BSP Spring Meeting 2019

University of Manchester

April 15th – 17th 2019

In Partnership with:

The Netherlands Society of Parasitology

The Belgian Society for Parasitology & Protistology

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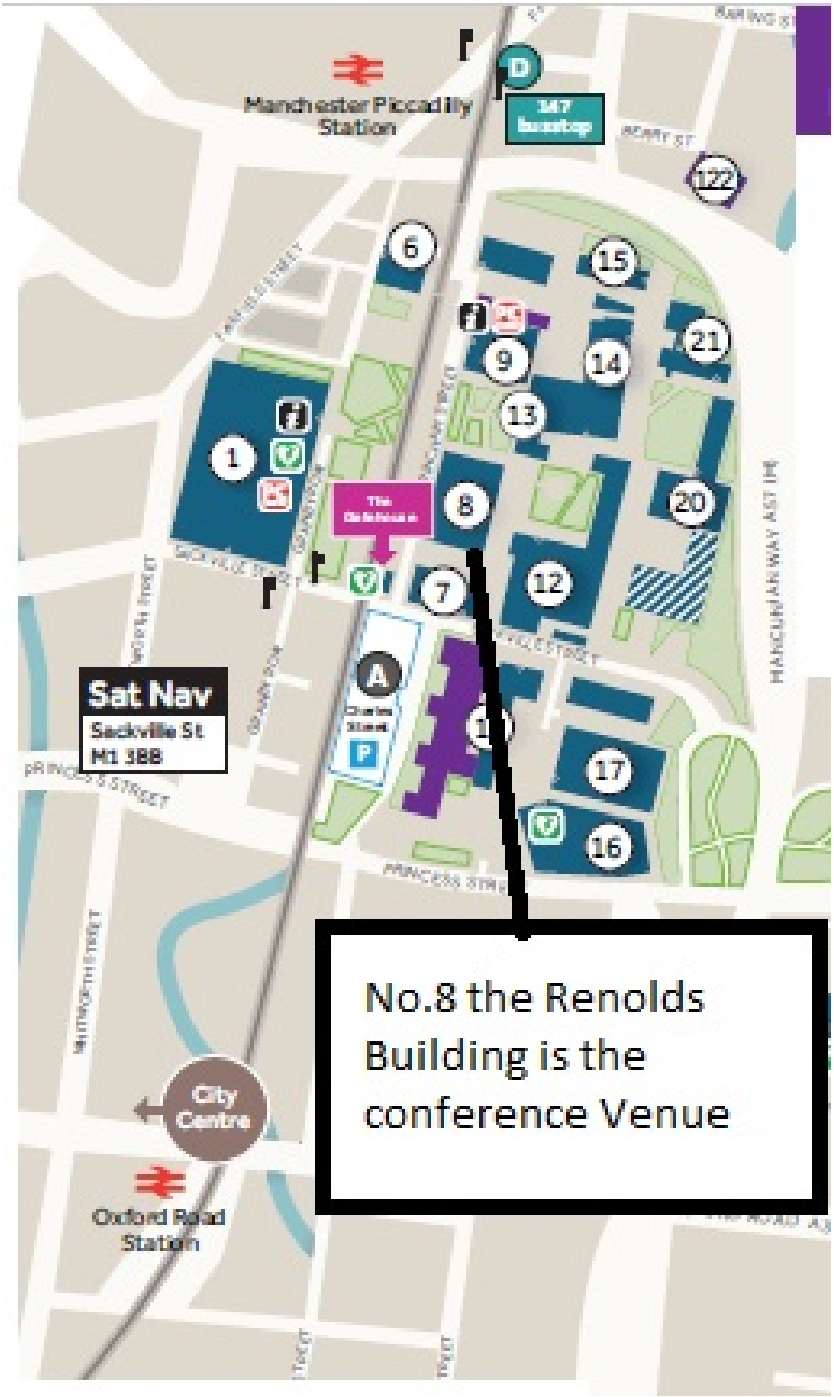
Manchester Piccadilly Station
347 bustop
Sat Nav
Sackville St
M1 3BB
City Centre
Oxford Road Station
No.8 the Renolds Building is the conference Venue

Welcome

We are delighted to welcome you to Manchester and to the University of Manchester for the 2019 Spring Conference of the British Society for Parasitology. This year the BSP is pleased to be hosting the Spring meeting jointly with the Belgian Society of Parasitology and Protistology and the Netherlands Society for Parasitology.

We sincerely hope that the conference will provide the perfect opportunity to develop collaborations and share knowledge for the goal of controlling parasitic diseases.

We have developed a series of exciting sessions and themes (Host Pathogen Interactions, Ecology and Ecosystems, Human Interventions, Cell Biology and Science Communication) under the overarching umbrella of "One Health." Notably we have organised these sessions by themes rather than by parasite in order to encourage cross fertilisation of ideas.

It has never been more important to be able to communicate your science succinctly and with clarity to a lay audience. Thus, in addition to the Science Communication session on Wednesday, we are running Science Communication workshops for delegates who have applied for this option through the abstract submission process. Delegates will be trained by Manchester experts in Science Communication, Dee-Ann Johnson and Ceri Harrop, learning about techniques and tools for building memorable flash talks. Delegates will create their own flash talks, with the top five recorded flash talks selected, based on Science Communication criteria, and presented as a film in the Science Communication session on Wednesday 17th April, with audience voting to select the top talk.
We have also offered "poster pitches" this year to accompany the poster presentations. Here, delegates will get a one minute opportunity to sell their poster as the one "not to be missed" during the themed sessions. Watch out for the poster pitch sessions on Monday and Tuesday, integrated within the theme sessions.

All the conference oral and poster sessions will be held in the Renold building. As well as a packed academic program we have a social program for delegates starting on Monday evening with a Drinks Reception in the Renold building to accompany the first of our two poster sessions. On Tuesday evening we have the Conference Dinner, in the adjacent Barnes Wallis building and after dinner Ceilidh entertainment provided by the Celtic Knot Ceilidh band. The Renold Building is of course only a short walk from Manchester City Centre with its many fine restaurants, museums, galleries, musical and other cultural offerings.

Contents

BSP Spring 2019 Conference Organisers

Ilaria Russo
Kathryn Else

Organising Committee and Session Organisers

Cell Biology: Ilaria Russo, Linda De Vooght, Paul Horrocks, Keith Matthews
Host pathogen interactions: Ron Hokke, Judi Allen, Richard Grencis, Jo Pennock, Carl De Trez
Ecology and Ecosystems: Geoff Hide, Mike Rogan, Joe Jackson, Kathryn Else, Johannes Charlier, Cathy Walton
Human Interventions: Guy Caljon Thomas Geurden, Maria Yazdanbakhsh, Sarah Hendrick
Science Communication : Dee-Ann Johnson, Cerri Harrop, Geoff Hide, Mike Rogan, Erinma Occhu, Ilaria Russo, Kathryn Else

Admin Support

Academic Events – Julian Fuller, Hazel Fuller , Cathy Fuller.

Sponsorship team:

ediHannah Smith, Sheila Macharia, James O'Sullivan

Poster pitch coordinator: Mel Lawson

Brief history of the University of Manchester

The Victoria University of Manchester was founded in 1851. In 2004, the Victoria University of Manchester and the University of Manchester Institute of Science and Technology merged, and the new university named The University of Manchester. Today, we are the largest single-site university in the UK. In total, 25 Nobel Prize winners have worked or studied here. We are ranked 34th in the world, eighth in Europe and sixth in the UK in the 2018 Academic Ranking of World Universities. What's more, we are well underway with one of the biggest investments in facilities undertaken by any UK university, something that is most noticeable if you get chance to explore the Oxford road campus whilst at the BSP.

Parasitology in Manchester

Parasitology in Manchester began in the 1980s, specialising in parasite immunology, building within the internationally renowned Immunology department but also having a significant representation in parasite cell biology. Primarily recognised for work in the area of immunity to gastro-intestinal nematode parasites (most notably Trichuris infection), Manchester now presents a unique range of preclinical models of parasite infection extending beyond the gut nematodes to include filarial parasites, schistosomes, malaria, toxoplasma and cestodes. In 2018, the Lydia Becker Institute of Immunology and Inflammation was launched with international excellence in parasitology recognised within one of the branches of the Institute, "Pathogens, parasites and commensals". Within this branch we have one of the strongest groups in the world working on immunity to helminths that is not only

defining new mechanisms of protective immunity and immunomodulation but also generating new information on fundamental immunity and tissue repair.

Just down the road from the University of Manchester, the University of Salford also offers significant strengths in parasitology with research interests including cestode and trematode biology, toxoplasma and malaria.

The University of Manchester has a longstanding commitment to building the parasitologists and parasite immunologists of the future, delivering parasitology units at second and final year undergraduate level. In addition, the postgraduate MRes in Infection Biology provides students with an in depth, up to date understanding of the mechanisms by which bacteria, fungi, viruses, parasites are able to colonise and establish infections, and the pathogen/host interactions that subvert/modify the ability of the host to respond to infection. Further, Manchester's PhD in Immunology programme offers a strong parasite immunology element, and the University of Manchester's Massive Open Online Course "Parasitic worms: life stories" which runs annually on the Canvas platform, enables a global reach for our teaching. Complementing these training opportunities, the University of Salford is launching a new MSc in Parasitology in 2019, building on the longstanding success of the Molecular Parasitology and Vector Biology masters, originally run jointly by the University of Salford, University of Keele and the University of Manchester.

