. Body mass was recorded and in addition, faecal samples were taken prior to treatment and again at the end of the study to detect any possible effect on internal parasites. Tick drags were also performed in the camps where the animals were kept to get an indication of field presence of immature stages of different tick species. The results obtained from the study showed no immediate solution for tick control but emphasised the importance of a thorough knowledge of the life cycle of the specific tick species in order to apply effective control. It also sets a platform for future similar studies in developing natural or biological tick control methods.

Diversity of monogenean parasites of freshwater fish of Africa

Milan Gelnar¹, Monika Mendlová¹, Nada Musilová¹, Iva Přikrylová¹ & Eva Řehulková¹

¹ *Department of Botany and Zoology, Faculty of Science, Masaryk University, Kotlarska 2, 611 37 Brno, Czech Republic. E-mail: gelnar@sci.muni.cz*

The ichthyofauna of sub-Saharan Africa is under heavy threat and conservation strategies and research on both fish host and fish parasite biodiversity are needed. In the monogenean fauna of Africa, far more oviparous parasites are known than viviparous parasites. Inasmuch as Lim (1998) and Whittington (1998) have assessed the number of monogenean species per fish species at three and five, respectively, with about 2 900 species of African freshwater fishes, the number of monogeneans expected to be found in this region is 8 700 – 14 500. In comparison with the number of species hitherto recorded (i.e. 370, or about 3.5 % of the expected number), our knowledge of monogenean diversity in this region is still poorly known. In the current study, the metazoan parasite fauna includes freshwater monogeneans. Fish originating from 25 localities from both the National Park Nikolo Koba, Senegal, West Africa (larger central river system) and Turkana Lake, Kenya, East Africa, were observed on site surveys carried out during eight field expeditions from 2004 – 2010. Altogether 985 specimens of freshwater fish belonging to 80 species have been investigated for monogenean parasites. Till now, almost 8 000 specimens of monogeneans have been identified and about 40 new monogenean species descriptions are going to be published in the near future. Moreover about 100 new original sequences of 18S rDNA, 28S rDNA and ITS1 (related to 50 monogenean species) have been analysed. The aim of this presentation was to partly compile monogenean parasites structural diversity, including phenotypic plasticity and molecular phylogeny.

Can monogeneans be a good biological model?

Milan Gelnar¹ & Andrea V. Simkova¹

¹ Department of Zoology and Ecology, Faculty of Science, Masaryk University, Kotlarska 2, 611 37 Brno, Czech Republic. E-mail: gelnar@sci.muni.cz

There is no doubt that modern biology tends to study problems rather than taxa. However, there is strong need for selection of suitable model which offers the best opportunity to answer the question. We think that the moment has come for Monogenea not to be studied for themselves only, but as models for parasitology in general and for biology in general. The fact that they have short life cycles, high fecundity, narrow specificity, a great number of species, a variety of habitats and diets and have been studied by specialists for years makes monogenean parasites excellent candidates to play this role. The main aim of our contribution is to demonstrate results of several monogenean parasite model systems investigated within the Central Europe (e.g. viviparous monogeneans belonging to the genus *Gyrodactylus* including oviparous monogeneans of the genera *Eudiplozoon* and *Dactylogyrus*). Patterns of morphological diversification have been the topic of various analyses and several hypotheses have been proposed to explain the morphological differences exhibited by related species. Co-existence of congeneric species occupying the same habitat or exploiting the same resources is the subject of many studies related to the questions of competition or reproductive isolation preventing the hybridisation of congeneric species. The potential relationships of those processes with phylogenetic patterns could be hypothesised. Several hypotheses connected with the coexistence of congeneric species could be proposed for parasites. Existence of the reproductive barriers should be connected to i) the morphological features of the parasite's reproductive organs preventing species hybridisation and/or ii) the morphology of the parasite's attachment apparatus connected with spatial segregation in terms of host specificity or niche preference within the host.

Metal bioaccumulation and partitioning in the pseudophyllidean cestode, *Bothriocephalus acheilognathi*

Beric M. Gilbert¹ & Annemarié Avenant-Oldewage¹

¹ *Department of Zoology, University of Johannesburg, P.O. Box 524, Auckland Park, Johannesburg, 2006, South Africa. E-mail: aoldewage@uj.ac.za*

Previous studies have indicated that acanthocephalans and cestodes have a greater capacity for the accumulation of heavy metals than their hosts and other free-living indicators. Further research into the accumulation of heavy metals by cestodes has revealed a partitioning in the metal concentrations between the anterior and posterior body segments. The aim of this investigation was to determine whether a difference occurs in the concentrations of the metals present in the different body sections of *Bothriocephalus acheilognathi* in comparison to the host fish. *Labeobarbus kimberleyensis* were sampled with the use of gill nets from the Vaal Dam. The cestodes were collected after dissection of the host fish and they were separated into sections, i.e. the scolex, mature proglottids and gravid proglottids, the premises that various sections differ in age and hence exposure time. Analysis of metal concentrations for the fish tissue was done with the use of ICP-MS and metal concentration analysis in the cestode tissue was performed using TXRF. Cestode segments were stained with a fluorescent probe to visually demonstrate the binding sites of heavy metals within the different body sections. The results for the metal concentration analyses show that metals are sequestered differentially between the different body segments of the cestodes, and the cestodes accumulated more metals than the host fish. The use of the fluorescent probe showed that the metal ions were binding to the eggshells of the cestodes and possibly to the embryo within the eggs. Fluorescence of the organs (e.g. uterus and testes) within the mature proglottids was also observed. In conclusion the tapeworms do indeed accumulate metals at greater concentrations than those present in the tissues of the host and the environment and there is partitioning in the accumulation of metals in the different body segments.

Entry of African trypanosomes into the central nervous system during early stages of disease

Dennis J. Grab¹, Sylvie Bisser² & Ute Frevert³

¹ Division of Medical Microbiology, Department of Pathology, The Johns Hopkins University School of Medicine, Baltimore, MD 21205, USA. E-mail: dgrab1@jhmi.edu

² Institut de Neurologie Tropicale, Universite de Limoges, Limoges, France. ³ Division of Medical Parasitology, Department of Microbiology, New York University School of Medicine, New York, NY 10010, USA.

Human African Trypanosomosis (HAT) is a vector-borne parasitic disease that has a major impact on human health and welfare in sub-Saharan countries. Based on animal models, it is currently thought that trypanosome manifestation in the brain occurs by initial infection of the choroid plexus and the circumventricular organs followed days to weeks later by dissemination to the brain parenchyma. However, *Trypanosoma brucei* bloodstream forms rapidly cross human brain microvascular endothelial cells in vitro and appear to be able to enter the murine brain without inflicting cerebral injury. Using a murine model and intravital brain imaging, we find that bloodstream forms of *T. b. brucei* and *T. b. rhodesiense* enter the brain parenchyma within hours, before a significant level of microvascular inflammation is detectable. Extravascular bloodstream forms were viable as indicated by motility and cell division, and remained detectable for at least three days post infection suggesting parasite survival in the brain parenchyma. Vascular inflammation as reflected by leukocyte recruitment and extravasation from cortical microvessels became apparent only with increasing parasitemia at later stages of the infection, but was not accompanied by neurological signs. Extravascular trypanosomes were predominantly associated with postcapillary venules suggesting that early brain infection occurs by parasite passage across the neuro-immunological blood brain barrier. To examine the potential clinical significance of these findings, we assessed cerebrospinal fluid (CSF) collected in Gabon and Angola using a detergent-enhanced LAMP assay. Remarkably, similar frequencies of CSF samples from patients diagnosed with Stage 1 or Stage 2 HAT were positive for parasite DNA regardless of disease stage. Together, these data suggest that trypanosomes invade the brain parenchyma during the early stages of the disease, before meningo-encephalitis is fully established.

The micromorphology of the flea *Xenopsylla philoxera* from the bushveld gerbil *Gerbilliscus leucogaster*

Eddie D. Green¹, Chantelle Baker² & Seth .J. Eiseb³

¹ Department of Anatomy, University of Limpopo, P.O. Box 232, Medunsa, 0204, South Africa. E-mail: Edward.Green@ul.ac.za

² Electron Microscope Unit, University of Limpopo, P.O. Box 232, Medunsa, 0204, South Africa

³ National Museum of Namibia, P.O. Box 1203, Windhoek, Namibia.

Gerbilliscus leucogaster is an important secondary host of the *Xenopsylla philoxera* fleas, which are important vectors of *Yersinia pestis* causing the wild-rodent plague in southern Africa. The thirty *Xenopsylla* species are not easily distinguished using traditional light microscopy (LM). This investigation using the scanning electron microscope (SEM) sought to reveal additional taxonomic characteristics as well as elucidating the functional micromorphology. The fleas were collected from trapped rodents in northern Namibia and fixed in 70% ethanol. Some of the fleas were cleared and mounted for identification under the LM, while the rest were routinely processed for SEM before being viewed in a Zeiss Supra 55 FE-SEM. *Xenopsylla philoxera* are compact fleas with the males measuring under 1mm in total length and the females approximately 1.5 mm. The frons of the head was well rounded lacking a genal comb. The eye with the preocular bristle was situated in the anterior corner of the deep antennal fossa which protects the lobed antenna. The two lobes of the stipes were medially fused protecting the underlying labial palps. These pointed tubular palps together with the enclosed serrated laciniae are used to penetrate the skin and blood vessels. The well-developed legs with large coxa and prominent outer internal ridges of the hind coxa, are typical of jumping fleas. The reported difference between the three pre-apical planter bristles on foretarsal segment 5 between the male and female was confirmed, but an additional 11 to 14 spiniforms were also observed here. The tarsal claws with lateral plates were specialised with ventral grooves for gripping the hairs of the host. The posterior tergites 8 housed the sensillum, the slit-like posterior spiracles and external genitalia, which were investigated. The male claspers bore the seven setae characteristic of this species. The SEM greatly enhanced the study of these taxomorphological specialisations of *Xenopsylla philoxera*.

The micromorphology of the rare flea *Macroscelidopsylla albertyni* from the elephant shrew

Eddie D. Green¹, Chantelle Baker² & Heike Lutermann³

¹ Department of Anatomy, University of Limpopo, P.O. Box 232, Medunsa, 0204, South Africa. E-mail: Edward.Green@ul.ac.za

² Electron Microscope Unit, University of Limpopo, P.O. Box 232, Medunsa, 0204, South Africa

³ Department of Zoology and Entomology, University of Pretoria, Hatfield, 0028, South Africa.

Before 2003 this rare flea had only been collected from elephant shrews from Aus in Namibia. Discovered amongst fleas collected from elephant shrews in Limpopo Province, provided an opportunity to investigate this relatively unknown flea using scanning electron microscopy. The fleas that had been preserved in 70% ethanol were identified using light microscopy, before being routinely processed for SEM and viewed in a Zeiss Supra 55 FE-SEM. These are small elongated fleas with the total length reflecting sexual dimorphism (males 1.3 mm and females 1.8 mm). The frons of the head was angular with two pairs of long setae just above the eyes and fine setae extended along the frons anterior to the first and second spines of the genal comb. The shape of each of the four flattened spines of the genal comb was specific and the innersides were ridged for sticking to the hairs of the host. The large eye was situated antero-dorsally and protected by a bean-shaped plate. The antennae were large and dorsally orientated, allowing for clear investigation. The mouthparts were composed of two serrated laciniae for penetrating the skin, and along with a rodlike epipharynx, were housed in a pair of tube-like labial palps. Twelve stout round bristles formed the prominent pronotal comb that was longitudinally ridged for hooking onto the hairs. The setation of the tibia of the hind legs confirmed this as a characteristic of this species. The structure of the ridged tarsal claws reflected their functional design to grasp the hairs. The spiracular openings on each of the abdominal tergites were mainly rounded except for the large slit-like posterior spiracles on tergite VIII. Short spines lined the posterior margin of each tergite. The sensillum and external genitalia were also investigated. A number of micromorphological specialisations were elucidated in this SEM study.

Unique morphological characteristics of *Neolinognathus elephantuli* lice revealed by scanning electron microscopy

Eddie D. Green¹, Martin L. Turner² & Heike Lutermann³

¹ Department of Anatomy, University of Limpopo, P.O. Box 232, Medunsa, 0204, South Africa. E-mail: Edward.Green@ul.ac.za

² Electron Microscope Unit, University of Limpopo, P.O. Box 232, Medunsa, 0204, South Africa

³ Department of Zoology and Entomology, University of Pretoria, Hatfield, 0028, South Africa.