Presentations

Information for Oral Presentations

Loading of oral presentations will take place in the lecture theatre appropriate to the session, and there is a desktop computer provided.

Please ensure that your presentation is loaded by 8.45 am at the latest if you are presenting in the morning sessions or by 1.45 pm if you are presenting in the afternoon sessions.

There will be a student volunteer or member of staff in each room who will help you load your presentation and assist you if any problems arise with the A/V equipment.

Speakers are respectfully requested to keep to their time slot so that delegates who wish to move between sessions can do so.

All presentations should be as follows

30 mins – 25 mins oral with 5 mins for questions.

15 mins - 10-12 mins oral with 3-5 mins for questions

10 mins – 7-8 mins oral with 3-2 mins for questions.

Information for Poster Presentations

Posters will be displayed in Reynolds C15.

Posters should be A0 size (841 mm wide x 1189 mm high) in portrait format, and be no larger than 900 mm wide x 1200 mm high).

You will find Velcro coins on the board ready to attach your poster. Please put up your poster on Monday before the first poster session and remove it on Wednesday afternoon.

Information for Poster Pitch Presentations
Prior to the meeting you will have submitted your single power point slide to us; we will have compiled these into a single powerpoint which will already be loaded on to the computer in the lecture theatre. The running order of presentations will be detailed in the programme handbook. At the start of the poster pitch session, presenters will be asked to line up and we will run through the short presentations one by one. There will be one overall prize for the best poster pitch.

There are two poster sessions during the conference: Monday from 18:30 to 20:00 and Tuesday from 14:30 till 16:00. Presenters should stand by their poster during these times.

Social Programme and Trade Fair

The BES Parasites and Pathogens Special Interest Group Social and Young Parasitologists Party will be held in collaboration at The Old Abbey Taphouse on 15th April from 19:00.

The Old Abbey Taphouse
Guildhall Close
Manchester Science Park
M15 6SY

There will be a light buffet, drinks and the opportunity to join a Pint Of Science quiz from 8pm at the pub. Rounding off the night will be the Pump Handle Blues Band from 9:30pm (http://www.pumphandleband.co.uk) (musicians including the likes of our very own BSP Vice President and this year's Wright Medalist!).
Please note that the Special Interest Group of the British Ecological Society – Parasites and Pathogens is free to join and you can sign up by following the link below to join this community of scientists interested in parasites.

https://www.britishecologicalsociety.org/membership-community/special-interest-groups/parasite-and-pathogen-ecology-and-evolution/

Sponsorship

The BSP Spring Meeting 2019 has been generously sponsored by:

British Ecology Society
Cambridge University Press
eLife
Elsevier
New England BioLabs
Nikon
Thermoscientific / Fisher
Royal Society
Qiagen

General Meeting information

Reception and Registration

Tuesday to Wednesday conference registration will be at the Renold building from 08:00. Monday will be from 12:00 onwards

The Conference programme starts on Monday at 10:00 in the Renold Building with the Science Communications Workshop (by invitation only). The main program kicks off at 14:00 with the opening plenaries.

House keeping

Food and Refreshments

All food and refreshment will be served in the Reynolds C15 and the Enigma Café

Internet Access

See the forms included in your bag for access then register at the Registration desk.

About the BSP

The BSP Council 2018-19

Professor Maria-Gloria Basanez- Council President 2018-2020
Professor of Neglected Tropical Diseases at Imperial College London

Dr Colin Sutherland - Vice-President (2018-2020)
Professor of Parasitology at London School of Hygiene and Tropical Medicine

Professor Paul Horrocks - Honorary General Secretary (2016-2019)
Professor in Molecular Parasitology at Keele University

Dr Paul Denny - Honorary Treasurer (2016-2019)
Associate Professor in Biosciences at Durham University

Professor Damer Blake - Meetings Secretary (2016-2019)
Professor of Parasite Genetics at the Royal Veterinary College

Dr Helen Price - Communications Secretary (2018-2021)
Senior Lecturer in Bioscience at Keele University

Dr Alvaro Acosta-Serrano - Ordinary Council Member (2016-2019)
Senior Lecturer in Parasite and Vector Biology, Liverpool School of Tropical Medicine

Dr Paul McVeigh - Ordinary Council member (2016-2019) (Incoming Meeting Secretary)
Research Fellow at Queen's University, Belfast

Dr Justin Pachebat - Ordinary council member (2016-2019) (Incoming Honorary Treasurer)
Senior Lecturer in Microbial Genomics at Aberystwyth University

Professor Joanne Cable - Ordinary Council Member (2015-2019)
Professor of Parasitology at Cardiff University
British Ecological Society Parasites and Pathogens BES Special Interest Group,

Professor Robert Hirt - Ordinary Council member (2018-2021)
Professor of Evolutionary Parasitology at Newcastle University
Dr Pegine Walrad - Ordinary council member (2018-2021)
Lecturer at University of York

Dr James LaCourse - Ordinary Council Member (2018-2021)
Senior Lecturer in Parasitology at Liverpool School of Tropical Medicine

Ms Alison Mbekeani - Student Representative
PhD student at Durham University

Mr Tom Pennance - Student Representative
PhD Student at the Natural History Museum and Cardiff University

BSP AGM

This is the second year of the CIO Charitable Incorporated Organisation the new status allows us to use more modern forms of communication, from and to the membership. Below are the accounts link for 2018, it should be noted they differ a little in their form from the old charity but we have wherever posibble to replicate the approach in previous accounts.

http://bsp.uk.net/wp-content/uploads/2019/04/BSP-Accounts-2019.pdf

Student travel awards are given at the end of the AGM.

Timetable

DAY 1 Timetable

Workshop I - (Renold F2)

15-April-2019, at 10:00 to 11:30
Chair - Ms Dee-Ann Johnston

Workshop II - (Renold F2)

15-April-2019, at 11:30 to 13:00
Chair - Dr Ceri Harrop

Plenary - (Renold C16)

15-April-2019, at 14:00 to 15:45
14:00 (50 mins)- *Primate Parasites in Madagascar: contrasting lemurs and humans* (Patricia Wright)
14:50 (50 mins) - *The impact of poultry disease on public health and welfare: a major development challenge* (Fiona Tomley)

Cell Biology - I - (Renold C2)

15-April-2019, at 16:15 to 17:45
16:15 (30 mins) - *Impact of Anopheles reproductive traits on the transmission of Plasmodium falciparum parasites* (Flaminia Catteruccia)
16:45 (15 mins) - *Using single-cell dual RNA sequencing to interrogate host immunity to pathogens* (Musa Hassan)
17:00 (15 mins) - An in vitro larval growth model of Dirofilaria immitis as a drug model for veterinary heartworm (Amy Marriott)
17:15 (15 mins) - *Distribution of trypanosomes in tsetse, cattle and humans in Southern Chad: Mandoul and Maro foci.* (Mahamat Alhadj Moussa Ibrahim)
17:30 (15 mins) - *The Plasmodium LAP complex affects crystalloid biogenesis and oocyst cell division* (Sadia Saeed)

Poster Pitches CB I - (Renold C2)

15-April-2019, at 17:45 to 18:15
Exploring the Nedd8 pathway of Plasmodium falciparum (Maryia Karpiyevich)
Nucleoside analogues against trypanosomatid parasites: phenotypic screening and mechanism-of-action (Camila Santos)
Vivaxin: a novel cell-surface gene family in Trypanosoma vivax with potential applications in an animal trypanosomiasis vaccine (Alessandra Romero Ramirez)
Functions of the BBSome protein complex in Leishmania mexicana (Helen Price)
The SUMO protease is important for flagellum biogenesis in Leishmania mexicana. (Meshal Daalah)
Dysregulated gene expression in oocysts of Plasmodium berghei LAP mutants (Annie Tremp)

Characterising in vitro G-Quadruplexes (G4) in S. mansoni (Holly M. Craven)
In silico analysis of putative cell surface proteins of Tritrichomonas foetus, the causative agent of bovine trichomoniasis. (Eleanor Senior)
Genetic diversity patterns of Haemonchus contortus isolated from sheep and goats in Bangladesh (Mohammad Zahangir Alam)
Impaired development of miltefosine-resistant Leishmania infantum in the sand fly vectors Phlebotomus perniciosus and Lutzomyia longipalpis (Lieselotte Van Bockstal)

Host-Pathogen interactions - I - (Renold C16)

15-April-2019, at 16:15 to 17:45
16:15 (30 mins) - *How does the African trypanosome surface mediate its interaction with its mammalian host?* (Matthew Higgins)
16:45 (15 mins) - *When to make an entrance.* (Petra Schneider)
16:45 (15 mins) - *Influence of paromomycin resistance on Leishmania fitness inside the sandfly vector* (Sarah Hendrickx)
17:00 (15 mins) - *Cercariae on the campus: a follow-up study of swimmer's itch acquired in a faculty pool* (Tomas Machacek)
17:15 (15 mins) - *Identifying the role of the different reservoir hosts of zoonotic schistosomiasis in West Africa* (Elsa Leger)

Poster Pitches HP I - (Renold C16)