Neolinognathus elephantuli is one of two lice species of the unique family Neolinognathidae host specific to *Elephantulus* shrews. Last described in 1922, it was considered necessary to revisit the descriptions of this louse using scanning electron microscopy (SEM). The lice were collected from trapped *Elephantulus myurus* and fixed in 70% ethanol. They were identified by light microscopy before being routinely processed for SEM and viewed in a Zeiss Supra 55 FE-SEM. These minute lice measured less than 1mm in total length. The thick cap-like clypeus covered the head anterior to the antennae. The uncovered areas of the head were protected by scales that also covered the thoracic segments. The sucking mouthparts were closed by two lateral flaps. The five-segmented antennae were not sexually dimorphic but revealed the typical sensory plate organs, one of which was situated on a unique pedunculate process on the tip of the distal segment. The long thin sternal plates were located between the coxae on the ventral thorax. The internal opening of the large lateral thoracic spiracles was lined by honeycomb patterned reinforcing which was similar in the large spiracles on abdominal segment VIII. Small abdominal stigmata were observed on the segments I to VII. Robust triangular scales demarcated the posterior margins of abdominal segments I to VI, with rounded scales alternating with sharp spinous scales that covered the abdomen. Abdominal setae were conspicuously absent. A pear-shaped genital plate with four short medial setae and a pair of claspers with three longer setae surrounded the female ovipositor. Two pairs of long setae occurred on each of segments VIII and IX. The claws of legs I are relatively thin and round compared to the robust flattened tarsal claws of legs II and III. This study reinforced the uniqueness of the micromorphology of these *Neolinognathus* lice.

Chewing lice of the genus *Myrsidea* (Phthiraptera: Menoponidae) in wild birds of Limpopo Province, South Africa

Ali Halajian¹, Oldrich Sychra², Wilmien Luus-Powell¹, Derek Engelbrecht¹, Johan Theron³ & Ivan Literak²

¹ Department of Biodiversity; ³ Aquaculture Research Unit, University of Limpopo, Private Bag X1106, Sovenga, 0727, South Africa. E-mail: ali_hal572002@yahoo.com.

² Department of Biology and Wildlife Diseases, Faculty of Veterinary Hygiene and Ecology, University of Veterinary and Pharmaceutical Sciences, Palackeho 1–3, 612 42 Brno, Czech Republic.

South Africa has nearly 850 bird species and South Africa's northernmost province, the Limpopo Province, boasts with more than 600 recorded bird species (approximately 420 breeding resident spp). Despite previous reports of *Myrsidea* spp. from South African birds, there has not been any detailed study of this louse genus, and from all the bird fauna of South Africa, only 20 (belonging to 13 families) are known to be hosts of 17 species of *Myrsidea*. The aim of this study is to present new data on the distribution of this genus in South Africa, including description of three new species. A total of 145 individuals of 46 bird species (from 20 families) were captured with mist nets, checked by visual examination and the fumigation chamber method for chewing lice. Sampling was done from November 2011 to March 2012 at five study sites in the Limpopo Province. These sites were: Golwe in the north-east of the province, Polokwane Nature Reserve, De Loskop near Mogwadi, Woodbush forest and the University of Limpopo, Turfloop Campus. A total of 19 birds representing eight species were parasitised by eight species of *Myrsidea*. Three of them were recently described. The new species and their type hosts are: *Myrsidea aynazae* ex *Phyllastrephus flavostriatus* (Sharpe) (Pycnonotidae), *Myrsidea eslamii* ex *Zoothera gurneyi* (Hartlaub) (Turdidae) and *Myrsidea mariquensis* ex *Bradornis mariquensis* Smith (Muscicapidae). Records of new host-lice associations are: *Phyllastrephus terrestris* Swainson (Pycnonotidae) for *Myrsidea* sp., *Ploceus intermedius* Ruppell (Ploceidae) for *Myrsidea* sp., and *Turdus libonyanus* (Smith) (Turdidae) for *Myrsidea* sp. Following lice genera were also found on the examined birds and are currently undergoing identification to species level, e.g. *Brueelia*, *Menacanthus*, *Penenirmus*, *Philopterus*, *Ricinus* and *Sturnidoecus*.

Sealice, systematics and sequences: working towards a robust phylogenetic framework for the Caligidae

Polly M. Hayes¹, Rony Huys¹ & Geoffrey A. Boxshall¹

¹ *Department of Life Sciences, The Natural History Museum, London SW7 5BD, UK. E-mail: polly.hayes@nhm.ac.uk*

Aquaculture is big business. Its inexorable growth is bringing more and more fish species into cultivation and aquaculture is on course to overtake capture fisheries during the 2030s in overall contribution to the human food chain. Currently, the biggest health hazard for farmed finfish is infestation with sealice (ectoparasitic copepods of the family Caligidae) – with global commercial losses in excess of \$100 million p.a. The Caligidae currently comprises over 450 valid species, the vast majority ectoparasitic on marine teleosts, and these are classified in 34 genera. However, the validity of several of these genera has been questioned and we lack a robust phylogenetic framework for the family. There is also uncertainty over the relationships between genera and the boundaries of the family, particularly with respect to genera formerly placed in the Euryphoridae. This taxonomic uncertainty is a barrier to developing an improved understanding of sealice biology. The aim of the current study is to establish a systematic framework for the family Caligidae using both comparative morphological and molecular data. Our approach is to: (i) build an updated character data matrix for phylogenetic analysis using an array of morphological characters, (ii) generate molecular sequence data for mitochondrial (Cox1, NADH1) and ribosomal (18S, 28S) markers, to be combined with existing published DNA sequence data (available for a limited number of species), and (iii) construct robust species phylogenies using in-depth phylogenetic inference (Bayesian analysis, Maximum Likelihood, & Maximum Parsimony). Morphological and molecular data sets will be treated both separately and combined, to achieve optimum phylogenetic resolution. Generating a better resolved phylogeny for the Caligidae will allow the significant conflict between, for example, life cycle patterns and the existing classification, to be resolved.

Morphological and molecular characterisation of a marine fish trypanosome from South Africa

Polly M. Hayes^{1,2}, Scott P. Lawton², Nico J. Smit³, Wendy C. Gibson⁴ & Angela J. Davies^{2,3}

¹ Department of Life Sciences, The Natural History Museum, London SW7 5BD, UK.

² School of Life Sciences, Faculty of Science, Engineering and Computing, Kingston University, Kingston upon Thames, Surrey KT1 2EE, UK. E-mail: ajdavies.russell@kingston.ac.uk

³ School of Biological Sciences, Potchefstroom Campus, North West University, Private Bag X6001, Potchefstroom, 2520, South Africa.

⁴ School of Biological Sciences, University of Bristol, Bristol BS8 1UG, UK.

Blood films were prepared from intertidal fishes captured intermittently on the west coast (Atlantic Ocean) and south coast (Indian Ocean) of South Africa between September 2003 and April 2010. Screening revealed a number of protists, the most obvious being trypanosomes, found in fishes of the genera *Clinus* and *Parablennius*. These fishes were also parasitised by haematophagous ectoparasites, namely juveniles of the isopod *Gnathia africana*, and/or adults and juveniles of the leech *Zeylanicobdella arugamensis*. The trypanosomes were morphometrically variable, even within single blood films. Individuals ranged from small, narrow, pale-stained forms through to those that were large, broad, and deep-stained. This suggested growth forms of one trypanosome type were present, or a mixed-species population. Examination of Giemsa-stained squashes of *G. africana* juveniles taken from infected fishes revealed none with trypanosome developmental stages. However, similar stained squashes from *Z. arugamensis* adults and juveniles demonstrated predominantly trypanosome epimastigotes. To determine whether trypanosomes in the fishes were of one or more genotypes, and whether the developmental stages in *Z. arugamensis* were those of fish trypanosomes, DNA was extracted from trypanosome-positive whole fish blood, or directly from stained fish blood films, as well as from slides with Giemsa-stained leech squashes. Fragments of the ssu rRNA gene were amplified by polymerase chain reaction (PCR) using trypanosome-specific primers and sequenced. The resulting sequence data were then compared with published trypanosome ssu rRNA sequences and used for phylogenetic analysis. Trypanosome sequences from fishes proved to be of one genotype, suggesting the presence of one, highly morphologically variable, trypanosome. Sequences from leeches were also of one trypanosome type, identical to that found in the fishes. Finally, sequence data, subjected to phylogenetic analysis, demonstrated that the South African trypanosome from intertidal fishes and its leech vector aligned closely with marine fish trypanosomes from the northern hemisphere.

Inside invertebrate hosts – using three-dimensional (3D) visualisation as a tool to investigate developmental stages of apicomplexan fish blood parasites and improve knowledge of host anatomy

Polly M. Hayes^{1,2}, David F. Wertheim³, Nico J. Smit⁴, Alan M. Seddon² & Angela J. Davies^{2,3}

¹ Department of Life Sciences, The Natural History Museum, London SW7 5BD, UK. E-mail: polly.hayes@nhm.ac.uk

² School of Life Sciences, Faculty of Science, Engineering and Computing, Kingston University, Kingston upon Thames, Surrey KT1 2EE, UK.

³ School of Computing and Information Systems, Faculty of Science, Engineering and Computing, Kingston University, Kingston upon Thames, Surrey KT1 2EE, UK

⁴ School of Biological Sciences, Potchefstroom Campus, North West University, Private Bag X6001, Potchefstroom, 2520, South Africa.

The application of three-dimensional (3D) imaging to parasitology appears limited to date but is becoming an increasingly more popular tool. We used 3D visualisation to investigate the developmental stages of a marine fish haemogregarine, *Haemogregarina curvata*, in their leech vector, *Zeylanicobdella arugamensis*, from southern Africa. 3D assessment of brightfield and confocal microscopy images through infected leech salivary gland cells demonstrated the morphology of the haemogregarine stages, their spatial layout, and their relationship with enlarged host cells showing reduced cellular content. Haemogregarine meronts, located marginally within leech salivary gland cells, were seen to have small tail-like connections to the host cell limiting membrane, revealing a previously unknown parasite-host cell interface and resulting in the likely first account of the use of 3D visualisation to study developmental stages of an apicomplexan parasite in its invertebrate vector. Similar techniques have also been employed in attempts to locate developmental stages of the cosmopolitan marine fish haemogregarine *Haemogregarina bigemina* within their probable vectors, juvenile stages of the gnathiid isopods *Gnathia africana* in South Africa and *G. maxillaris* in the UK. The internal anatomy of *Gnathia* spp. is generally not well known and neither are their digestive cycles. Preliminary 3D visualisations of histological sections of the two *Gnathia* species showed potential for future reconstruction of the entire internal anatomy of gnathiids, which would allow the sites of development of the haemogregarine to be clearly defined and potentially help to elucidate the mode of passage of *H. bigemina* from gnathiid to fish.

***Cosmiomma hippopotamensis*: An endangered tick species?**

Heloise Heyne¹ & Ivan G. Horak^{2,3}

¹ *Parasites, Vectors and Vector-borne Diseases (PVVD), ARC-Onderstepoort Veterinary Institute, Private Bag X05, Onderstepoort, 0110, South Africa. E-mail: heyneh@arc.agric.za*

² *Department of Veterinary Tropical Diseases, University of Pretoria, Private Bag X04, Onderstepoort, 0110, South Africa*

³ *Department of Zoology and Entomology, University of the Free State, P.O. Box 339, Bloemfontein, 9300, South Africa.*

In 1843, Henry Denny, an English entomologist described two ticks collected from what was thought to be a hippopotamus somewhere in the South African interior. He named the male *Ixodes hippopotamensis* and the female *Ixodes bimaculatus*. A year later Koch (1844) realised that *I. hippopotamensis* and *I. bimaculatus* were sexes of the same species and he, as first reviser, gave name priority to *I. hippopotamensis* and placed it under the genus *Amblyomma*. It was later transferred to the genus *Hyalomma* followed by *Dermacentor* to finally reside in the monospecific genus *Cosmiomma* as *C. hippopotamensis*. These two species were finally grouped as one species, *Cosmiomma*, Schultze, 1919. For more than a 100 years this tick species was not collected in southern Africa, until 1959, when Gertrud Theiler received some preserved specimens reportedly collected from goats, Koakoland, northern Namibia. Attempts to find live ticks and their hosts were unsuccessful. In 1971, Dürr Bezuidenhout, a veterinarian in Windhoek, received live specimens from northern Namibia. He and fellow veterinarian H. Schneider tried feeding them on various hosts. In what can be described as serendipitous he discovered the natural host. Armed with this knowledge they went walking on the game tracks used by this tick species' natural host and collected about 80 live ticks from vegetation, mainly Mopani. Subsequent forays into Koakoland have been unsuccessful, as the host has apparently been exterminated in the area. Despite numerous surveys, this tick species was never again found in South Africa.