15-April-2019, at 17:45 to 18:15
Population genetics as a tool for the detection of vertical transmission of Toxoplasma gondii in a wild population of Apodemus sylvaticus (long-tailed woodmouse) from Malham Tarn, UK (Sameena Haq)
A *review on parasites of Australian cormorants* (Shokoofeh Shamsi)
Genome-led vaccine target discovery for animal African trypanosomiasis (Gavin Wright)
M2 macrophage-associated protein Ym1 mediates parasite expulsion in T. muris infection (Hannah Smith)
Nanopore sequencing significantly improves genome assembly of the protozoan parasite Trypanosoma cruzi (Florencia Díaz-Viraqué)
Tick-borne pathogens in passerine migratory birds in Lithuania (Vesta Matulaitytė)
Prevalence of parasitic infections in surgically removed appendices: parasitological and histopathological studies (Alaa Amer)
The vector biology of ectoparasites on rodents from the 'Asir Region of Saudi Arabia (Samia Alghamdi)
Gastrointestinal parasites on cattle in Kulon Progo district of D.I. Yogyakarta, Indonesia (Fitrine Ekawasti)
More than just chips: what are you getting with your fish? (Shokoofeh Shamsi)
Mechanisms of pyrethroid resistance in Aedes aegypti populations from Saudi Arabia (Ashwaq Alnazawi)

Human Interventions - I - (Renold C9)

15-April-2019, at 16:15 to 17:45
16:15 (30 mins) - *Anti-parasitic vaccines as global health technologies: Building their public health value propositions and business cases* (Maria Elena Bottazzi)

16:45 (15 mins) - *Early diagnosis of acute schistosomiasis by detection of the circulating antigen CAA in serum and urine in a cluster cohort of 34 Belgium travellers exposed in South Africa*. (Lisette van Lieshout)
17:00 (15 mins) - *Evaluating the evidence for lymphatic filariasis elimination thresholds* (Emma Davis)
17:15 (15 mins) - Im*proving variability in egg excretion during controlled human hookworm infection: the road to testing vaccines.* (Marie-Astrid Hoogerwerf)

Poster Pitches Hl l - (Renold C9)

15-April-2019, at 17:45 to 18:15
A Global Network for Neglected Tropical Diseases: towards new therapeutic solutions for Chagas disease and Leishmaniasis (Mags Leighton)
The effect of a single dose of oral ivermectin on human volunteers (Adrian Wolstenholme)
Diagnostic screening for Plasmodium falciparum by Illumigene. (Foekje F. Stelma)
Diagnostic performance of the Alere™ Ultra-sensitive rapid diagnostic test for Plasmodium falciparum malaria infections in asymptomatic pregnant women in Timika, Indonesia (Vera Unwin)
Knowledge, attitudes and practices (KAP) of owners, veterinarians and policy makers in relation to animal schistosomiasis risk and control in Senegal: a One-Health approach. (Louise Vince)
Hand washing as an effective method for intestinal parasites control among school children in Gaza city: Public Health point of view (Adnan Al-Hindi)
Profiling the best-performing community medicine distributors for mass drug administration: a comprehensive, data-driven analysis of treatment for schistosomiasis, lymphatic filariasis, and soil-transmitted helminths in Uganda (Goylette Chami)
Novel water treatments for the zoonotic waterborne pathogen Cryptosporidium (Bozo Lugonja)
Test-and-treat with doxycycline as an alternative strategy for the acceleration of onchocerciasis elimination in a loiasis co-endemic region of South-West Cameroon (Armelle Forrer)

Day 2 Timetable

Cell Biology - ll - (Renold C2)

16-April-2019, at 09:00 to 10:30
09:00 (30 mins) - *Cellular mechanisms of immunity and pathology in filariasis* (Joseph Turner)
09:30 (15 mins) - *Exposing a role for liver fluke stem cells in the flukicide response* (Nathan Clarke)
09:45 (15 mins) - *First profile of long non-coding RNAs in the liver fluke, Fasciola hepatica* (Paul McVeigh)
10:00 (15 mins) - *Transcriptomics of Brugia malayi larval stages reveal insights into Wolbachia metabolism switch during population expansion* (Shannon Quek)
10:15 (15 mins) - *Drug selection and CRISPR-Cas for schistosome transgenesis* (Gabriel Rinaldi)

Cell Biology - lll - (Renold C2)

16-April-2019, at 11:00 to 12:30
11:00 (30 mins) - *On the expansion of an exported kinase family in virulent malaria* (Heledd Davies)
11:30 (15 mins) - *A membrane component of the apical annuli structures in Toxoplasma gondii is essential for parasite survival and replication* (Huiling KE)

11:45 (15 mins) - *The effect of formulation and radiation – a quantitative imaging-based analysis of sporozoite motility* (Clarize de Korne)
12:00 (15 mins) - *RH5-basigin binding tropisms within the Laverania reveal a key event in the origin of Plasmodium falciparum malaria* (Gavin Wright)
12:15 (15 mins) - *New insights into the drug susceptibility of the primate malaria parasite P. knowlesi in vitro and in vivo* (Colin Sutherland)
12:30 (20 mins) -*Proline, a "metabolic penknife" for the dangerous lifestyle of Trypanosoma cruzi (Ariel M Silber)*

Special Lecture - (Renold C16)

16-April-2019, at 14:00 to 14:30
14:00 (30 mins) - *Reducing the time from Innovation to Impact for infectious disease prevention* (Janet Hemingway)

Wright Medal Lecture - (Renold C16)

16-April-2019, at 16:00 to 16:30
16:00 (30 mins) - *Some personal reflections on Connections, Collaborations and Cross-overs: Three important 'Cs' in a career in schistosomiasis research and control* (Russell Stothard)

BSP AGM - (Renold C16)

16-April-2019, at 16:30 to 17:30
Collect Travel awards

Presidents Lecture - (Renold C16)

16-April-2019, at 17:30 to 18:00
17:30 (15 mins) - *Cryptosporidium, a genetically tractable parasite* (Mattie Pawlowic)

Host-Pathogen interactions - II - (Renold C16)

16-April-2019, at 09:00 to 10:30
09:00 (30 mins) - *Leishmania-myeloid cell interactions at the tissue level* (Paul Kaye)
09:30 (30 mins) - *Full development of tsetse-transmitted trypanosomes in advanced human skin tissue models* (Markus Engstler)
10:00 (15 mins) - *Investigating the role of eosinophils in barrier function in infection* (Sheila Macharia)
10:15 (15 mins) - *Assessing the role of neutrophils in vector-transmitted Trypanosoma brucei infections* (Dorien Mabille)

Host-Pathogen interactions - III - (Renold C16)

16-April-2019, at 11:00 to 12:30
11:00 (30 mins) - *Chronic infection and virulence: a role for the Plasmodium pir gene family?* (Jean Langhorne)
11:30 (15 mins) - *Disparate education of inflammatory and patrolling monocytes underpins tissue-specific immunity during gastrointestinal infection*. (Kelly Wemyss)

11:45 (15 mins) - *Filarial-associated pathological lymphatic remodelling is rapidly induced post-larval infection and is mediated by both interleukin 4 receptor alpha-dependent adaptive immune responses as well as recruited inflammatory CCR2+ monocytes.* (Julio Furlong-Silva)
12:00 (15 mins) - *The unexpected role of Natural Killer cells in the anti-filarial nematode innate immune response* (Nicolas Pionnier)
12:15 (15 mins) - *Neuropathogenic schistosomes in the spinal cord: does the peripheral immunity register the infection?* (Martin Majer)

Poster Pitches HP III - (Renold C16)

16-April-2019, at 12:30 to 13:00
Bioavailability improvement of Artemisinin through cocrystal approach: in-vivo and in vitro studies (Manreet Kaur)
Miltefosine restores the infectivity of miltefosine resistant Leishmania parasites by attenuating the innate immune response (Dimitri Bulté)
Evaluating the effect of hen age on poultry red mite feeding and mortality (Francesca Nunn)
Inferring clearance and reinfection dynamics of Schistosoma mansoni from Kato-Katz and circulating cathodic antigen-based diagnostics (Jessica Clark)
A library of Schistosoma mansoni cell surface and secreted proteins for the identification of vaccine candidates and early serological markers of infection (Cecile Crosnier)
Small RNAs with a role in parasitism by Strongyloides nematodes (Vicky Hunt)
Spatial patterns of geo-helminths in soil environment at the Adankolo campus of Federal University Lokoja, an endemic area in North Central Nigeria (Patrick Amidu Audu)
Diagnosis of intestinal schistosomiasis by POC-CCA. A new field applicable approach to quantify score intensities. (Miriam Casacuberta Partal
Novel cystatin of Trichinella spiralis inhibits inflammation mediated by bone marrow-derived macrophages (Porntida Kobpornchai)
The role played by B cells in supporting protective immunity against Trichuris muris infection is dependent on host genetic background and is independent of antibody (Rinal Sahputra)

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Ecology and Ecosystems - I - (Renold C9)

16-April-2019, at 09:00 to 10:30
09:00 (30 mins) - *Theory and practice of parasite management in multi-host systems* (Josephine Walker)
09:30 (15 mins) - *Survival costs of reproduction are mediated by immune responses and parasites in wild Soay sheep* (Adam Hayward)
09:45 (15 mins) - *Patterns of genetic variation in the parasitic nematode Strongyloides ratti.* (Rebecca Cole)
10:00 (15 mins) - *A non-invasive sampling coupled with high-throughput sequencing for helminth characterisation from cetacean faecal samples* (Natalia Fraija-Fernández)
10:15 (15 mins) - *Exploring trophic niches and parasite communities of sympatric Arctic charr and brown trout populations of southern Norway* (Rachel Paterson)

Ecology and Ecosystems - II - (Renold C9)

16-April-2019, at 11:00 to 12:30

11:00 (30 mins) - *Environmental impacts on host susceptibility in mesocosms for This Wormy World* (Andrea Graham)

11:30 (15 mins) - *Single nucleotide polymorphism linkage groups define population structure in Cryptosporidium hominis* (Anna Paziewska-Harris)

11:45 (15 mins) - *Epidemiology of "neglected" tick-borne infections in Nigeria: A (hopefully) early quest of USALTI-Afrique* (Richard Birtles)

12:00 (15 mins) - *Freshwater snails of biomedical importance in the Niger River Valley, Bulinus spp., Biomphalaria pfeifferi and Radix natalensis: a longitudinal survey reveals evidence of spatial and temporal patterns in abundance and distribution.* (Muriel Rabone)

12:15 (15 mins) - *Totiviruses in Leishmania* (Ahmad Garziz)

Poster Pitches EE II - (Renold C9)

16-April-2019, at 12:30 to 13:00

Assessing selective pressure in Fasciola hepatica: challenges and relevance to drug and vaccine gene targets (Olukayode Daramola)

Out of sight: do eye flukes alter predator-prey interactions? (Meg Huggins)

A plan to sequence the genomes of all parasite species from the British Isles (Adam Reid)

The metabolic energy budget of the nymphs (Ixodes ricinus) (Saeed Alasmari)

Regulatory influence of Procambarus clarkii, Girad (Decapoda: Cambaridae) on schistosome-transmitting snails in lotic habitats within the River Athi Basin, Kenya (Geoffrey Maina)

Host specificity of bat flies in South-Eastern Europe (Áron Péter)

Speaking with a forked tongue: pentastomid parasites in man's best friend (Shokoofeh Shamsi)

T. b. gambiense; evidence of absence in NW Uganda (Lucas Cunningham)

Revising the transmission biology of schistosomiasis in Zanzibar (Tom Pennance)

Day 3 Timetable

Cell Biology - IV - (Renold C2)

17-April-2019, at 09:00 to 10:30

09:00 (30 mins) - *The Delivery and Activity of late blight effector proteins that suppress plant immunity* (Paul Birch)

09:30 (15 mins) - *Divergent roles of the RH5 complex components, CyRPA and RIPR in human-infective malaria parasites* (Ellen Knuepfer)

09:45 (15 mins) - *Using CRISPR-Cas9 genome-editing to study Plasmodium falciparum var genes* (Alex Rowe)

10:00 (15 mins) - *Tailored CRISPR screening in Toxoplasma gondii identifies novel virulence factors in vivo* (Joanna Young)

10:15 (15 mins) - *Inhibition of fatty acid oxidation: a new treatment strategy for Primary Amoebic Meningoencephalitis?* (Maarten Sarink)

Cell Biology - V - (Renold C2)

17-April-2019, at 11:00 to 13:00

11:00 (30 mins) - *Mutually Assured Destruction - Wolbachia and the role of host autophagy in population control, antibiotic mode of action and viral protection* (Mark Taylor)

11:30 (30 mins) - *Flagellum length control during the trypanosome life cycle* (Philippe Bastin)

12:00 (15 mins) - *Trafficking itinerary of aquaglyceroporin 2 in T. brucei: new insights into the mode of action of pentamidine*. (Juan Quintana)

12:15 (15 mins) 975 - *In vitro activity of chitosan and derivatives against Leishmania major and Leishmania mexicana* (Alaa Riezk)

12:30 (15 mins) - *Trypanosomal peptidases-promising targets for point of care animal African trypanosomiasis diagnostics* (Theresa Coetzer)

12:45 (15 mins) - *Developmental competence and surface antigen switch frequency can be uncoupled in Trypanosoma brucei* (Keith Matthews)

Host-Pathogen interactions - IV - (Renold C16)

17-April-2019, at 09:00 to 10:30

09:00 (30 mins) - *Heligmosomoides polygyrus secretes multiple immunomodulators of early innate immune responses* (Henry McSorley)

09:30 (15 mins) - *TGF-β bioactivity in Trichuris muris can induce Foxp3+ T regulatory cells and inhibit Th1 and Th2 polarisation.* (Adefunke Ogunkanbi)

10:00 (15 mins) - 3D X-ray microscopy (XRM) for investigating host-parasite interactions and helminth biology reveals a potential novel behavioural-based survival strategy (James O'Sullivan)

10:15 (15 mins) - *Towards the development of a novel vaccine for Trichuris trichiura* (Ayat Zawawi)

Host-Pathogen interactions - V - (Renold C16)

17-April-2019, at 11:00 to 13:00

11:00 (30 mins) - *Immune-driven control of Toxoplasma gondii in human cells* (Eva Frickel)

11:30 (30 mins) - *Adopting helminth-induced regulatory strategies: who is exploiting who?* (Hermelijn Smits)

12:00 (15 mins) - *A controlled human Schistosoma mansoni infection model to accelerate the development of novel medicine, vaccines and diagnostics*. (Marijke C C Langenberg)

12:15 (15 mins) - *The diagnostic potential of glycan specific antibodies in schistosomiasis assessed by glycan microarrays* (Anna Kildemoes)

12:30 (15 mins) - *Cellular immunological analysis of naïve European and pre-exposed African volunteers infected with P. falciparum sporozoites* (Mikhael Manurung)

12:45 (15 mins) - *Elucidating the pulmonary immune response in schistosomiasis* (Emma Houlder)

Ecology and Ecosystems - III - (Renold C9)

17-April-2019, at 09:00 to 10:30

09:00 (30 mins) - *Unravelling the factors that affect immune variability in wild rodents* (Jan Bradley)

09:30 (15 mins) - *The value of museum collections: a case study to investigate the length relationship between cymothoid isopods and their fish hosts* (Wynand Malherbe)

09:45 (15 mins) - *Semi-field evaluation of wAlbB Wolbachia potential for population replacement of dengue vector Ae. aegypti from Lahore, Pakistan* (Nusrat Jahan)
10:00 (15 mins) *3 - Human schistosomiasis in the Senegal River Basin: does wildlife matter?* (Stefano Catalano)
10:15 (15 mins) - *The sweet spot between the lab and the real world - detailed analysis of the immune response against T. muris in a wild house mouse population* (Iris Mair)

Human Interventions - II - (Renold C9)

17-April-2019, at 11:00 to 13:00
Chair - Prof Guy Caljon
11:00 (30 mins) - *Challenges for academia to sustain innovative drug discovery against neglected tropical diseases: focus on Leishmaniasis* (Louis Maes)
11:30 (30 mins) - *Is host specificity beneficial to mosquitoes? – the case of the Anopheles gambiae complex* (Willem Takken)
12:00 (15 mins) - *Anthelmintic resistance in sheep farms using pasture in Quebec, Canada* (Roger Prichard)
12:15 (15 mins) – *Screening for antiparasitic leads from a library of natural products from temperate zone plants(Paul Horrocks)*
12:30 (15 mins) - *The action of ivermectin against filarial nematodes; new clues from RNASeq and C. elegans genetics* (Adrian Wolstenholme)
12:45 (15 mins) - *Exploring cyclic nucleotide phosphodiesterases as drug targets in Schistosoma mansoni* (Harry De Koning)

Science Communications - (Renold C2)

17-April-2019, at 14:00 to 15:20
14:00 (50 mins) - *The science communication imperative* (Andy Miah)
14:50 (30 mins) - *Increasing awareness and dialogue around the themes of Infection and Immunology in non-native English Speakers* (Sheena Cruickshank)

Awards and Close - (Renold C2)

17-April-2019, at 16:00 to 16:30

List of oral abstracts by time

Day 1 Orals

Plenary - (Renold C16)

15-April-2019, at 14:00 to 15:45

14:00 (50 mins

Primate Parasites in Madagascar: contrasting lemurs and humans - *A16563*

Presenter: **Prof Patricia Wright**, *Stony Brook University*

P Wright[1];
[1] Stony Brook University, USA

Madagascar, the fourth largest island worldwide, is one of the most biodiversity rich countries on Earth. Yet, in contrast, it is the sixth poorest country for human economies. Over 30 years we have studied lemurs (non-human primates) in a rainforest ecosystem, and human residents in rural villages around Ranomafana National Park (RNP). These lemurs lived in isolation from humans and other primates for at least 40 million years, resulting in the evolution of unique species and genera of helminth and protozoan parasites. For example, the Lemuroidea malaria parasites are monophyletic and share a common ancestor to all Catarrhini (old world monkeys and apes) malarias with the exception of those related to *P. falciparum*. However, recently, we have demonstrated that lemurs living in areas of frequent overlap with humans are at risk to spillover of parasitic infections including *Cryptosporidium hominis* (Bodager et al. 2015) and *Entamoeba histolytica* (Ragazzo et al. 2018). As would be expected, we have seen similar patterns of spillover with directly-transmitted pathogenic enteric bacteria within this system (Bublitz et al. 2014, 2015). By examining the ecology o f the host and its parasites, we have gained insights into parasite ecosystems both in humans and lemurs.

14:50 (50 mins)

The impact of poultry disease on public health and welfare: a major development challenge

Presenter: **Prof Fions Tomley**, *Royal Veterinary College*

F Tomley[1];
[1] Royal Veterinary College, UK

Professor Fiona Tomley is the former Head of the Department of Pathology & Pathogen Biology at the Royal Veterinary College. She has chaired major grant funding committees and is leading the newly funded £18M UKRI GCRF One Health Poultry Hub which focuses on an interdisciplinary One Health framework to reduce public health risks posed by rapid intensification of poultry. Fiona is an internationally recognised expert on infectious diseases in chickens, and has published extensively on the protozoan parasite Eimeria.