Utilising *Diplozoon* as a sentinel organism for metal pollution

Ebrahim Hussain¹ & Annemarié Avenant-Oldewage¹

¹ Department of Zoology, University of Johannesburg, P.O. Box 524, Auckland Park, Johannesburg, 2006, South Africa. E-mail: aoldewage@uj.ac.za

Previously studies have been conducted on the use of endoparasites (acanthocephalans and cestodes) as sentinels for heavy metals. These studies revealed that endoparasites accumulate metals in concentrations far above that of their respective host. There have been no conclusive results regarding the use of ectoparasites as such sentinels. When using an endoparasite as a sentinel the respective host has to be sacrificed, this is not the case with monogenean ectoparasites which can be removed with little damage to the host. Thus the use of the *Diplozoon* spp, found on the gills of *Labeo umbratus*, as a sentinel organism for metal pollution was evaluated. Fish and parasite samples were collected from the Vaal Dam. *Labeo umbratus* was chosen as a test fish because they have a high prevalence of diplozoans and they have been shown to accumulate metals. This parasite-host combination was deemed appropriate for the biomonitoring of the Vaal Dam due to its wide distribution throughout this system. The Vaal Dam was chosen as the study site due to its vast economic importance to three of South Africa's major industrial provinces. This dam also provides drinking water to more than 10 million people within the greater Pretoria-Witwatersrand-Vereeniging area. Five different tissue types (muscle, gills, liver, kidney and spinal cord) as well as the parasites were removed from the fish for metal analysis. Tissue samples were analysed using an Inductively coupled plasma-mass spectrometry (ICP-MS) and the parasites were analysed using Total reflection X-Ray fluorescence (TXRF). This study has revealed that the *Diplozoon* species does in fact accumulate certain metals such as Fe, Pb, Cu, Ni, Cr and Zn in concentrations above those found in the fish host and ambient environment. These results illustrate the potential use of such a parasite for the biomonitoring of metal contamination within the aquatic environment.

Plant parasitic nematodes from the Bakwena Cave, South Africa

Candice Jansen van Rensburg¹ & Antoinette Swart²

¹ Department of Zoology and Entomology, University of the Free State, P.O. Box 339, Bloemfontein, 9300, South Africa. E-mail: jvrensc@ufs.ac.za

² Nematology Unit, Biosystematics Division, Agricultural Research Council-Plant Protection Research Institute, Private Bag x134, Queenswood, 0121, South Africa.

Nematodes are among, if not the, most abundant multicellular animals on earth. Worldwide plant parasites are known to infect a number of agricultural crops and can lead to great economic losses annually in crops such as maize, wheat and potatoes, to name but a few. Surveys forming part of the Bakwena cave project were carried out from January 2009 to January 2012 at Bakwena Cave, South Africa. The main aims of these nematode surveys were: 1) to contribute to the biodiversity of the Bakwena Cave and 2) to increase our current knowledge and understanding of parasitic and free living nematodes from South Africa. Nematodes were collected from seven localities, representing different habitats, which ranged from outside the cave to a pool 30m underground. Nematodes were extracted from the soil using the sieving-centrifugal-flotation method and fixed using standard techniques. Results showed that the highest diversity of plant parasites was found from the area outside the cave. Plant parasitic nematodes found associated with this locality included: *Scutellonema* spp., *Helicotylenchus* spp. and *Rotylenchus* spp. The underground pool showed the lowest diversity of plant parasitic nematodes, with *Trichodorus parorientalis*, a predominantly plant parasite being found from this locality. The remaining localities were dominated by bacteriovorous nematodes such as *Panagrolaimus* spp., *Diploscapter coronatus* and *Plectus* spp. This nematological study is the first of its type from South Africa and also contributes to the study of nematodes from cave environments worldwide.

Development of species-specific PCR, real-time PCR and LAMP for detection of *Anaplasma marginale* infections in South Africa

Zamantungwa Khumalo¹, Sibusiso M Mtshali¹ & Oriel M.M. Thekiso²

¹ National Zoological Gardens of South Africa, P.O. Box 754, Pretoria, 0001. E-mail: mantungwa1@webmail.co.za

² Parasitology Research Program, Department of Zoology and Entomology, University of the Free State, Qwaqwa campus, Private Bag X13, Phuthaditjhaba, 9866, South Africa.

Currently there is no molecular assay that has been developed to rapidly diagnose *Anaplasma marginale* infections in livestock in South Africa. Polymerase chain reaction (PCR) is an established molecular detection method which is now widely in use in the developed countries because of its specificity and sensitivity. Loop-mediated isothermal amplification (LAMP) is a novel DNA amplification technique which is also highly specific and sensitive. Furthermore, LAMP is rapid, simple and cost effective and can be easily adopted for use in resource-poor laboratories/countries. The main objective of the study was to develop DNA molecular assays for detection of *A. marginale* infections. Conventional PCR, real-time PCR and LAMP assays were successfully developed for detection of *A. marginale* infections in cattle, targeting the major surface protein 1b (MSP1b) gene. These three assays specifically amplify only *A. marginale* and do not amplify other related and co-existing pathogens including *A. centrale*, *Babesia bigemina*, *B. bovis* and *Ehrlichia ruminantium*. The assays were specific with different detection limits. We are currently using the newly developed assays for detection of *A. marginale* infections from cattle samples collected from different provinces of South Africa.

Myxosporea beyond the Arctic Circle

Alena T. Kodádková^{1,2}, Tomáš Tymi^{1,2}, Oleg Ditrich², Eva Kašparová^{3,4}, Šárka Mašová⁵, Michal Tušer^{3,6} & Ivan Fiala¹

¹ Institute of Parasitology, Biology Centre of the AS CR, v.v.i., Branišovská 31, 370 05 České Budějovice, Czech Republic. E-mail: alena.kodadkova@gmail.com

² Faculty of Science, University of South Bohemia in České Budějovice, Branišovská 31, 370 05 České Budějovice, Czech Republic.

³ Institute of Animal Physiology and Genetics AS CR, v.v.i., Rumburská 89, 277 21 Liběchov, Czech Republic.

⁴ Faculty of Science, Charles University in Prague, Albertov 6, 128 43 Prague, Czech Republic.

⁵ Faculty of Science, Masaryk University, Kotlářská 2, 611 37 Brno, Czech Republic.

⁶ Institute of Hydrobiology, Biology Center of the AS CR, v.v.i., Na Sádkách 7, 370 05 České Budějovice, Czech Republic.

Polar regions such as the Arctic Ocean are unique environments. It is the most extreme ocean with regard to the seasonality of light and its year-round existing ice cover. The Arctic Ocean is the shallowest ocean and the entire ecosystem possesses low biodiversity. In order to examine the diversity of myxozoan parasites, we dissected 234 fishes belonging to seven species (*Myoxocephalus scorpius*, *Clupea harengus*, *Mallotus villosus*, *Gymnocanthus tricuspis*, *Boreogadus saida*, *Hippoglossoides platessoides*, *Lumpenus lampretaeformis*) from Petunia Bay in Svalbard. We found eight myxosporean species: *Ceratomyxa* cf. *longispina*, *Myxidium gadi* and *Sinuolinea* sp. in *M. scorpius*, *Parvicapsula* sp. in *G. tricuspis*, *Zschokkella hildae* in *B. saida*, *Parvicapsula* sp. and *Shulmania aenigmatica* in *H. platessoides* and *Latyspora* sp. in *C. harengus*. Four taxonomically undescribed species: *Latyspora* sp., *Sinuolinea* sp. and two species of the genus *Parvicapsula* were morphologically characterised by light microscopy. As the phylogenetic position of *Z. hildae* and *M. gadi* is already known, we added new molecular data to four species from the urinary bladder and the analysis confirmed their position within the marine urinary clade according to tissue tropism. Further, two different *Parvicapsula* spp. and *Latyspora* sp. cluster within the *Parvicapsula* subclade and *S. aenigmatica* clusters within the *Zschokkella* subclade. *Shulmania aenigmatica* is the first sequenced species of the genus and we provide new detailed data about its ultrastructure. *Latyspora* sp. is the second discovered species of its genus; however, its distant relation to the type species *L. scomberomori* causes the genus *Latyspora* to be paraphyletic. The low number of discovered myxosporean species in comparison to the abundance and diversity of fish is an interesting contrast to myxosporean diversity in tropical or subtropical fishes. This work was supported by grants of the Czech Science Foundation (P505/12/G112), GAJU (04-135/2010/P), Czech Ministry of Education (CzechPolar) and European social fund (CZ.1.07/2.2.00/28.0190).

Innovative approaches to veterinary product evaluations

Dawie J. Kok¹ & Leon J. Fourie¹

¹ CLINVET INTERNATIONAL (PTY) LTD, Uitsig Road, Bainsvlei, Bloemfontein, South Africa. E-mail: Dawie.Kok@clinvet.com

Parasites that infect/infest livestock and companion animals cause production losses, loss of condition, irritation and some are zoonotic. Many parasiticides are available to the public and in the animal health industry there is a continuous race for the development and registration of new efficacious and environmentally friendly active ingredients. At least one of the reasons is that the selection pressures associated with regular treatment lead to resistance against parasiticides thus creating a necessity for new actives. Globally regulatory authorities set very high standards and strict requirements for the registration of parasiticides as effective and safe to use in target animals. At ClinVet International new actives are evaluated to determine if the intended claims can be supported or are unfounded. As a leading CRO ClinVet has to be innovative in its approach to the evaluation of new actives in order to remain on the forefront of product development and to offer clients in addition to existing models also sound new models for product evaluation. This presentation will focus on some artificial infection/infestation models with a novel approach against parasites such as *Spirocerca lupi*, *Dipylidium caninum*, *Taenia taeniaeformis*, babesiosis and ehrlichiosis, including the use of molecular techniques. The aim to use the Three Rs as guiding ethical principles for all involved in the animal health industry will also be mentioned.

Adaptive evolution in African species of *Schistosoma* blood flukes and potential problems for vaccine design

Scott P. Lawton¹

¹ *Molecular Parasitology Laboratory, School of Life Sciences, Kingston University London, KT1 2EE, Surrey, United Kingdom. E-mail: s.p.lawton@kingston.ac.uk*

Schistosomiasis is one of the most prevalent parasitic diseases globally with over 200 million people infected across 74 countries worldwide and a further 600 million at risk of infection. Vaccine development has become a priority with several tegumental associated antigenic proteins being targeted as potential targets. The tetraspanins are a family of tegumental trans-membrane proteins which have been focused on as potential vaccine targets. This is because they are expressed on the outer surface of the schistosome, directly interact with the host's immune system, and in fact, represent the proteins that most specific antibodies are raised against. However, several studies have shown that definitive hosts do not maintain complete immune memory and are susceptible to subsequent reinfection regardless of any previous infection or prototype vaccination. The current study shows that the vaccine target tetraspanin 23 (TSP 23) is hypervariable not only between species of *Schistosoma* but within species also. DNA and protein sequence analysis shows high levels of antigenic variation within the extracellular loops of TSP 23 and that they are allelic as well as undergoing positive selection with most of the mutations affecting the chemical constitution of the resultant protein. Phylogenetic reconstruction of TSP 23 shows no congruence with the true species relationships and may indicate TSP 23 to be under convergent evolution with several different species occupying the same host producing clades. These results suggest that not only species specific vaccines need to be considered but also host specific vaccines could be required. If this is the case then the validity and practicality of vaccines in schistosome control programs may need to be readdressed.

Tricky taxonomy, tantalising trees and terrifying ticks; tinkering with the molecular systematics of *Amblyomma*

Scott P. Lawton¹ & Angela J. Davies¹

¹ *Parasitology Laboratory, School of Life Sciences, Kingston University, Kingston upon Thames, Surrey, KT1 2EE, United Kingdom. E-mail: s.p.lawton@kingston.ac.uk*

The genus *Amblyomma* are ixodid ticks that are of major medical and veterinary importance not only as haemophageous endoparasites but also as vectors of blood parasites and other pathogens. Being found throughout the world, *Amblyomma* parasitise a range of vertebrate hosts from reptiles to mammals including humans. However, in spite of their relative importance the systematics of the genus *Amblyomma* remains much debated and unresolved. Historically, tick species have been identified and characterised based on morphological characteristics, which has lead to erroneous conclusions to species resurrection and interrelationships. More recently, molecular markers have been used, especially the rDNA ITS region and the mitochondrial 16s gene, not only to identify species but also to provide a robust phylogenetic framework for the systematics of the genus *Amblyomma*. However, although ITS and 16s markers are excellent for species identification and for providing inferences in population genetics and molecular epidemiology this study questions the utility of these markers in providing phylogenetic inference. Both MUSCLE and Clustal approaches of constructing DNA alignments of both ITS and 16s not only produce data sets that are poorly compared but also produce phylogenies that are poorly resolved with low nodal support. Phylogenies based on both markers do provide phylogeographical inferences, producing clades with species from the same continent together, however, the true relationships within those clades remain problematic. These results suggest that other markers with higher resolution should be used as a standard DNA “barcode” that not only provide species identification but also give true phylogenetic resolution.

Vector potential of *Amblyomma hebraeum* in the transmission of lumpy skin disease virus

Jimmy C. Lubinga¹, Eava S.M. Tuppurainen², Jacobus A.W. Coetzer¹, Wilhelm H. Stoltz¹
& Estelle H. Venter¹

¹ Department of Veterinary Tropical Diseases, Faculty of Veterinary Science, University of Pretoria, Private Bag X04, Onderstepoort, 0110, South Africa. E-mail: jimlubinga@yahoo.com

² Institute for Animal Health, Ash Road, Pirbright, Surrey, GU24 0NF, UK

Lumpy skin disease is an economically important disease of cattle, caused by lumpy skin disease virus (LSDV), a *Capripoxvirus* within the family *Poxviridae*. It is characterised by fever, circumscribed skin lesions and enlarged lymph nodes. The transmission of the virus by *Aedes aegypti* -mosquitoes and *Stomoxys calcitrans* (stable fly) has previously been demonstrated. Mechanical/intrastadial transmission by *Rhipicephalus appendiculatus* male ticks was recently reported by the authors. The vector potential of *Amblyomma hebraeum* by mechanical, transstadial and transovarial routes was investigated in this study. Laboratory-reared *A. hebraeum* nymphal and adult ticks were fed on viraemic cattle (donors) that were artificially infected with LSDV. In order to test for mechanical transmission, male ticks were only partially fed on the donor animals and then transferred to uninfected recipient animals. Females and nymphs were fed to repletion on the donor animals. Females were allowed to oviposit and their eggs to hatch while nymphs were allowed to moult. The emergent larvae and adults were similarly placed on respective recipient animals to test for transovarial and transstadial transmission of the virus. Successful transmission of LSDV was determined in recipient animals by monitoring the development of clinical signs, testing of blood samples for LSDV by real-time PCR and virus isolation and the detection of antibodies using a serum neutralisation test. Confirmatory testing of ticks (adults and larvae) used in the transmission study, for the presence of LSDV by real-time PCR and virus isolation was also performed. The results demonstrated, for the first time, mechanical, transstadial and transovarial transmission of LSDV by *A. hebraeum*. These findings implicate *A. hebraeum* as a possible maintenance host in the epidemiology of lumpy skin disease.

Effects of tick abundance and captivity on body condition measures in sengis

Heike Lutermann¹, Katarina Medger¹ & Nigel C. Bennett¹

¹ Department of Zoology and Entomology, University of Pretoria, Private Bag X20, Hatfield, 0028, South Africa. E-mail: hlutermann@zoology.up.ac.za

Parasites can greatly affect the amount of resources available to their host. In accordance with such resource depletion, decreases in body condition and body mass loss are frequently observed in infested individuals. Parasite invasion is often accompanied by concomitant increases of glucocorticoids (GCs, e.g. cortisol). Due to the detrimental effects of long-term GC increases, elevated GC levels may not be sustained during chronic infestation. Parasitised individuals may, however, exhibit an impaired ability to cope with additional stressors. We tested these hypotheses in eastern rock sengis (*Elephantulus myurus*) that harbour large tick burdens throughout the year. For 109 sengis captured from September 2007 to August 2008 in Goro Game Reserve in the Limpopo Province we measured the effects of tick burden and captivity stress on body condition, cortisol-levels and body mass loss. Body condition was significantly greater during the breeding season (August-March) compared to the non-breeding season (April-July) and better in adults compared to juveniles. Contrary to our predictions body condition improved significantly with larval burdens of *Rhipicephalus* near *warburtoni*. Cortisol levels were significantly increased during breeding season and in adults vs. juveniles but not affected by tick burdens. Similarly, body mass loss was greater during the breeding compared to the non-breeding season and increased with cortisol-level. For pregnant females only body mass loss was significantly correlated with larval tick abundance. Our results suggest minor detrimental effects of tick burdens possibly due to a down-regulated response as a result of the chronic nature of the infestation. However, under the additional stressors captivity and gravity costs of tick parasitism became apparent suggesting that hosts may successfully employ compensatory mechanisms to cope with the ticks. The positive correlation between body condition and tick abundance may indicate a tick preference for hosts of high nutritional value.

***Ergasilus* sp. from the skin of freshwater fish: An epidemic?**

Wilmien J. Luus-Powell¹, Annemarié Avenant-Oldewage³, Willem J. Smit¹, Hendrik E. Hattingh¹, Lourens J.C. Erasmus², Modibe E. Raphahlelo¹, Tshepiso P. Ramalepe¹, M. Eunice Mogashoa¹, N. Martin Chabalala¹ & Kgokong Mazwi¹.

¹ Department of Biodiversity, University of Limpopo, Private Bag X1106, Sovenga, 0727, South Africa. E-mail: Wilmien.Powell@ul.ac.za

² Department of Physiology and Environmental Health, University of Limpopo, Private Bag X1106, Sovenga, 0727, South Africa

³ Department of Zoology, University of Johannesburg, P.O. Box 524, Auckland Park, Johannesburg, 2006, South Africa.

Ergasilus Nordmann, 1832 is the largest genus (with more than 180 nominal species) of the family Ergasilidae (Copepoda). The majority of the *Ergasilus* spp. is recorded from freshwater fishes but some records of hosts from marine and brackish environments are found. The adult females are usually attached to the gills of hosts although there are two records from the skin and base of pectoral fins. We reported a small *Ergasilus* sp. from the skin and fins of *Oreochromis mossambicus* from Flag Boshielo Dam and *Labeo capensis* from the Vaal Dam in 2010. Since then, this *Ergasilus* sp. was found on several fish species from different localities from the Limpopo and Olifants River Systems. Parasites were fixed and preserved in 70% ethanol. *Ergasilus* sp. was recorded from the following hosts (with mean intensity indicated after number of hosts) from the Olifants River System: *Oreochromis mossambicus* (n=3; 3.7), *Tilapia rendalli* (n=18; 36.5), *Labeo rosae* (n=55; 6.2), *Hypophthalmichthys molitrix* (n=52; 66.1), *Synodontis zambezensis* (n=46; 28.5), *Marcusenius macrolepidotus* (n=9; 3.0), *Clarias gariepinus* (n=2; 2.0) from Flag Boshielo Dam; *Schilbe intermedius* (n=60; 1.0) from Phalaborwa Barrage; *O. mossambicus* (n=16; 1.25) from Loskop Dam (Mpumalanga). From the Limpopo River System: *Labeobarbus marequensis* (n=19; 1.0) from Nandoni Dam and *M. macrolepidotus* (n=10; 1.0) from Nwanedi-Luphephe Dams. Although it is mostly found on the skin and fins of hosts, occasionally it loosely attaches on the gills. Since 2010, the mean intensity values of *Ergasilus* sp. increased for all fish species and this new copepod species is now recorded from several river systems and hosts from South Africa.

Life cycle of *Lamproglena clariae* under laboratory conditions

Grace N. Madanire-Moyo¹ & Annemarié Avenant-Oldewage¹

¹ Department of Zoology, University of Johannesburg, P.O. Box 524, Auckland Park, Johannesburg, 2006, South Africa. E-mail: gmoyo@uj.ac.za

Lamproglena clariae Fryer, 1956 is endemic to Africa and attaches to gill filaments of freshwater fish of the family Clariidae. The adult stage of this parasite has been extensively studied and described and a brief description of the nauplius stages of this parasite has previously been recorded. The only species in this genus whose life cycle has been described is *L. chinensis*. Literature provides detailed and comprehensive findings on the life cycle of *Lernaea cyprinacea*, a parasite belonging to a different genus of the same family of Lernaeidae. The current study aimed at determining the number of life stages of *L. clariae* and further studying and recording their morphology. Adult specimens of *L. clariae* were collected from the gills of fish. Egg sacs were collected and maintained in tap water to allow the larvae to hatch. After the third naupliar stage the larvae were transferred to suitable hosts in aquaria in the laboratory. Fish were killed at different intervals, various larval stages of the parasites recovered and preserved in 70% ethanol. Preserved specimens were cleared in 90% lactic acid, mounted and drawn with the aid of a Zeiss light microscope equipped with digital imaging software. Three nauplii and four copepodite stages were observed. Nauplius stages are translucent, elliptical bodies filled with a mass of yolk, which is reduced as the nauplius develops. Copepodite stage 1 develops 14-21 days after hatching, and in the absence of a host fish, parasite larvae die before reaching stage II. Peristaltic movement of the gut was observed to commence with the emergence of Stage I. Significant morphological changes in copepodites with passage from one stage to the next are expressed mainly by increase in the number of free abdominal segments and appendages, increased segmentation of the appendages and in the general increase in body length.

Morphological studies on some African fish nematodes

Šárka Mašová¹, Vlastimil Baruš¹, František Moravec², Božena Koubková¹ & Iveta Hodová¹

¹ Department of Botany and Zoology, Faculty of Science, Masaryk University, Kotlarska 2, 611 37 Brno, Czech Republic. E-mail: masova@sci.muni.cz

² Institute of Parasitology, Biology Centre, Academy of Sciences of the Czech Republic, Branisovská 31, 370 05, Ceske Budejovice, Czech Republic.

During parasitological research carried out in Senegal and Kenya between 2005 and 2009, the following species of fish nematodes were recorded among other parasites: *Procamallanus (Procamallanus) laeviconchus* (Wedl, 1862), *P. (Spirocamallanus) spiralis* (Baylis, 1923) and *Procamallanus* spp. (Camallanidae); *Cithariniella citharini* Khalil, 1964, *C. khalili* Petter, Vassiliadès et Troncy, 1972 and *C. gonzalesi* Van Waerebeke, Chabaud, Bain et Georges, 1988 (Pharyngodonidae); *Multicaecum heterotis* Petter, Vassiliadès et Marchand, 1979 (Ascarididae) and *Mexiconema africanum* Moravec, Jirku, Charo-Karisa et Mašová, 2009 (Daniconematidae). Specimens were recovered mainly from stomachs and intestines of catfishes belonging to Mochokidae, Clariidae, partly to Bagridae (Siluriformes) and Citharinidae (Characiformes), and one fish of the family Arapaimidae (Osteoglossiformes). Light microscopy (LM) was used for morphological studies of important differentiation features of nematodes. For structures poorly recognisable by LM, scanning electron microscopy (SEM) and environmental scanning electron microscopy (ESEM) were used. Nematodes are characterised mainly by the form of mouth opening, position of cephalic papillae and amphids, form of deirids, presence/absence of vulval lips, arrangement, form and number of caudal papillae on tails, structure of eggs and the type of definitive hosts e.g. *C. khalili* has chitinoid ribbed flaps and eggs with filaments; *M. heterotis* possesses denticular ridges on lips; *M. africanum* has fine transverse striation of cuticle visible only by SEM; *Procamallanus* spp. are mutually recognisable by the mouth opening with or without the oral flange and by the number and shape of projections on female tail tips. This study was supported by the Department of Botany and Zoology, Faculty of Science, Masaryk University and by the Czech Science Foundation (No. P505/12/G112).

Nutritional implications of *Giardia lamblia* infections among new-born children in northern Limpopo, South Africa

Dikeledi E. Mathatha¹, Phindile Ntekele¹, Nesamvuni Cebissa¹, Rebecca Dillingham², Richard L. Guerrant², Pascal O. Bessong¹ & Samie Amidou¹

¹ Department of Microbiology, University of Venda, Private Bag X5050 Thohoyandou 0950, Limpopo, South Africa. E-mail: samieamidou@yahoo.com

² Centre for Global Health, University of Virginia, Virginia, USA

Giardia lamblia is one of the most common intestinal parasites in humans. Although people of all ages harbour these organisms, infants and children are more often infected than adults. However, the prevalence of *Giardia* and its effect on child growth is poorly documented in South Africa. In the present study, stool samples were collected from children participating in the Mal-Ed cohort on a monthly basis from birth up to the age of 12 months with anthropometric measurements and nutrition assessment conducted monthly by field workers. The stool samples were tested for *Giardia* using microscopy and ELISA. Polymerase chain reaction (PCR) amplification of the triose phosphate isomerase gene was used for genotyping. A total of 1400 stool samples were tested from 161 participants, with number of samples varying from 1 to 12 per participant. From the 161 participants 53.4% were female. From all the samples, 40 (2.9%) were positive for *Giardia* by ELISA and Microscopic analysis. However, from the 160 children followed, 28 had at least one infection making it an incidence of 17.5%. Of all the children, 20% of the boys were infected compared to 15% of the girls. Although children with low birth weight had higher rates of infection, the difference was not statistically significant. Children that were stunted, underweight or wasted were more infected compared to those that were not, although the differences were not statistically significant. The genotyping results indicated that most of the infections were due to Assemblage B (42%) while 31.4% had Assemblage A with 25% having mixed infections. *Giardia* poses a significant health threat to children living in rural areas, and may lead to diarrhoea, malnutrition and growth retardation. Therefore, public health education and proper water treatment and sanitation measures are necessary to help reduce the prevalence and spread of *Giardia* among children.

Evolution and diversification of cichlid parasites

Monika Mendlova¹, Yves Desdevises^{2,3}, Kristina Civanova¹ & Andrea V. Simkova¹

¹ Department of Botany and Zoology, Faculty of Science, Masaryk University, Kotlarska 2, Brno, 611 37, Czech Republic. E-mail: mendlova@sci.muni.cz

² UPMC Univ Paris 06, UMR 7232, BIOM, Observatoire Oceanologique, F-66650, Banyuls/Mer, France.

³ CNRS, UMR 7232, BIOM, Observatoire Oceanologique, F-66650, Banyuls/Mer, France.