Cell Biology - I - (Renold C2)

15-April-2019, at 16:15 to 17:45

16:15 (30 mins)

Impact of *Anopheles* reproductive traits on the transmission of *Plasmodium falciparum* parasites - *A16556*

Presenter: **Prof Flaminia Catteruccia**, *Professor, Immunology & Infectious Diseases, Harvard T.H. Chan School of Public Health*

F Catteruccia[1]; K Werling[1]; P Marcenac[1]; W R Shaw[1]; M A Itoe[1]; K A Westervelt[1]; A L Smidler[1]; A South[1]; T Lefèvre[2]; E G Kakani[3]; N Mitchell[3];
[1] Department of Immunology and Infectious Diseases, Harvard T.H. Chan School of Public Health, United States; [2] MIVEGEC, IRD, CNRS University of Montpellier, France; [3] Verily Life Sciences, South San Francisco, United States

The reproductive fitness of *Anopheles* mosquitoes is an important component of vectorial capacity, as it ensures large densities for the transmission of *Plasmodium* parasites. In the major malaria vector *Anopheles gambiae*, female reproduction is profoundly affected by the function of the steroid hormone 20-hydroxyecdysone (20E), which is both transferred by males during mating and produced by females after blood feeding. Upon sexual transfer, male 20E induces vast signaling cascades that permanently reshape female physiology, impacting blood feeding-induced processes that are regulated by female 20E and that affect egg development. We show how the human malaria parasite *Plasmodium falciparum* exploits the physiological environment created by mating and blood feeding in the female Anopheles to optimize its own transmission while minimizing fitness costs to its vector. Mosquitoes that produce high number of eggs also support higher infection loads, unveiling a positive correlation between fecundity and *P. falciparum* infection intensity. Impairing oogenesis by multiple manipulations of female 20E levels decreases parasite intensities. These manipulations, however, accelerate *Plasmodium* growth, allowing sporozoites to become infectious sooner. Interestingly, impairing female reproductive factors that are regulated by sexual transfer of male 20E disrupts the positive egg-parasite correlation and induces a fitness cost to infection, leading to decreased egg production in infected females. Finally, we reveal that *Plasmodium* parasites have adopted an evolutionary strategy of resource exploitation to optimize transmission while minimizing fitness costs to its mosquito vector.

16:45 (15 mins)

Using single-cell dual RNA sequencing to interrogate host immunity to pathogens - *A17334*

Presenter: **Dr Musa Hassan**, *Chancellor's Fellow, University of Edinburgh*

M Hassan[1];
[1] University of Edinburgh, UK

Infectious diseases are a major cause of mortality and morbidity worldwide and our ability to treat them is hampered by the rise of antimicrobial resistance. How our immune cells respond to pathogens determines the outcome of an infection. Within the same person, individual immune cells will produce either beneficial or detrimental responses, with some cells fighting off the pathogens and others succumbing to the infection. Understanding why and how this occurs has been challenging because established experimental approaches limited us to measure cell responses in bulk cell or pathogen populations, which obscured individual cell responses. With recent technological advances, we can now measure cell-wide responses with single cell resolution. We exploited these technologies to simultaneously measure host and pathogen gene expression in one infected monocyte at a time. We used *Toxoplasma gondii*, which the World Health Organization ranks 4th among

foodborne parasites with the greatest global impact, and human monocytes, which are the major immune cells that respond to *Toxoplasma* in humans, to perform a cell-by-cell analysis of gene expression in *Toxoplasma*-infected monocytes, and identified the genes that and a subset of cells that regulate monocyte response to *Toxoplasma* at the single cell level. We analysed *Toxoplasma* gene expression in individual monocytes to evaluate the relationship between parasite's virulence and response to monocyte intracellular conditions, which vary between cells. Insights and methods from this study have the potential to reveal new approaches for managing *Toxoplasma* and other important human pathogens.

17:00 (15 mins)

An *in vitro* larval growth model of *Dirofilaria immitis* as a drug model for veterinary heartworm

Presenter: **Miss Amy Marriott**, *Research Associate, Liverpool School of Tropical Medicine* *- A17321*

A E Marriott[1]; J Furlong-Silva[1]; A Steven[1]; J Archer[1]; M J Taylor[1]; J D Turner[1];
[1] Centre for Drugs and Diagnostics Research Department of Tropical Disease Biology, Liverpool School of Tropical Medicine, UK

Dirofilaria immitis and *D. repens* are mosquito-borne filarial parasites that cause heartworm disease in cats and dogs. Left untreated, they can cause life-threatening morbidities, including congestive heart failure and cardiopulmonary embolism. *Dirofilaria* species are also capable of causing zoonotic pathologies in humans.
In recent years, disease incidence has increased in USA and Europe, in tandem with geographical expansion due to spread of *Aedes* mosquito habitats and more favourable climatic conditions for transmission. Current prophylactic treatments rely on continuous, monthly administration of macrocyclic lactones (ML) to block larval development in client owned cats or dogs; however cases of ML resistance have been identified. Curative treatment with melarsomine can cause potentially fatal adverse reactions in dogs and there is no safe drug cure for cats. A new, alternative approach treatment is the blockade of the endosymbiont, *Wolbachia,* to prevent larval development or to block transmission and cure adut heartworm. However, with a heavy reliance on cat or dog *in vivo* models for drug testing, the evaluation of new therapies is time-consuming, laborious and expensive.
To more rapidly assess candidates with matching or improved efficacy against gold-standard ML or anti-*Wolbachia* treatments and to reduce the number of severe experimental procedures in cats or dogs in line with '3Rs' principles in animal experimentation, we have developed an *in vitro* larval model utilising a canine kidney cell line co-culture system. The co-culture reproducibly supports the development and full viability of *D. immitis* L4 larvae for a minimum of 28 days. We demonstrate the optimisation of the larval growth culture model using molecular and morphological parameters as markers of *in vitro* 'fitness' and have validated the system as a drug model using reference ML drugs (ivermectin, moxidectin) or the anti-*Wolbachia* treatment, doxycycline. We are now beginning to deploy the model to scrutinise advanced anti-*Wolbachia* drug candidates, including repurposing opportunities and new chemical entities with narrow spectrum activity, with proven efficacy against human filarial disease, in order to identify a portfolio of alternative prophylactic and potentially curative treatments targeting veterinary heartworm.

17:15 (15 mins)

Distribution of trypanosomes in tsetse, cattle and humans in Southern Chad: Mandoul and Maro foci. *- A17295*

Presenter: **Mr Mahamat Alhadj Moussa Ibrahim**, *Student, University of Bremen*

M A Ibrahim[1];
[1] University of Bremen, Germany

Human African Trypanosomiasis (HAT) and Animal African Trypanosomiasis (AAT) are caused by a parasite of the genus *Trypanosoma*. In Eastern Africa, HAT is caused by *T. brucei rhodesiense* while in Central and Western Africa it is *T. b. gambiense*. AATis predominantly caused by *T. vivax*, *T. congolense*, and *T. b. brucei*, because of their predominance throughout sub-Saharan Africa and of their economic impact on animal production. Trypanosomes are transmitted by tsetse vector, flies of the genus *Glossina*. The general objective is to study the distribution of the trypanosomes in southern Chad, where HAT and AAT are common. The surveys have been conducted during 2017 and 2018 in the Mandoul and Maro foci. A total of 721 humans and 542 cattle were sampled and 183 tsetse were collected. DNA were extracted from human and cattle blood as well as from the midgut and proboscis tissues of the tsetse. Nested PCR targeting trypanosomal ITS1 performed on cattle and fly samples gave a high prevalence. 182 cattle were positive for trypanosomal DNA. The overall species distribution was *T. congolense* with 34%, followed by *T. theileri* (29%), *T. godfreyi* (25%), *T. vivax* (17%) and *T. brucei* ssp.(10%). 22% of the positive cases were mixed infections. No *T. congolense* were detected in the Mandoul focus, while *T. vivax* was in 5% and *T. theileri* in 24% of the sampled cattle.

17:30 (15 mins)

The *Plasmodium* LAP complex affects crystalloid biogenesis and oocyst cell division - *A17286*

Presenter: **Dr Sadia Saeed**, *Research Fellow, London school of hygiene and tropical medicine*

S Saeed[1];
[1] Department of Pathogen Molecular Biology, London School of Hygiene and Tropical Medicine, Keppel Street, London, WC1E 7HT., UK

Malaria parasite oocysts located in the mosquito midgut generate sporozoites by a process called sporogony. *Plasmodium berghei* parasites express six LCCL lectin domain adhesive-like proteins (LAPs), which operate as a complex and share localisation in the crystalloid – an organelle found in the ookinete and young oocyst. Depletion of LAPs prevents crystalloid formation, increases oocyst growth, and blocks sporogony. LAP4 is also one of the member of LAP protein family and its mutant has abnormal crystalloid biogenesis and produces oocysts that display reduced growth and premature sporogony. These findings provide evidence for a role of the LAP complex in regulating oocyst cell division via the crystalloid.