African freshwater fish of the family Cichlidae are parasitised by five genera of monogeneans belonging to the Dactylogyridea (*Cichlidogyrus*, *Scutogyrus*, *Onchobdella*, *Enterogyrus* and *Urogyrus*). *Cichlidogyrus* is the most diverse genus of monogeneans parasitising cichlid fish distributed among a wide range of cichlid species. *Scutogyrus* species are restricted to mouthbrooders of the genus *Sarotherodon* and *Oreochromis*. The objectives of this study were to perform phylogenetic analyses of monogeneans parasitising cichlid fish in West Africa based on ribosomal DNA sequences, to investigate phylogenetic relationships within West African cichlid fish based on mitochondrial cytochrome b sequences and to assess host-parasite cophylogenetic history and reveal the presence of host-parasite cospeciation. All phylogenetic analyses showed the monophyletic origin of the *Cichlidogyrus/Scutogyrus* group, and suggested that *Cichlidogyrus* is polyphyletic and *Scutogyrus* is monophyletic. The phylogeny of Cichlidae supported the separation of mouthbrooders and substrate-brooders and is consistent with the hypothesis that the mouthbrooding behavior of *Oreochromis* and *Sarotherodon* evolved from substrate-brooding behaviour. The cophylogenetic analyses indicated a significant fit between host and parasite phylogenetic trees using distance-based methods, but no significant co-speciation signal was found using tree-based methods, which suggests the presence of parasite duplications and host switches on related host species. This research was supported by Czech Science Foundation No. P505/12/G112.

Plant parasitic nematodes from the Seekoeivlei Nature Reserve, Memel, South Africa

Ayesha Mobarra¹ & Candice Jansen van Rensburg¹

¹ Department of Zoology and Entomology, University of the Free State, P.O. Box 339, Bloemfontein, 9300, South Africa. E-mail: mobaraa@ufs.ac.za

The Seekoeivlei Nature Reserve is situated in the northeastern corner of the Free State Province near the town of Memel. The wetland is the largest on the southern African Highveld and was declared a Ramsar Site in 1997. A survey was carried out over a period of eight months, from October 2011 to May 2012. This included three sampling occasions that incorporated a pre-liminary study, a winter and a summer occasion. The aim of this study was to: 1) identify plant parasitic as well as free-living nematodes collected to genus level; 2) to taxonomically describe new species from the different habitats within the system, and 3) to determine whether plant parasitic nematodes can be used as bio-indicators in assessing the health of the system. Nematodes were extracted from soil samples using the sieving-centrifugation-flotation method. All the nematodes were fixed using standard techniques for light and scanning electron microscopy. Nematodes were examined under a compound light microscope and identified up to genus level and classified according to their feeding types. Results indicated that plant-parasitic nematodes were more abundant during the winter months when water levels were relatively low in comparison to the summer months. Genera of plant parasitic nematodes found included amongst others: *Rotylenchulus*, *Helicotylenchus*, *Ditylenchus*, *Tylenchorhynchus* and *Criconema*.

Molecular detection of zoonotic tick-borne pathogens in the different provinces of South Africa

Khethiwe Mtshali¹, Chihiro Sugimoto² & Oriel M.M. Thekiso¹

¹ Department of Zoology and Entomology, University of the Free State – Qwaqwa Campus, Private Bag X13, Phuthaditjhaba, 9866, South Africa. E-mail: kmtshali@yahoo.com

² Research Center for Zoonosis Control, Hokkaido University, Sapporo, 060-0818, Japan

Ticks and tick-borne diseases are a burden in the livestock industry where they decrease productivity and compromise food security causing a high socioeconomic impact on agroexporting nations each year. Not only do the ticks act as agricultural pests but they have the capacity to spread diseases of public health concern, many a people are not aware of. It is therefore the aim of this study to conduct a retrospective survey of tick-borne zoonotic pathogens which include among others *Coxiella burnetii*, *Rickettsia africae*, *Ehrlichia*, *Anaplasma phagocytophilum*, *Borrelia burgdorferi* sensu lato, as well as other common tick-borne pathogens. Preliminary results indicate that tick species identified in the collection include *Amblyomma hebraeum*, *Rhipicephalus* spp., *Haemaphysalis elliptica* and *Hyalomma* spp. The overall prevalence of infection of ticks with *E. ruminantium* in the five sampled provinces was 83% for sheep; 85% for goats; and 48% for cattle ticks. *Rhipicephalus africae*, sheep for 75%; goats for 27%; cattle for 15 %; and 20% of the tick samples collected from the vegetation. Other *Rickettsia* species isolated from sheep and cattle ticks gave an overall percentage of 2.8% and 20% respectively. *Coxiella burnetii* in sheep was 75%, goats 100%, cattle 75%, dogs 40%, and in 100% of the tick samples collected from the vegetation. An overall percentage of 17% *E. canis* was detected in the screened dog tick samples. None of the pooled samples screened for *A. phagocytophilum* (n=87) and *B. burgdorferi* s. l. (n=40) across all sampled animals were positive for the bacteria. PCR positive results were sequenced to validate the findings.

A comparison between branchiuran reproductive organs and sperm transfer methods

Louelle Neethling¹ & Annemarié Avenant-Oldewage¹

¹ Department of Zoology, University of Johannesburg, PO Box 524, Auckland Park, Johannesburg, 2006, South Africa. E-mail: aoldewage@uj.ac.za

In the last 50 years, some attention has been paid to the morphology of the reproductive system and the method of sperm transfer in certain branchiurans, both to fill the gap in knowledge as well as a means to understand the life cycle and to control these parasites. The internal and external reproductive structures of *Dolops ranarum* as well as *Argulus japonicus* and the method of sperm transfer is known. It is believed that the difference in body form of *C. australis* to *A. japonicus* and *D. ranarum* will affect sperm transfer. A study was thus conducted on *Chonopeltis australis* to describe the internal and external reproductive structures. Male and female specimens were studied via whole mount analysis using light and scanning electron microscopy as well as standard histological techniques. Micrographs were obtained. The micrographs of the histological sections were reconstructed using digital 3D techniques. The images created were then compared to those already known for *Argulus* and *Dolops*. A comparison with other Branchiura to determine similarities in structures could elucidate the mechanism of sperm transfer. In both *D. ranarum* and *A. japonicus*, their bodies are short and squat and their legs are more or less equidistant. The male specimens of *D. ranarum* bear external reproductive structures limited to a small peg, whereas the male specimens of *A. japonicus* display elaborate peg and socket systems that assist with spermatophore transfer. In *Chonopeltis* the bodies are long and narrow, but their legs are further apart from each other. The male specimens also possess elaborate peg and socket systems. This similarity in secondary reproductive structures suggests a similarity in the sperm transfer mechanism.

Tiny worms from a mighty continent: uncovered diversity and new phylogenetic lineages of African monogeneans

Iva Přikrylová¹, Maarten P.M. Vanhove^{2,3}, Steven B. Janssens⁴, Paul A. Billeter⁵ & Tine Huyse²

¹ Department of Botany and Zoology, Faculty of Science, Masaryk University, Kotlářská 2, 611 37 Brno, Czech Republic. E-mail: ivaprik@sci.muni.cz

² Laboratory of Biodiversity and Evolutionary Genomics, Department of Biology, KU Leuven, Ch. Debériotstraat 32, B-3000 Leuven, Belgium.

³ Department of African Zoology, Royal Museum for Central Africa, Leuvensesteenweg 13, B-3080 Tervuren, Belgium.

⁴ Laboratory of Plant Systematics, Department of Biology, KU Leuven, Kasteelpark Arenberg 31, B-3001 Leuven, Belgium.

⁵ Department of Biological and Physical Sciences, College of Southern Maryland, P.O. Box 910, LaPlata, Maryland 20646-0910, USA.

The phylogenetic relationships between gyrodactylid monogeneans of African freshwater fishes and other representatives of Gyrodactylidae, covering a wide range of species and genera from both freshwater and marine systems were investigated. New complete SSU RNA sequences of 18 gyrodactylid species of eight genera together with ITS rRNA gene sequences of eight species representing seven genera were generated and complemented with GenBank sequences. The maximum likelihood and Bayesian analyses pointed to a paraphyletic nature of African *Gyrodactylus* species. They formed well-supported clades possibly indicating speciation within host taxa: 1) parasites of cichlids (Cichlidae); 2) parasites of catfishes (Siluriformes), consisting of a lineage infecting mochokids and one infecting clariids. *Macrogryrodactylus* spp. firmly clustered into a monophyletic group. The phylogenetic position of *Diplogyrodactylus* and *Afrogyrodactylus* was not well resolved. We found that *Swingleus* and *Fundulotrema* are very closely related and clearly cluster within *Gyrodactylus*. This supports earlier claims as to the paraphyly of *Gyrodactylus* and necessitates a revision of *Swingleus* and *Fundulotrema*. Furthermore, our analyses demonstrated the systematic value of morphological affinities in a few cases (*Gyrodactyloides* and *Laminiscus*; *Gyrodactylus* spp. of mainly oreochromine cichlids; *Gyrodactylus thysi* and a new congener; gyrodactylids from African characiform hosts). Molecular dating estimates confirmed a relatively young, certainly post-Gondwanan, origin of current gyrodactylid diversity.

Enhanced taxonomy, is DNA the answer? Southern Africa ergasilid phylogeny

Ruaan Schlebusch¹ & Liesl L. van As¹

¹ Department of Zoology and Entomology, University of the Free State, P.O. Box 339, Bloemfontein, 9300, South Africa. E-mail: Schlebuschr@ufs.ac.za

The exactness of species descriptions in taxonomy, taking only morphology into account, has long been debated over. Parasitic crustacean systematics, in particular the classes Copepoda and Branchiura of Africa, are often perplexing and solely based on morphological characteristics. Worldwide no one taxon for any certain group is agreed upon, causing pointless confusion. Morphological differentiation between the orders in the classes Copepoda and Branchiura are difficult and the differences between species mostly subtle. A molecular approach appears to be the answer to more accurate identification, albeit a more rapid process. The availability of molecular information of the class Branchiura would ease the process of molecular work being done on the classes, but the copepods and the branchiurans are not as closely related and therefore the branchiurans cannot be used in the rooting of a phylogenetic tree. The lack of molecular information in both classes leaves a gaping hole in the understanding of crustacean systematics and ecological importance. Due to work done in China (Song, Wang, Yao, Gao & Nie, 2007) on the genus *Ergasilus* (Family Ergasilidae) molecular studies on this particular genus in Africa can now readily be done. Although the family Ergasilidae is not a great threat to the fish populations of Africa, the availability of samples and information on morphological traits makes this family a good starting point in the use of molecular work on the parasitic crustaceans of Africa. Thus the phylogeny of southern African ergasilids based on the 18S and 28S rDNA sequences with specifically designed primers (used in the Chinese study) coupled with the morphological characteristics is therefore the focus of this study. The family Lernaevidae (using the genus *Lernaea*), closely related to the genus *Ergasilus*, is to be used as an out-group.

Biodiversity and ecology of fish parasitic gnathiid isopods and fish blood protozoans from Lizard Island, Great Barrier Reef, Australia

Nico J. Smit¹, Alexandra S. Grutter² & Angela J. Davies³

¹ School of Biological Sciences, Potchefstroom Campus, North West University, Private Bag X6001, Potchefstroom, 2520, South Africa. E-mail nico.smit@nwu.ac.za

² School of Biological Sciences, University of Queensland, Brisbane QLD 4072, Australia.

³ School of Life Sciences, Kingston University, Kingston upon Thames, Surrey, KT1 2EE, UK.

Coral reefs are marine ecosystems with among the greatest species diversity in the world. The Great Barrier Reef (GBR) is one of the richest and most complex of these systems. Gnathiid isopods are abundant on coral reefs and their juveniles (larvae) are common ectoparasites, where they feed on the blood and tissue fluids of teleost and elasmobranch fishes. When not feeding on fishes, gnathiids are cryptic and widely distributed, especially among coral reef habitats living in cavities, crevices, sponges, coral rubble, or sediment. Twelve genera are recognised and among these are almost 200 described species, the majority in the genus *Gnathia*. Gnathiids have a biphasic life cycle with three parasitic larval stages; the latter are also known as pranizae when engorged with fish blood and tissue fluids and zupheae when unfed. Species descriptions rely on the morphology of adult males. When juveniles or females are found, their identification can be difficult, a problem that will be discussed in this presentation. The juveniles of gnathiids are also known to be the main food source of the coral reef cleaner fish *Labroides dimidiatus*. These small ectoparasites have been found feeding on 70% of 56 species of reef fish surveyed on the Great Barrier Reef. This paper focuses on the research done during the past 10 years at Lizard Island, Great Barrier Reef, Australia and will report on the discovery of new gnathiid species from teleost and elasmobranch hosts, host parasite interactions, laboratory elucidated life cycles, the effect of feeding in aquaria and in the wild, as well as the role of gnathiids as vectors of fish blood protozoans in the tropics.