Poster Pitches CB I - (Renold C2)

15-April-2019, at 17:45 to 18:15

Exploring the Nedd8 pathway of Plasmodium falciparum (Maryia Karpiyevich)

Nucleoside analogues against trypanosomatid parasites: phenotypic screening and mechanism-of-action (Camila Santos)

Vivaxin: a novel cell-surface gene family in Trypanosoma vivax with potential applications in an animal trypanosomiasis vaccine (Alessandra Romero Ramirez)

Functions of the BBSome protein complex in Leishmania mexicana (Helen Price)

The SUMO protease is important for flagellum biogenesis in Leishmania mexicana. (Meshal Daalah)

Dysregulated gene expression in oocysts of Plasmodium berghei LAP mutants (Annie Tremp)

Characterising in vitro G-Quadruplexes (G4) in S. mansoni (Holly M. Craven)

In silico analysis of putative cell surface proteins of Tritrichomonas foetus, the causative agent of bovine trichomoniasis. (Eleanor Senior)
Genetic diversity patterns of Haemonchus contortus isolated from sheep and goats in Bangladesh (Mohammad Zahangir Alam)
Impaired development of miltefosine-resistant Leishmania infantum in the sand fly vectors Phlebotomus perniciosus and Lutzomyia longipalpis (Lieselotte Van Bockstal)

Host-Pathogen interactions - I - (Renold C16)

15-April-2019, at 16:15 to 17:45
16:15 (30 mins)

How does the African trypanosome surface mediate its interaction with its mammalian host? - *A16553*

Presenter: **Prof Matthew Higgins**, *Oxford University*

M Higgins[1];
[1] Oxford University, UK

The surfaces of the African trypanosomes are the interfaces between host and parasite. They are coated with a dense layer of variant surface glycoproteins, allowing a population of parasites to use mechanisms of antigenic variation to persist despite the attack of the mammalian immune system. Within this layer operate receptors which are used by the trypanosomes to scavenge nutrients and are exploited by human innate immunity as a route for lytic factor uptake. This talk will present our recent structural insights into how these receptors bind to their ligands and how they have evolved to avoid the mammalian immune defences.

16:45 (15 mins)

When to make an entrance. - *A17314*

Presenter: **Dr Petra Schneider**, *researcher, University of Edinburgh*

P Schneider[1]; A J O'Donnell[1]; S E Reece[1];
[1] University of Edinburgh, Institute of Evolutionary Biology, UK

Recently, we highlighted the importance of daily rhythms of both mosquitoes and hosts/parasites for the transmission of malaria parasites from the vertebrate host to mosquitoes. But how important is the time of transmission for entering the vertebrate host? Asking whether transmission from mosquito to vertebrate host is more - or less - efficient during the daytime versus night time matters given reports of mosquitoes changing the time-of-day they blood feed in response to bednet use. Here we investigate how well *Plasmodium berghei* establishes liver-stage infections in mice, after night time (host active phase) or daytime (host resting phase) transmission. We control for any role of mosquito and parasite rhythms to focus on the importance of host time-of-day for the successful establishment and replication of incoming parasites. Furthermore, we also examine whether pyrimethamine prophylaxis mediates the effects of host time-of-day. We find that liver infections reach higher levels in hosts that are infected by mosquitoes during the daytime (host resting phase) compared to the night time (host active phase). Pyrimethamine reduces liver infection levels and negates any time-of-day effects. Our results could be explained by differences in host rhythms for immunity and/or metabolism. Making an entrance at the right time helps parasites establish successful liver infections. If we extrapolate our results from malaria in nocturnal mice to malaria in humans (with the usual caveats), liver infection levels would reach higher levels - and prophylaxis would

have higher relative efficacy -after night time compared to daytime infections. This could have implications for epidemiology and disease control, especially if bednet use alters mosquito biting times.

16:45 (15 mins)

Influence of paromomycin resistance on *Leishmania* fitness inside the sandfly vector - *A17479*

Presenter: **Mrs Sarah Hendrickx**, *postdoctoral researcher, Universiteit Antwerpen*

S Hendrickx[2]; J Sadlova[1]; P Volf[1]; G Caljon[2]; L Maes[2];
[1] Charles University, Prague, Czech Republic; [2] Laboratory of Microbiology, Parasitology and Hygiene (LMPH), University of Antwerp, Belgium

Background: Previous research showed that experimental selection of paromomycin resistance (PMM-R) in *Leishmania infantum* triggered an increase in parasite fitness. Although no fitness gain was observed between wild type (WT) and PMM-R promastigotes, intracellular growth and *in vivo* infection capacity were clearly increased in PMM-R amastigotes. Given this enhanced fitness in the mammalian host, this laboratory study aimed to extend these findings by assessing the overall fitness of PMM-R parasites in the sandfly vector.
Materials and Methods: Female sandflies (*Lutzomyia longipalpis* and *Phlebotomus perniciosus* or *P. argentipes*) were artificially infected with WT and PMM-R promastigotes of *L. infantum* (MHOM/FR/96/LEM3323-cl4) or *L. donovani* (MHOM/NP/03/BPK275/0-cl18). Progression of the infection was closely monitored by microscopic evaluation of the parasite localization in dissected fly guts and quantification of the total parasite burdens at days 2, 5 and 9 post-infection.
Results: Although *L. longipalpis* is recognized as a susceptible fly for various *Leishmania* species, the infection burdens, metacyclogenesis rate and colonization of the stomodeal valve were considerably higher in the natural vectors *P. perniciosus* and *P. argentipes*. Despite these intrinsic differences in parasite susceptibility between both sand fly species, none of the models demonstrated significant dissimilarities between WT and PMM-R parasites.
Conclusion**:** The fitness gain linked to PMM-R is not observed in promastigotes. Despite their unaffected behavior in the vector, the enhanced virulence observed for PMM-R amastigotes in the mammalian hosts may nevertheless represent an advantage for transmission as this may lead to higher numbers of parasites acquired by bloodfeeding sandflies. To challenge this hypothesis, sandfly transmission studies on hamsters infected with either WT or PMM-R parasites are now being conducted.

17:00 (15 mins)

Cercariae on the campus: a follow-up study of swimmer's itch acquired in a faculty pool - *A17278*

Presenter: **Mr Tomas Machacek**, *PhD student, Charles University, Faculty of Science, Prague*

T Macháček[1]; L Turjanicová[1]; J Bulantová[1]; J Hrdý[2]; P Horák[1]; L Mikeš[1];
[1] Charles University, Faculty of Science, Prague, Czech Republic; [2] Charles University, First Faculty of Medicine & General University Hospital, Prague, Czech Republic

Human cercarial dermatitis (CD), also known as swimmer's itch, is a re-emerging disease frequently reported from all continents. It is a skin immune reaction provoked by antigens of schistosome cercariae. Avian species, such as the genus *Trichobilharzia*, are responsible for most of the cases. Although the symptoms of CD are generally known, the data on immune response in human patients are sporadic and rather incomprehensive.

Here we present a unique set of clinical and immunological data obtained from ten persons accidentally exposed to *Trichobilharzia szidati* cercariae during voluntary management of a faculty pool. In particular, we attempted to correlate the symptoms, personal history, and time course of CD with differential cell counts, dynamics of selected cytokines, and dynamics and character of antibody response. As revealed by a personal questionnaire, the onset of CD was significantly faster, and the symptoms were more severe in the participants with a previous history of CD if compared to the naive ones. The repeatedly infected persons had an elevated proportion of eosinophils 1 week after exposure and a stronger parasite-specific IgG but not IgM response. Increased serum levels of IL-4 occurred 1 and 3 weeks after exposure in all participants, but no clear pattern was noticed for IL-10. As for immunoblots, there was high interindividual variability in IgG reactivity patterns. No antigen with a universal diagnostic potential was confirmed.
Taken together, we had an exceptional chance to study a unique set of accidentally infected individuals who were monitored for 9 weeks after exposure to the parasite. To our knowledge, no similarly complex follow-up study has been conducted. From a practical point of view, our analysis suggests that a complex approach can improve the accuracy of the diagnosis of CD, but particular results of immunodiagnostic methods should be interpreted carefully.

17:15 (15 mins)

Identifying the role of the different reservoir hosts of zoonotic schistosomiasis in West Africa - *A17195*

Presenter: **Dr Elsa Leger**, *Postdoctoral researcher, Royal Veterinary College, University of London*

E Leger[4]; S Catalano[4]; A M Borlase[4]; C B Fall[5]; S D Diop[1]; L Yasenev[4]; B Webster[3]; A M Emery[3]; D Rollinson[3]; K Bâ[2]; N D Diouf[6]; M Sene[6]; J P Webster[4];
[1] IFSAR - Université de Thiès, Bambey, Senegal; [2] Institut de Recherche pour le Développement, Senegal; [3]Natural History Museum, UK; [4] Royal Veterinary College, University of London, UK; [5] Universite Cheikh Anta Diop de Dakar, Senegal; [6] Universite Gaston Berger de Saint Louis, Senegal

Schistosomiasis is a neglected tropical disease caused by *Schistosoma* parasitic worms, which inflicts a significant burden on human and animal populations, particularly across sub-Saharan Africa. Anthropogenic land-use changes affect the distribution and availability of suitable definitive and intermediate hosts, increasing opportunities for hybridization between human and animal schistosomes with subsequent zoonotic transmission. This can have a substantial impact on the dynamics and distribution of schistosomiasis, with further challenges and constraints for effective control. Our aim was to elucidate the role of different definitive hosts as reservoirs of zoonotic *Schistosoma* single species and hybrids in a region of northern Senegal subject to important anthropogenic change. Extensive and systematic parasite sampling from human, livestock, and rodent definitive hosts, combined with snail intermediate hosts, were performed over three years across key transmission sites in northern Senegal. Multi-locus molecular analyses of all *Schistosoma* isolates, followed by Maximum Likelihood (ML) and Bayesian Inference (BI), were used to infer phylogenetic and transmission dynamics between the circulating zoonotic *Schistosoma* species/hybrids and their hosts. Molecular analyses confirmed the presence of widespread viable hybridization within and between *Schistosoma* species of humans and animals. Phylogenetic analyses indicated shared transmission of zoonotic *Schistosoma* species and hybrids between humans and animals (both wild and domestic), providing unique insights into the role of different host species in maintaining transmission. Our study emphasizes the need for a One Health multi-host framework for schistosomiasis control in both people and animals living in high zoonotic transmission zones of sub-Saharan Africa.

Poster Pitches HP I - (Renold C16)

15-April-2019, at 17:45 to 18:15

Population genetics as a tool for the detection of vertical transmission of Toxoplasma gondii in a wild population of Apodemus sylvaticus (long-tailed woodmouse) from Malham Tarn, UK. (Sameena Haq)

A *review on parasites of Australian cormorants* (Shokoofeh Shamsi)

Genome-led vaccine target discovery for animal African trypanosomiasis (Gavin Wright)

M2 macrophage-associated protein Ym1 mediates parasite expulsion in T. muris infection (Hannah Smith)

Nanopore sequencing significantly improves genome assembly of the protozoan parasite Trypanosoma cruzi (Florencia Díaz-Viraqué)

Tick-borne pathogens in passerine migratory birds in Lithuania (Vesta Matulaitytė)

Prevalence of parasitic infections in surgically removed appendices: parasitological and histopathological studies (Alaa Amer)

The vector biology of ectoparasites on rodents from the 'Asir Region of Saudi Arabia (Samia Alghamdi)

Gastrointestinal parasites on cattle in Kulon Progo district of D.I. Yogyakarta, Indonesia (Fitrine Ekawasti)

More than just chips: what are you getting with your fish? (Shokoofeh Shamsi)

Mechanisms of pyrethroid resistance in Aedes aegypti populations from Saudi Arabia (Ashwaq Alnazawi)

Human Interventions - I - (Renold C9)

15-April-2019, at 16:15 to 17:45

16:15 (30 mins)

Anti-parasitic vaccines as global health technologies: Building their public health value propositions and business cases - *A16560*

Presenter: **Prof Maria Elena Bottazzi**, *Associate Dean and Professor, Baylor College of Medicine National School of Tropical Medicine*

M Bottazzi[1];

[1] Baylor College of Medicine National School of Tropical Medicine, United States

The neglected tropical diseases (NTDs) are the most common infections of the poorest people in the world and who live on less than US$2 per day. They include ancient parasitic scourges such as hookworm and other soil-transmitted helminth infections, Chagas disease, amoebiasis, schistosomiasis, and leishmaniasis. Together, the NTDs produce a burden of disease that in certain regions even exceeds HIV/AIDS, while simultaneously trapping "bottom billion" in poverty through their deleterious effects on child physical and intellectual development, pregnancy outcome, and worker productivity. The high prevalence and incidence of the major parasitic NTDs afford an opportunity for joint cooperation and alliances to address these conditions and accelerate the development of novel and complementary global health technologies, such as vaccines, to combat them. One of the major hurdles in the critical path for the development and testing of novel and translational discoveries is overcoming the "valleys of death", or product development gaps for taking a bench discovery to the point where it shows a clear path to the clinic and later into licensure and delivery. A perspective of the sustainable business model, applied by Texas Children's Hospital Center for Vaccine Development, a Product Development Partnership, and the advances of the development and testing of the human hookworm and schistosomiasis vaccines will be presented.

16:45 (15 mins)

Early diagnosis of acute schistosomiasis by detection of the circulating antigen CAA in serum and urine in a cluster cohort of 34 Belgium travellers exposed in South Africa. - *A17342*

Presenter: **Dr Lisette van Lieshout**, *Parasitologist, Leiden University Medical Center*

L Van Lieshout[2]; P T Hoekstra[2]; M Van Esbroeck[1]; L Cnops[1]; J De Vries[2]; P L Corstjens[2]; G J Van Dam[2]; J Clerinx[1];
[1] Institute of Tropical Medicine Antwerp, Belgium; [2] Leiden University Medical Centre, Netherlands

In non-endemic settings, travellers or migrants are generally diagnosed with schistosomiasis by detection of specific antibodies in serum. Although serology is sensitive and specific, it cannot distinguish active from past infection while it may take several weeks or even months for seroconversion to occur. A more accurate diagnostic tool is detection of adult worm circulating antigen (i.e. CAA) in serum or urine, which reflects the presence of viable parasites. Here we explored three diagnostics tests in a cluster of 34 Belgian travellers who were recently and simultaneously exposed to *Schistosoma* during a short travel to South Africa. These cases were seen at the Institute of Tropical Medicine, Antwerp, Belgium (ITM), during the early symptomatic phase 4-5 weeks after exposure, at week 7-8 when treatment with praziquantel was given and at week 12-14. While no eggs were seen in microscopic examination of stool and urine samples, all 34 travellers were confirmed to have acquired a *Schistosoma* infection based on the 100% cumulative positive outcome of the PCR test for the detection of the *Dra1* sequence of the *S. haematobium* complex in serum.(1)While the serum *Dra1* PCR was able to diagnose infection at a much earlier stage than any of the other applied ITM standard diagnostic tests, including serology, the *Dra1* PCR was also found to be similarly unsuitable for short-term monitoring the effect of drug treatment.(1) Stored urine (4 mL) and serum (0.5 mL) samples of this cluster were retrospectively examined for CAA concentrations by utilizing the highly specific and ultrasensitive quantitative *Schistosoma* Up-Converting Phosphor Lateral Flow CAA assay (UCP-LF CAA). Additional antibody testing was done by performing two in-house serology assays which are routinely applied at the Leiden University Medical Center for the diagnosis of imported schistosomiasis, i.e. an immunofluorescence assay (IFA) detecting IgM directed against adult *S. mansoni* worm gut antigen and an enzyme immuno assay (EIA) detecting IgG directed against *S. mansoni* soluble egg antigen (SEA). Urine and serum CAA concentrations and the outcome of IgM-IFA and IgG-EIA were compared with data of the Dra1 PCR and serology previously performed at ITM. Findings showed detectable CAA levels as early as 4-5 weeks after exposure in 27% (8/30) of the urine samples and 91% (30/33) of the serum samples, with a final CAA detection rate in serum of 97% (33/34) before praziquantel treatment was given. Following treatment with the anthelminthic drug CAA levels dropped significantly. No CAA was detected in 30 urine samples and 34 serum samples, except one serum showing a CAA concentration just above the cut-off level, all tested 6-8 weeks after treatment. IgM-IFA and IgG-EIA showed higher numbers of positive cases than the previously used serology tests, with a final detection rate of 82% (28/34), but, as expected b

17:00 (15 mins)

Evaluating the evidence for lymphatic filariasis elimination thresholds - *A17326*

Presenter: **Miss Emma Davis**, *PhD student, University of Warwick*

E Davis[4]; L J Reimer[1]; L Pellis[2]; T D Hollingsworth[3];
[1] Liverpool School of Tropical Medicine, UK; [2] University of Manchester, UK; [3] University of Oxford, Big Data Institute, UK; [4] University of Warwick, UK

In the global drive for elimination of lymphatic filariasis, 14 countries have brought prevalence below the WHO-specified thresholds for halting mass treatment. These thresholds were set as practical targets with the expectation that reducing prevalence to this level would lead to transmission fading away in most settings. This has been undermined by recent evidence of ongoing transmission in some areas. As more countries cease interventions it is vital that we ensure this process is well-informed, as prematurely halting control programs could pose a serious threat to global targets. There is a strong mathematical and biological basis for the existence of a break-point for lymphatic filariasis: a threshold below which transmission cannot be sustained, but we often neglect to consider that it is possible for stochastic extinction to occur even before this break-point is reached. The probability of lymphatic filariasis elimination, given a particular prevalence (e.g. 1%), can be calculated by considering the probability a chain of transmission will die out, dependent on certain key biological parameters. We use these methods to demonstrate how the probability of elimination explicitly depends on the accuracy of these parameters, many of which have a poor evidence base. We conclude that the existing experimental evidence does not support a high probability of elimination at the current thresholds, partially due to uncertainties in parameters which could be experimentally assessed.

17:15 (15 mins)

Improving variability in egg excretion during controlled human hookworm infection: the road to testing vaccines.

Presenter: **Mrs Marie-Astrid Hoogerwerf**, *MD, PhD student, Leiden University Medical Center*

M A Hoogerwerf[4]; J P Koopman[2; 3]; J J Janse[2; 3]; E A Brienen[2; 3]; M C Langenberg[4]; Y Kruize[2; 3]; L E Coffeng[1]; S J de Vlas[1]; L G Visser[4]; L van Lieshout[4]; M Yazdanbakhsh[4]; M Roestenberg[4];
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Introduction: Hookworm control programs are proving to be very challenging due to re-infection and insufficient coverage of mass drug administration. A vaccine would be needed to reach the ultimate goal of elimination. However, field testing of potential vaccine candidates needs large sample sizes, is a lengthy process and costly. Experimental infection of humans with hookworm, can provide a more controlled setting for preliminary testing of vaccine efficacy and down-selection of the most promising candidates, thereby cutting time and costs. Current controlled human hookworm infection studies only result in low egg counts and as such do not reflect the natural infection setting. This trial aims to investigate the effect of repeated exposure on median egg count and egg excretion variability in order to develop a suitable model for future vaccine testing. Methods: Twenty-four healthy, male and female volunteers were randomized in a double blind fashion to receive either one, two or three doses of 50 L3 *Necator americanus* larvae at 2-week intervals divided over four infection sites. Volunteers visited the trial center weekly for twenty weeks after which they were treated with albendazole to clear the infection. Adverse events were collected at each visit, eosinophil counts were measured weekly and faecal samples were collected for Kato-Katz slides from week 6 onwards. Results: Three volunteers received early treatment because of severe abdominal adverse events after the infection. One withdrew informed consent after the first visit for reasons unrelated to the study. Skin adverse events were mild. We found no relation between infectious dose and adverse events, although a trend towards a longer duration of adverse events was seen in the highest dose group which received 150 L3. All volunteers showed patent infection by Kato-Katz 6-9 weeks after first exposure to larvae. At 12 to 16 weeks after first exposure, egg counts reached a plateau phase. Median egg count for the group exposed to 50 L3 for this plateau was significantly lower (480 epg) than the median count for the 100 L3 and 150 L3 group (both 1200 epg). Variability in egg excretion was highest in the 50 L3 group and lowest in the 150 L3 group. Conclusions: Repeated infection reduces the variability in egg excretion without producing a corresponding increase in adverse events. We conclude that doses of 100 or 150 L3 larvae are well tolerated and result in mild-

to-moderate level infections according to WHO criteria, thus reflecting egg excretion levels as observed in endemic regions. These improvements in the controlled human hookworm model can accelerate the development of hookworm vaccines.