Acanthocephalans of Iran, a review with new records

Sareh Tavakol^{1,2}, Ali Halajian¹, Omar Amin³ & Wilmien Luus-Powell¹

¹ Department of Biodiversity, University of Limpopo, Private Bag X1106, Sovenga, 0727, South Africa. E-mail: ali_hal572002@yahoo.com

² Islamic Azad University, Tonekabon Branch, Tonekabon, Iran

³ Institute of Parasitic Diseases, 11445 E. Via Linda, #2-419, Scottsdale, Arizona, 85259, USA.

Acanthocephala is a cosmopolitan phylum of parasitic helminths that can infect a wide range of hosts in their life cycles, from crustaceans to vertebrates. In Iran, acanthocephalans have been reported from different animals including fishes, birds, rodents and carnivores with a small number of human infections reported. To date, the fauna of acanthocephalans in Iran is represented by 29 species, which include 21 genera, from 12 families. The highest diversity of acanthocephalans has been reported from fishes (with 13 species from 9 genera and 7 families) followed by birds with 10 species (8 genera, 5 families), carnivores with five species (5 genera, 3 families), rodents with one species (1 genus, 1 family) and one species (1 genus, 1 family) from humans. Many potential hosts from Iran have not been investigated for possible infection with thorny-headed worms. In this review several other available hosts were studied to add to the list of fauna from Iran. All acanthocephalans were fixed and preserved in 70% ethanol. Several fish species, especially from the Caspian Sea and adjoining rivers, the Caspian seal (*Pusa caspica*), 48 species of birds and two species of hedgehogs (*Haemiechinus auritus*, *Erinaceus concolor*) were studied for possible acanthocephalan infection. *Centrorhynchus spinosus* (from Tawny Owl), *Nephridiacanthus major* (from long-eared hedgehog and Eastern European hedgehog), *Plagiorhynchus (Prosthorhynchus) nicobarensis* (from Common Starling), *Sphaerostris picae* (from Magpie, Crow and Rook) were identified as new records for Iranian fauna and *Plagiorhynchus (Prosthorhynchus) cylindraceus* (Blackbird) as new host record. In the case of *Corynosoma*, *Sphaerostris* and *Nephridiacanthus*, histopathology and ultrastructural studies are included in this review.

Life cycles of haemogregarines (Apicomplexa: Adeleorina) infecting *Pseudocordylus* spp. and their possible definitive hosts from the Free State highlands

Johann van As¹, Nico J. Smit², Angela J. Davies^{2,3} & Neil J.L. Heideman⁴

¹ Department of Zoology and Entomology, University of the Free State, Qwaqwa campus, Private Bag X13, Phuthaditjaba, 9886, South Africa. E-mail: vanasj@qwa.ufs.ac.za

² School of Biological Sciences, Potchefstroom Campus, North West University, Private Bag X6001, Potchefstroom, 2520, South Africa.

³ School of Life Sciences, Kingston University, Kingston upon Thames, Surrey, KT1 2EE, United Kingdom

⁴ Office of the Dean, Faculty of Natural & Agricultural Sciences, University of the Free State, P.O Box 339, Bloemfontein, 9300, South Africa

The study of blood parasites of reptiles is a relatively new and unexplored field of research in South Africa. The object of this paper is to give an overview of two new *Hepatozoon* species of high-altitude cordylid lizards, *Pseudocordylus melanotus* and *P. subviridis*, and to show the elucidated life cycle stages in infected lizard tissues as well as in their possible definitive host vectors. Lizards were captured at various altitudinal gradients on the Sentinel Trail area at the top of the Tugela Falls and Namahali Pass, and at the top of Platberg, near Harrismith. A rich diversity of un-described infections, likely of the genus *Hepatozoon*, was found in the blood of *P. melanotus* and *P. subviridis* from the two disjunct study sites, mostly accompanied by other infections including *Sauroplasma*, filarial nematodes and various forms of saurian malaria. The life cycle stages of the presumptive *Hepatozoon* spp. in the internal organs of the lizards as well as in mosquitoes were elucidated by means of stained squashes. Merogonic stages occurred in smears of lizard tissues and haemogregarine gamonts were observed with digested blood in the gut of squashed mites. However, culicid mosquitoes, [*Culex (Afroculex) lineata*] appeared the more likely vector and they were collected at night feeding on infected lizards. Mosquito squashes revealed early sporogonic stages including oocysts, sporocysts and sporozoites. Experimental transmission studies with laboratory bred *Culex* and *Aedes* species revealed ingested gamonts, but no further developmental stages were observed in these invertebrates. Complete life cycles of these new *Hepatozoon* species are presented in this paper.

The history of *Lernaea* with emphasis on *L. cyprinacea*

Liesl L. van As¹

¹ Department of Zoology and Entomology, University of the Free State, P.O. Box 339, Bloemfontein, 9300, South Africa. E-mail: vanasll@ufs.ac.za

The name Carl Linnaeus is known to all of us, but what is not known is the fact that the genus *Lernaea* Linnaeus, 1758 and the type species *L. cyprinacea* is amongst the oldest of the parasitic copepods known to science. Up until the 1920's only 17 species were described, 53% (9 spp) from North America, a mere 6% (1 spp) from South America, 24% (4 spp) were known from Africa and 17% (3 spp) from Europe. The absence of information from Asian waters was because only a few freshwater species have been examined. More than 40 species of the genus have since been described. Severe outbreaks of *L. cyprinacea*, which is now a cosmopolitan species, were reported, especially over the last few years. *Lernaea cyprinacea* was first recorded in Africa in the early 1960s and introduced to southern Africa twenty years later and have since been found in the Limpopo, Olifants, Orange, and Vaal River Systems. In Africa *L. cyprinacea* have been recorded from the following fish species: *Oreochromis aureus*, *O. mossambicus*, *O. placidus*, *Labeo altivelis*, *L. capensis*, *L. congora*, *L. rosae*, *L. ruddi*, *L. umbratus*, *Labeobarbus kimberlyensis*, *Barbus marequensis* and *Tilapia rendalii*.

During fish parasitological surveys in Bloemhof Dam, we collected *L. cyprinacea* from *Labeo capensis*, *Labeobarbus aeneus* (highest infestation), *Cyprinus carpio*, and *Ctenopharyngodon idella*. In the case of *L. cyprinacea* the different developmental stages are found on separate hosts, but we collected copepodites and adult worms from the same host. Numerous epibionts have been found associated with *Lernaea* species. In the present study suctorians were encountered, which has never been recorded before. More astonishing is the fact that it was found not only on the adult anchor worms, but also on the copepodites.

Tick resistance status of *Rhipicephalus (Boophilus) decoloratus* against chemical control in the KwaZulu-natal and Eastern Cape Provinces

Ellie M.S.P. van Dalen¹ & Christa du Rand¹

¹ *Pesticide Resistance Testing Facility, Department of Zoology and Entomology, University of the Free State, P.O. Box 339, Bloemfontein, 9300, South Africa. E-mail: vdalenem@ufs.ac.za*

Blue ticks parasitising livestock in South Africa are the cause of great financial losses to stock producers due to their direct feeding activities and ability to act as vectors for the transmission of diseases. To restrict these losses tick infestations are mainly controlled by the use of acaricides especially in areas where the climate is favorable for tick survival. Intensive use of these acaricides leads to the development of tick resistance against these chemical control strategies causing an even greater financial impact on cattle farming. A nation-wide tick resistance survey conducted on blue ticks from 1998 to 2001 showed at least one population of 200 tested to have resistant individuals to all three acaricide groups available to control ticks. More frequent treatments were also associated with higher levels of resistance. Since then more cases of resistance against all three acaricides were detected on farms in the KwaZulu-Natal and Eastern Cape Provinces from samples sent in to our facility for resistance testing. In this study the current status of tick resistance in KwaZulu-Natal and Eastern Cape Provinces is reviewed by comparing data from the previous national survey to resistance information acquired since then to determine by which measure tick resistance in these areas deteriorated. In both provinces a dramatic increase of resistance against especially synthetic pyrethroids and amidines were detected. Limited knowledge of resistance development and contradictorily information received from various sources by the producers seems to be the main culprit for the lack of effective tick control.

Poster presentations:

The remarkable nematode of the genus *Subulura* molin, 1860 parasitising

Vlastimil Baruš¹, Šárka Mašová¹, Božena Koubková¹ & Jiljí Sitko²

¹ Department of Botany and Zoology, Faculty of Science, Masaryk University, Kotlarska 2, 611 37 Brno, Czech Republic. E-mail: masova@sci.muni.cz

² Moravian Ornithological Station, Comenius Museum, Horní náměstí 1, 751 52 Prerov, Czech Republic.

The study of nematodes collected from the intestine of a Eurasian scops owl (*Otus scops* L.), found in April 2011 near Prerov in the Czech Republic after a car crash, has recovered the specimens of a rare genus *Subulura* Molin, 1860. Only two works about helminthofauna of *O. scops* have been done until now and only one work reports the record of *Subulura* spp. nematodes, however without morphometric data and species determination. Morphology of the cephalic end with hexagonal mouth opening, lateral cervical allae, inconspicuous vulva and caudal end with mucron in females, and ten pairs of caudal papillae (three pre-, two para- and five post-cloacal) in males is described and documented. Another observed feature is the topography of three pairs of papillae near the end of the tail with two phasmids. The presence of a single papilla on the upper lip of the cloaca is described for the first time in the *Subulura* genus. Two unequal spicules are alated. The alae ends approximately 70 µm from the acerate top of spicule. Only one species, *S. subulata* (Rudolphi, 1819) from the host *Caprimulgus europaeus* L., was reported in the Czech Republic. On the basis of the morphometric features our specimens belong to the group of species from the genus *Subulura*, whose males have markedly unequal spicule lengths. It differs from the most similar morphospecies *S. glaucidii* (López-Neyra, 1945) from *Glaucidium passerinum* L. in body length, tail length, spicule length, number of caudal papillae and the presence of a single cloacal lip papilla in males, egg size, ratio of the distance between the anterior end of the body and vulva, and the total body length (in %) in females. These differential features are strong enough to consider it clearly as a new species. This study was supported by the Department of Botany and Zoology, Faculty of Science, Masaryk University and by the Czech Science Foundation (No. P505/12/G112)

Evaluation of radiation sensitivity of *Glossina brevipalpis* and *Glossina austeni* (Diptera, Glossinidae)

Chantel J. de Beer¹ & Gert J. Venter¹

¹ Parasites, Vectors and Vector-borne Diseases, Agricultural Research Council-Onderstepoort Veterinary Institute, Private Bag X5, Onderstepoort, 0110, South Africa. E-mail: DeBeerC@arc.agric.za

Tsetse eradication is assuming increasing importance within Africa as it has become evident that the tsetse and trypanosomosis is a contributing factor to perpetuating rural poverty. Therefore, the adoption of an area-wide approach for integrated pest management where conventional methods are used in combination with the Sterile Insect Technique (SIT) to eliminate tsetse can have a major impact on socio-economic development by increasing land available for agricultural exploitation and increase livestock development. In north-eastern KwaZulu-Natal, *Glossina brevipalpis* and *G. austeni* preferring densely vegetated habitats, are potential candidates for eradication using SIT. Colonised males of both species were irradiated at doses of 40, 80, 100, 120 and 140 Gy, using a Caesium Gammacell delivering a dose rate of 0.69 Gy/min, mated with females and fecundity and survival determined. Dissection of females, at the end of the experiment after 60 days, showed that the insemination rate in both species exceeded 98%, thus indicating that radiation did not affect the insemination ability of the males. A significant negative linear correlation found between dose and fecundity for *G. brevipalpis* ($R^2 = 0.7$) and *G. austeni* ($R^2 = 0.8$) indicated fecundity to be dose depended. An irradiation dose of 40 Gy for *G. brevipalpis* and 80 Gy for *G. austeni* induced 98% sterility. Although no mortalities were observed immediately after irradiation preliminary results indicate that increases in the irradiation dose can lead to a decrease in survival of both species. The results show that irradiation can successfully be used to sterilise males of both species, and that the dose in *Otus scops* (Strigiformes) needed to achieve this did not have any significant negative effect on the survival and mating capabilities of the colonised flies. The effect of irradiation on the behaviour, competitiveness and dispersal capacity of these two species under field conditions still needs to be determined.

The infection biology of a diplozoid on *Labeo umbratus* Smith, 1841 in the Vaal Dam, South Africa

Quinton M. Dos Santos¹ & Annemarié Avenant-Oldewage¹

¹ Department of Zoology, Faculty of Science, University of Johannesburg, P.O. Box 524, Auckland Park, Johannesburg, 2006, South Africa. E-mail: aoldewage@uj.ac.za

Diplozoidae are oviparous macroscopic ectoparasites which occur primarily on the gill lamellae of cyprinid fish. These diplozoids are unique among the platyhelminths as they display precocious sexual behaviour with two hermaphrodite individuals forming a permanent cross-copula in the adult stage. Little information is available on the diplozoid parasites of the indigenous cyprinids of South Africa in terms of infection biology. As these parasites show great potential as sentinels as well as a tool for identifying hosts, it is essential to study them. *Labeo umbratus* Smith, 1841 were collected from the Vaal Dam, around the UJ Island, and the Vaal River, in the Visgat area, using gill nets. The fish were examined for diplozoids while noting the position of the parasites on the gill as well as the gill arch on which each parasite was found. The data was then analysed statistically to determine whether these parasites show any specificity when selecting an attachment site. The parasites showed a prevalence of 28.71%, a mean intensity of 2.31 and an abundance of 0.66. The results showed that the parasites were not more abundant on one side of the gill chamber than the other. In terms of the specific sites on the gills, all the parasites were found on the central area of the gills while the dorsal and ventral areas were almost equally selected for attachment with 50.7% and 47.7% of the parasites respectively. The first and fourth gill arches exhibited the highest parasitism with 41.8% and 46.2% respectively. Thus these parasites do not attach randomly, but are instead found on specific areas in the gill chamber. It may be postulated that site selection is associated with turbulence created by water flowing over the gills as well as finding a mate.

Occurrence of tick-borne haemoparasites in the African buffalo (*Syncerus caffer*) from two geographical areas in Botswana

Dewald Eygelaar¹, Ferran Jori², Mokganedi Mokopasteso³, Elizabeth Debeila¹, Nicola Collins¹, Ilse Vorster¹, Milana Troskie¹ & Marinda Oosthuizen¹

¹ Department of Veterinary Tropical Diseases, Faculty of Veterinary Science, University of Pretoria, South Africa. E-mail: hillfoxx@gmail.com

² Mammal Research Institute, Department of Zoology and Entomology and RP-PCP, CIRAD, UPR AGIRs, Montpellier, France

³ FAO-ECTAD Office for Southern Africa, Gaborone, Botswana

The African buffalo (*Syncerus caffer*) is host for many pathogens known to cause economically important diseases and is considered an important wildlife reservoir for livestock diseases. Theileriosis, heartwater, babesiosis and anaplasmosis are the most important tick-borne diseases of livestock in sub-Saharan Africa, resulting in extensive economic losses to farmers in endemic areas. The most pathogenic and economically significant *Theileria* species in sub-Saharan Africa is *Theileria parva*, which causes East Coast fever (ECF), Corridor disease and January disease in cattle. There are no official reports on the presence of *T. parva* in Botswana and information on detrimentally significant tick-borne haemoparasites especially in Northern Botswana is scarce. The aim of the study was to screen buffalo samples for the presence of *Theileria*, *Babesia*, *Ehrlichia* and *Anaplasma* species using the reverse line blot (RLB) hybridisation assay. DNA was extracted from buffalo blood smear samples obtained from two geographically different areas in Northern Botswana; the Chobe National park (n=64) and the Okavango Delta (n=57). A fragment of the 18S ribosomal RNA (rRNA) gene was amplified using genus-specific primers and amplicons were identified by RLB hybridisation to species-specific probes. Samples were also screened for the presence of *T. parva* using a *T. parva*-specific real-time PCR assay. Of the *Theileria* spp. present, *T. parva* (33%) and *T. mutans* (21%) were most prevalent. Other species of interest were: *Anaplasma centrale* (46%), *A. marginale* (32%), *Babesia occultans* (24%) and *Ehrlichia ruminantium* (6%). Real-time PCR results indicated that 74% of the samples tested positive for the presence of *T. parva*. This is the first report of *T. parva* in the buffalo population from Northern Botswana. Buffalo are asymptomatic reservoirs for these haemoparasites, and when infected buffalo share the same home ranges with cattle, haemoparasites can be transmitted to cattle through infected tick bites. This information on the circulation of tick-borne diseases can contribute to raise awareness among veterinary officials and cattle owners so that control measures (prevention of wildlife-cattle contacts, regular dipping) can be implemented to mitigate their economic impact.

Epidemiology of *Cryptosporidium* spp among household animals in rural communities in Malamulele and Giyani, Limpopo Province

Alone Hlungwane¹, Samie Amidou¹ & Peter A. Mbat¹

¹ *Molecular Parasitology and Opportunistic infections program, Department of Microbiology, University of Venda, Private Bag X5050, Thohoyandou, South Africa. E-mail: samieamidou@yahoo.com*

Cryptosporidium species are coccidian protozoans that infect the intestine of humans and animals and are responsible for diarrhea particularly among immuno-compromised patients. In livestock, a certain number of *Cryptosporidium* spp have been reported to cause morbidity and outbreaks of disease. Although *Cryptosporidium* has been described in the Limpopo Province among humans very little research has been conducted in animals. In the present study, stool samples were collected from animals in rural households in three villages situated in the Vhembe and Mopani Districts and tested for *Cryptosporidium*, using the modified Ziehl Neelsen and a real time PCR assays. A total of 314 stool samples were collected from 64 households. Of the 314 samples 98 (31.2%) tested positive for *Cryptosporidium*. Sheep (48%) and goat (45%) appeared to be the most infected of all types of animals tested compared to cattle (25%) and chicken (5%). From the 64 households surveyed, 43 (67.2%) had at least one or more infected animals. The prevalence of infected animals in the households varied from 11% to 100% of all the animals kept in a specific household. Adult animals were more infected (32%) compared to young animals (29%) but the difference was not statistically significant ($p=0.793$). The sex of the animals as well as the consistency of the stool did not affect the occurrence of *Cryptosporidium*, however; the level of education as well as the sex of the owners significantly affected the prevalence of *Cryptosporidium* among the animals they kept. The prevalence of *Cryptosporidium* was higher among animals that were kept by widows (67%) while the prevalence of *Cryptosporidium* was lower among animals owned by individuals that were married (26%). This study indicated the high prevalence in domestic animals, which could be a health threat to both animals and humans in these regions. Community education will be useful in helping reduce the impact of these infections.

Metazoan parasite infestation of red-nose labeo from two dams characterised by dissimilar water constituents

Jeffrey Lebepe¹, Wilmien J. Luus-Powell¹ & Willem J. Smit¹

¹ Department of Biodiversity, University of Limpopo, Private Bag X1106 Sovenga 0727, South Africa. E-mail: Wilmien.Powell@ul.ac.za

Loskop and Flag Boshielo Dams are located in the Olifants River System that is one of the most polluted river systems in South Africa. To evaluate parasitic infestation in these dams, water samples were collected during winter (July 2011) and summer (November 2011) and analysed. Fifteen fish specimens from each dam were collected using gill nets and examined for metazoan parasites. The concentrations of nutrients and ions were higher at Loskop Dam whereas most metal concentrations were found to be higher at Flag Boshielo Dam. Although the concentrations were shown to be dissimilar, there were no significant differences between localities ($p > 0.05$). A total of five ectoparasite species (*Dactylogyrus pianaari*, *Paradiplozoon* sp., *Ergasilus* sp., *Lamproglena* sp. and *Lernaea cyprinacea*), and two endoparasites (*Nematobothrium* sp. and *Paracamallanus cyathopharynx*) were recorded at Flag Boshielo Dam. One endoparasite species (*Nematobothrium* sp.) and one ectoparasite (*Dactylogyrus pianaari*) were recorded at Loskop Dam. For ectoparasites, Flag Boshielo Dam exhibited higher prevalence, mean intensity and mean abundance values than Loskop Dam. However, higher mean abundance and mean intensity values were recorded for endoparasites at Loskop Dam but with higher prevalence at Flag Boshielo Dam. A Margalef index value of 0.0 was recorded for both ecto- and endoparasites at Loskop Dam with values of 7.95 and 2.17 being recorded for ecto- and endoparasites respectively at Flag Boshielo Dam. Based on the results, elevated concentrations of metals at Flag Boshielo Dam did not seem to affect the ectoparasite infestation negatively. There might be a correlation between nutrients and metazoan parasite diversity as a lower species diversity was recorded at Loskop Dam.

First record of fish trypanosomes from Lake Liambezi, Namibia

Kyle J. McHugh¹, Nico J. Smit¹ & Olaf L.F. Weyl²

¹ Water Research Group, School of Environmental Sciences and Development, Potchefstroom Campus, North West University, Private Bag X6001, Potchefstroom, 2520, South Africa. E-mail: Nico.Smit@nwu.ac.za

² South African Institute for Aquatic Biodiversity, Private Bag 1015, Grahamstown, 6140, South Africa

In August 2011 the opportunity presented itself to sample fish from Lake Liambezi, Namibia, a lake that in 2009 filled for the first time since 1985. The lake has a surface area of 300 km² with an average depth of 3.5 m and a maximum depth of 5.0 m. This large inland lake is filled by floodwaters from three rivers, the Kwando, Chobe and Zambezi Rivers. The contribution of each to the lakes water budget is variable and depends on the rainfall in its individual catchment. When flooded, the lake is home to some 43 fish species. Gill nets, electro shocking and recreational fishing methods were used to collect as many of these species as possible. Thirteen fish species from the Cichlidae, Characidae and Clariidae were sampled, thin blood smears were made on clean microscope slides, fixed in absolute methanol on site and later stained in phosphate-buffered Giemsa and screened for blood parasites. The peripheral blood of nine of the thirteen fish species studied was infected with trypanosomes. The trypanosomes had a wide variety of smaller and large parasites with a total body length ranging from 18.73 µm to 55.14 µm. These parasites corresponded in overall morphometrics and staining properties to that of the widely distributed *Trypanosoma mukasai* Hoare, 1932. To our knowledge, this is the first record of fish trypanosomes from Lake Liambezi, Namibia and the first record of this parasite in the blood of *Clarias ngamensis*, *Sargochromis codringtonii* and *Tilapia rendalli*.

The parasites of grass carp, found in Bloemhof Dam

L. Katlego Mogorosi¹ & Liesl L. van As¹

¹ Department of Zoology & Entomology, University of the Free State, P.O Box 339, Bloemfontein, 9300, South Africa. E-mail: mogorosilk@ufs.ac.za

The grass carp, *Ctenopharyngodon idella*, was introduced to South Africa in the 1970s by the then Natal Parks board. This invasive species of fish is native to eastern Asia and occurs from the Northern parts of Vietnam all the way up to the Amur River on the China-Siberia border. The grass carp was originally introduced to the KwaZulu-Natal of South Africa as sterile individuals. However, fertile individuals were able to escape and have now spread through the Vaal River, and can be found as far as Bloemhof Dam, with more and more reports from anglers indicative of grass carp being present in their catches. The introduction of grass carp to South Africa has had many implications for the local fauna of South Africa. One important factor with regards to the introduction of grass carp has to do with the parasites that are naturally associated with them. These parasites are not native to South African river systems. During fish parasitological surveys grass carp were caught in various parts of Bloemhof Dam, together with other fish species and examined externally and internally to determine the parasite biodiversity of this alien fish. The parasites found included: *Lernaea cyprinacea*, *Argulus japonicus*, and *Bothriocephalus acheilognathi* as well as *Trichodinella epizootica*. The majority of these parasites were also found to occur naturally on the grass carp, meaning that they were probably introduced to South African river systems along with the grass carp and the common carp. Furthermore it was found that the grass carp found in the Bloemhof Dam fed mainly on algae, as there is not much vegetation in the dam itself.

Anthelmintic effects of medicinal plants (*Artemisia afra* and *Mentha longifolia*) on parasitic gastro-intestinal nematodes of livestock

Nthatsi I. Molefe¹, Ana M. Tsotetsi^{1,2}, Oriel M.M. Thekiso¹ & Tom A.O. Ashafa¹

¹ Department of Zoology and Entomology, University of the Free State - Qwaqwa Campus, Private Bag X13, Phuthaditjhaba, 9866, South Africa. E-mail: nthatisimolefe@gmail.com

² Parasite, Vectors and Vector-borne diseases, ARC-Onderstepoort Veterinary Institute, Private Bag X05 Onderstepoort 0110, South Africa.

Gastrointestinal nematodes are the most widespread and economically important class of the helminths. The major threat posed by nematode infections is productivity loss due to their ability to disrupt nutrient utilisation of livestock resulting in hunger and malnutrition. Considering the poor socio-economic situation of small stock farmers coupled with daily infection of the livestock by nematodes, an alternative way of controlling the infection is needed. Acetone and water extracts of the shoot of *Artemisia afra* and *Mentha longifolia* were tested for anthelmintic activity using the egg hatch, larval development and larval mortality assays. The *A. afra* water extracts had 13.55, 2.46 and 9.83 egg hatch inhibition percentages, while acetone extracts exhibited 30.09, 19.99 and 22.50, for 2.5, 5.0 and 7.5 mg/ml, respectively. Similarly, *M. longifolia* water extracts exhibited 0.98, 0.67 and 1.05 whereas the acetone extracts showed 26.09, 22.85 and 14.81 for 2.5, 5.0 and 7.5 mg/ml, respectively. No larval development was observed for all extracts at the lowest concentration of 2.5 mg/ml. All the extracts reduced larval numbers at the highest concentration of 7.5 mg/ml for the larval mortality test as compared to negative control (distilled water). Water extracts from the two plants resulted in a total death of the larvae within one week, whereas the acetone extracts displayed the same results after two weeks of experimentation. Generally the acetone extracts from the two plants were most effective against parasitic gastrointestinal nematodes of livestock.

***Afrogyrodactylus* Paperna, 1968 (Gyrodactylidae: Monogenea) parasites of alestid fishes**

Iva Prikrylová¹, Radim Blažek² & Wilmien J. Luus-Powell³

¹ Department of Botany and Zoology, Faculty of Science, Masaryk University, Kotlarska 2, 611 37 Brno, Czech Republic. E-mail: ivaprik@sci.muni.cz

² Department of Fish Ecology, Institute of Vertebrate Biology, Academy of Sciences of the Czech Republic, Květná 8, 603 65 Brno, Czech Republic

³ Department of Biodiversity, University of Limpopo, Private Bag X1106, Sovenga, 0727, South Africa

Until recently, the taxonomical status of *Afrogyrodactylus* Paperna, 1968 has been unclear. During parasitological surveys of freshwater fishes in several African countries, parasites of this genus have been recorded on alestid fish only.

In 2004, one specimen of *Afrogyrodactylus* was recorded on the fin of nurse tetra, *Brycinus nurse* (Rüppell, 1832) in Niokolo Koba National Park, Eastern Senegal and in 2010, many of them were collected from the fins of the same host from the Nile River in Sudan. In March 2012, during additional sampling in South Africa, these parasites were discovered on the gill arches of the silver robber, *Micralestes acutidens* (Peters, 1853) in the Nwanedi River, Limpopo Province. Parasites of the genus *Afrogyrodactylus* are small viviparous gyrodactylids which can be easily identified based on the typical morphological character of the haptor sclerites, simple ventral bar without membrane without any lateral processes and hamuli with well developed inner processes/ root. An additional particular characteristic is the tubularly- shaped male copulatory organ with a spinous reinforcement and with the internal duct opening into the parasite's body surface. Morphometrical and molecular analyses confirmed the finding of two undescribed species, *Afrogyrodactylus* sp. 1 from *B. nurse* and *Afrogyrodactylus* sp. 2 from *M. acutidens*.

Metazoan parasites of *Clarias gariepinus* and *Cyprinus carpio* in the Houtriver Dam

Tshepiso P. Ramalepe¹, M. Eunice Mogashoa², Modise E. Raphahlelo¹, Wilmien J. Luus-Powell¹ Lourens J.C. Erasmus² & Willem J. Smit¹

¹ Department of Biodiversity, University of Limpopo, Private Bag X1106, Sovenga, 0727, South Africa; E-mail: Wilmien.Powell@ul.ac.za

² Department of Physiology and Environmental Health, University of Limpopo, Private Bag X1106, Sovenga, 0727, South Africa

Despite an increase in parasitological research in South Africa, there are still a number of smaller impoundments from which no records are available. One of these is the Houtriver Dam (30 km west of Polokwane, Limpopo) that forms part of the Limpopo River System. The hosts, *Clarias gariepinus* (n=14) and *Cyprinus carpio* (n=30), were collected in autumn, winter and spring of 2011 using conventional angling gear and investigated for parasites. All parasites were collected, fixed and preserved using standard methods. Infestation parameters (prevalence, mean intensity and mean abundance) were calculated and are indicated for each parasite. The parasites recorded for *C. gariepinus* included three monogenean species, i.e. *Gyrodactylus rysavyi* (33%, 1, 0.33) from the skin, *Macrogyrodactylus clarii* (49.5%, 3.25, 0.85) and *Quadriacanthus clariadis* (55.5%, 2.6, 3.24) from the gills; one copepod species, i.e. *Lamproglana clariae* from the gills (22.8%, 1.75, 1.42); and one branchiuran, i.e. *Argulus japonicus* (33%, 1, 0.33) from the skin. Endoparasites included two nematodes, i.e. *Contracaecum* sp. larvae from the body cavity (51.5%, 7.4, 4) and *Paracamallanus cyathopharynx* from the intestine (7.7%, 12, 4.95); the cestode, *Tetracampos ciliotheca* (33%, 1, 0.33) and the digenean, *Glossidium pedatum* (66%, 2, 1.33) from the intestine. Parasites recorded for *C. carpio* included two branchiuran species, i.e. *Argulus japonicus* (46.5%, 3.6, 0.86) and *Dolops ranarum* (25%, 0.5, 0.55) from the skin; two monogenean species, i.e. *Dactylogyrus* sp. (67%, 1, 0.07) and *Gyrodactylus* sp. (45.5%, 7.5, 1) from the gills. The endoparasites recorded included the larval nematode *Contracaecum* sp. (66%, 1, 0.06) from the body cavity and an unidentified cestode (3.3%, 1.8, 1) from the intestine. The water quality was good with only aluminium above the Target Water Quality Range for aquatic ecosystems. Both fish harboured a wide range of parasite species that could be linked with the good water quality of this dam.

Helminth parasites of the brown squeaker *Synodontis zambezensis* from the Lepelle River System, South Africa

Modibe E. Raphahlelo¹, Matshwele M. Matla¹, Johan Theron³, Wilmien J. Luus-Powell¹, Willem J. Smit¹, Lourens J.C. Erasmus², Tshepiso P. Ramalepe¹, M. Eunice Mogashoa² & N. Martin Chabalala¹

¹ Department of Biodiversity, University of Limpopo, Private Bag X1106, Sovenga, 0727, South Africa

² Department of Physiology and Environmental Health, University of Limpopo, Private Bag X1106, Sovenga, 0727, South Africa

³ Aquaculture Research Unit, University of Limpopo, Private Bag X1106, Sovenga, 0727, South Africa. E-mail: Matshwele.Matla@ul.ac.za

Synodontis Cuvier, 1817 is the most species-rich and widespread of the mochokid catfishes, with more than 120 described species distributed throughout Africa. *Synodontis zambezensis* Peters, 1852 is the southern most representative of the genus *Synodontis*. Forty-six (46) specimens of the brown squeaker were collected from Flag Boshielo Dam (24°50'S, 29°18'E) in the Lepelle River System (formerly known as the Olifants River System). Fish were sampled monthly with angling gear from February to June 2012 and examined for helminth parasites. Parasites were fixed and relaxed using standard methods and stored in 70% ethanol. The preliminary results are reported in terms of morphology, prevalence (p) expressed in percentage, mean intensity (mi) and mean abundance (ma). The helminth parasites found comprised of a gill monogenean *Synodontella zambezensis* (p=75%; mi=61.0; ma=46.0), intestinal cestode *Tetracampos ciliotheca* (p=7%; mi=2.5; ma=0.2) as well as an unidentified cestode (p=15%; mi=2.8; ma=0.4) and the intestinal nematodes *Synodontisia thelastomoides* (p=62%; mi=16.0; ma=10.0) and *Spirocamallanus daleneae* (p=72%; mi=8.4; ma=6.1). The monogenean had the highest infestation indices while the two intestinal nematode species identified were both high in terms of prevalence but had lower mean intensity and mean abundance values. This is a first report for the monogenean *S. zambezensis* from this fish species for South Africa (previously only recorded from Zimbabwe).

Metazoan parasites of the Mozambique tilapia (*Oreochromis mossambicus*) from Lake Urema, Mozambique

Willem J. Smit¹, Joseph R. Sara² & Wilmien J. Luus-Powell¹

¹ Department of Biodiversity, University of Limpopo, Private Bag X1106, Sovenga, 0727, South Africa. E-mail: Willem.Smit@ul.ac.za

² Aquaculture Research Unit, University of Limpopo, Private Bag X1106, Sovenga, 0727, South Africa.

A total of 15 specimens of *Oreochromis mossambicus* (Mozambique tilapia) were collected from Lake Urema (Sofala Province, Mozambique) and investigated for metazoan parasites. Monogeneans were removed and mounted on slides with glycerine jelly dissolved over a flame. All other parasites were fixed and preserved in 70% ethanol. A total number of 349 ectoparasites and 15 endoparasites consisting of five species were collected during this study. Two different groups of ectoparasites were recovered (mean abundance indicated): two species of copepods i.e., *Ergasilus* sp. (7.8) from the gills and *Lernaea cyprinacea* (9.7) from the skin and the monogenean *Cichlidogyrus halli* (5.7) from the gills. Two larval endoparasites were also recorded: these were the trematode *Euclinostomum* sp. (0.1) embedded in the muscle tissue and the nematode *Contracaecum* sp. (0.9) found within the body cavity. The parasite community was dominated by ectoparasites where all hosts were infested with *Ergasilus* sp. and *C. halli* whereas 13 (prevalence 86.7%) hosts were infested with *L. cyprinacea*. *Contracaecum* sp. was recorded from nine (prevalence 60%) and *Euclinostomum* sp. from two (prevalence 13.3%) of the hosts examined. The mean abundance of ectoparasites was also notably higher than those of endoparasites. As found, it was expected to find high infestations of copepods in Lake Urema as it is known that this group of parasites thrives in shallow waters at high temperatures. These results presented here are new parasite records for *O. mossambicus* from Mozambique as well as a new host record for *Ergasilus* sp.

Could the occurrence of the testicular coccidian, *Eimeria sardinae* (Reichenow, 1921), in South African sardine *Sardinops sagax* (Jenyns, 1842) be a concern for fisheries management?

Nurudean Ssempe¹, Cecile C. Reed² & Carl D. van der Lingen^{2,3}

¹ Zoology Department, University of Cape Town, Private Bag X3, Rondebosch 7701, South Africa.

² Marine Research Institute, University of Cape Town, Private Bag X3, Rondebosch 7701, South Africa. E-mail: cecile.reed@uct.ac.za

³ Branch of Fisheries Management, Department of Agriculture, Forestry and Fisheries, Private Bag X2, Rogge Bay 8012, South Africa.

Sardine support important fisheries in many countries including South Africa, where annual catches of sardine (*Sardinops sagax*) have averaged around 130 000t for the past 60 years. Studies from elsewhere have shown that sardine, like other small pelagic fish species are susceptible to infection by coccidian parasites of the genus *Eimeria*. One of these parasites, *Eimeria sardinae*, leads to reduced body condition and even parasitic castration has been reported in some studies. To date very little is known about the prevalence and physiological effects of this testicular coccidian parasite on infected fish from southern Africa. A total of 553 male sardines were collected between 2010 and 2012 from around southern Africa and examined. Sardine from Namibia and from South Africa's east coast showed no infection by *E. sardinae*, whereas fish from the South Africa's west and south coasts had almost similar average prevalence of 49% ± 7 SD and 48% ± 8 SD, respectively. Infection intensity had a significant negative effect (ANOVA, p<0.05) on gonado-somatic index (GSI) values of fish from both the west and south coasts. The marked negative effect of heavy infection intensity on GSI, possibly leading to parasitic castration, has potentially important implications for fisheries management and thus requires further research.

First record of the seriously pathogenic and potentially invasive monogenean *Neobenedenia melleni* from South Africa with serious implications for biosecurity and the marine aquaculture industry

David B. Vaughan¹ & Kevin W. Christison²

¹ Aquatic Animal Health Research, Two Oceans Aquarium, P.O. Box 50603, Victoria & Alfred Waterfront, Cape Town, 8002, South Africa. Current address: Amanzi Biosecurity, Private Bag x15, Hermanus, 7200, South Africa

² Directorate Aquaculture Research, Department of Agriculture Forestry and Fisheries, Private Bag X2, Roggebaai, 8012, South Africa. E-mail: KevinCH@daff.gov.za

Neobenedenia melleni has been labelled a lethal pathogen of captive marine teleosts in public aquaria and aquaculture from as early as 1927 because of its apparent lack of host-specificity and unreliable taxonomy. Historic geographic localities suggest that its origin may be situated along the Pacific and Western Atlantic North American coastlines including the Caribbean Sea and the Gulf of Mexico. The spread of *Neobenedenia melleni* worldwide to some additional localities may be linked to the movement of infected aquaculture stock. The live fish trade is a global system linking fishing communities from areas including the Pacific and Indian Ocean islands, the Caribbean and markets, primarily in Hong Kong and mainland China. A significant portion of the estimated global trade value in live fishes is contributed by the global ornamental fish trade with an estimated annual value of US\$ 220-300 million. Of the recorded host families, representatives of three coral reef-dwelling families, Acanthuridae, Chaetodontidae and Pomacanthidae make up significant imports into South Africa from wild-caught fishes from China, South East Asia, Sri Lanka and Kenya. An initial outbreak of *N. melleni* at a public aquarium in Durban was thought to have originated from species representing Acanthuridae donated from home aquarists (hobbyists) in 2005. However, sporadic purchases of imported coral reef fishes from several ornamental fish retailers in Cape Town by a public aquarium from 2008-2012 revealed parasitism by *N. melleni* on species representing all three families, notably originating from Sri Lanka. Currently there is a significant lack of control or regulation of the ornamental fish trade in South Africa. The confirmation of this pathogen in South Africa and the identification of at least one transmission pathway suggest that our ports of entry are not biosecure, and that finfish aquaculture along our coastline may now be at risk.