Poster Pitches HI I - (Renold C9)

15-April-2019, at 17:45 to 18:15

A Global Network for Neglected Tropical Diseases: towards new therapeutic solutions for Chagas disease and Leishmaniasis (Mags Leighton)

The effect of a single dose of oral ivermectin on human volunteers (Adrian Wolstenholme)

Diagnostic screening for Plasmodium falciparum by Illumigene. (Foekje F. Stelma)

Diagnostic performance of the Alere™ Ultra-sensitive rapid diagnostic test for Plasmodium falciparum malaria infections in asymptomatic pregnant women in Timika, Indonesia (Vera Unwin)

Knowledge, attitudes and practices (KAP) of owners, veterinarians and policy makers in relation to animal schistosomiasis risk and control in Senegal: a One-Health approach. (Louise Vince)

Hand washing as an effective method for intestinal parasites control among school children in Gaza city: Public Health point of view (Adnan Al-Hindi)

Profiling the best-performing community medicine distributors for mass drug administration: a comprehensive, data-driven analysis of treatment for schistosomiasis, lymphatic filariasis, and soil-transmitted helminths in Uganda (Goylette Chami)

Novel water treatments for the zoonotic waterborne pathogen Cryptosporidium (Bozo Lugonja)

Test-and-treat with doxycycline as an alternative strategy for the acceleration of onchocerciasis elimination in a loiasis co-endemic region of South-West Cameroon (Armelle Forrer)

Day 2 Orals

Cell Biology - II - (Renold C2)

16-April-2019, at 09:00 to 10:30

09:00 (30 mins)

Cellular mechanisms of immunity and pathology in filariasis - *A16558*

Presenter: **Dr Joseph Turner**, *Senior Lecturer, Liverpool School of Tropical Medicine*

J Turner[1];

[1] Liverpool School of Tropical Medicine, UK

Lymphatic filariasis is the third leading cause of global disability, and the major cause of secondary lymphoedema, affecting ~40 million patients. Whilst elimination of LF may be achievable within the next decade, pre-existing pathology patients will face a life time of progressively debilitating disease. Because current treatment is generally limited to symptom management, novel strategies to ameliorate pathology are urgently required. A first step to developing new therapies is to detail the underlying aetiology of lymphatic disease following filarial infection. Our laboratory has utilised mouse models of *Brugia malayi* filarial infection and developed bioimaging technologies to interrogate adaptive immune control of infection and lymphatic pathology development. In this talk I will detail the cellular and molecular effector mechanisms controlled by the initial CD4+ T-helper 2 polarised immune response to

larval *B. malayi* infection which are successful in control of infection yet mediate profound lymphatic remodelling and dysfunction.

09:30 (15 mins)

Exposing a role for liver fluke stem cells in the flukicide response - *A17274*

Presenter: **Mr Nathan Clarke** , *PhD student, Molecular Parasitology, Queen's University Belfast*

N Clarke [1]; E Gardiner[1]; E McCammick[1]; P McCusker[1]; P McVeigh[1]; A Mousley[1]; J Coulter[1]; J Hodgkinson[2]; N J Marks[1]; A G Maule[1];
[1] Queen's University Belfast, UK; [2] University of Liverpool, UK

Liver fluke parasites from genus *Fasciola* are the causative agents of fascioliasis/fasciolosis, a disease of socioeconomic importance with impacts upon animal health/global food production and upon human health as a neglected tropical disease. Treatment of infections is reliant on a small arsenal of flukicides, of which only triclabendazole is effective against both the acute and chronic stages of infection. Increasing reports of triclabendazole resistance necessitate novel drug target discovery. Our *in vitro* culture platform facilitates the growth and development of juvenile fluke towards an adult-like phenotype, a process dependent on neoblast-like stem cells. These neoblast-like stem cells are sensitive to ionising radiation, possess the capacity for self-renewal and exhibit asymmetric division, traits associated with neoblasts in other flatworms. RNAi of the cell cycle transcript, *histone-2b* results in reduced expression of neoblast markers, accompanied by a reduction in juvenile growth and neoblast proliferation, highlighting the importance of neoblasts to fluke development and their appeal as a resource for novel flukicide targets. Similarly, triclabendazole treatment reduces juvenile growth and neoblast proliferation in a dose-dependent manner. Observed triclabendazole-neoblast interplay supports a role for neoblasts in drug responses and drug tolerance/resistance. Comparing the levels of neoblast proliferation between triclabendazole susceptible and resistance strains reveals a greater proliferative rate in drug resistant fluke, supporting the hypothesis that neoblast proliferation dynamics can support drug resistance. This greater capacity for cell turnover could impose an advantage in navigating both the harsh host environment, as well as tolerating/recovering from flukicide-induced damage.

We acknowledge funding provided by the Biotechnology and Biological Sciences Research Council and Merial Ltd. (BB/K009583/1), the National Centre for the 3Rs (NC/N001486/1) and the Department for the Economy of Northern Ireland.

09:45 (15 mins)

First profile of long non-coding RNAs in the liver fluke, Fasciola hepatica - *A17481*

Presenter: **Dr Paul McVeigh**, *Senior Research Fellow, Queen's University Belfast*

P McVeigh[1]; E McCammick[1]; N J Marks[1]; A G Maule[1];
[1] Queen's University Belfast, UK

Long non-coding (lnc)RNAs are a relatively newly-designated subset of non-coding RNAs, arbitrarily defined as RNA transcripts longer than 200 nucleotides that do not code for protein. A burgeoning research field has identified lncRNAs in animals, plants, yeast and prokaryotes, with roles in transcriptional control, protein localization, apoptosis and stem cell pluripotency. However the vast majority of lncRNAs still have unknown functions. The first descriptions of flatworm lncRNAs describe thousands in *Schistosoma* spp., some of which appear to be co-expressed with mRNAs, suggesting a regulatory function. We have developed an *in-silico* pipeline to mine lncRNAs from transcriptomic resources for the liver fluke, *Fasciola hepatica*, from which we have identified more

than 32,000 lncRNA-like transcripts. Sequential comparisons between intra-mammalian life stages (metacercariae, newly-excysted juveniles, 21-day juveniles, adult parasites) show that a small proportion of these (7%) are significantly differentially expressed ($p<0.001$) during development. Of these, RNAseq data (validated by droplet digital PCR) indicate that thirteen are expressed solely in the most pathogenic life stage, the 21-day liver-stage juvenile. Notably, these are also expressed in 21-day old worms maintained *in vitro* with our published maintenance methods, enabling us to study lncRNA biology in worms maintained *in vitro*. RNAi analyses link selected lncRNAs with functions in growth and/or development of juvenile parasites.

10:00 (15 mins)

Transcriptomics of *Brugia malayi* larval stages reveal insights into *Wolbachia* metabolism switch during population expansion - *A17107*

Presenter: **Mr Shannon Quek**, *PhD student, Liverpool School of Tropical Medicine*

S Quek[1]; C Bronowski[2]; S Wagstaff[1]; M J Taylor[1];
[1] Liverpool School of Tropical Medicine, UK; [2] University of Liverpool, UK

Lymphatic filariasis and onchocerciasis are diseases caused by filarial nematodes, which combined have a morbidity estimate of up to 108 million people. The ability for these, and other, filarial nematodes to thrive is known to be dependent on the presence of the obligate intracellular bacterium, *Wolbachia.* Removal of *Wolbachia* via antibiotics causes significant deleterious effects in the nematode, including a cessation of embryogenesis, reduced lifespan, and arrested development. *Wolbachia* populations in these nematodes are known to expand significantly during the L3 to L4 stages of development in preparation to assist the nematode host for development past L4 and to adult stages. The mechanisms behind this population explosion remain unexplored. This study employs a transcriptomics approach to investigate the development of *Brugia malayi* L3 larval stages in the two weeks immediately after it enters a mammalian host, sampling at 3, 7, 11, and 14 days post-infection. Using a combined approach of differential expression and pathway analysis, as well as Gene Set Enrichment analysis, we observe discrete changes in the *Wolbachia* endosymbiont's glycolysis-gluconeogenesis pathway in a manner similar to cancer, or other rapidly proliferating cells. This observation is accompanied by the upregulation of haem and nucleotide biosynthesis pathways in *Wolbachia*, which have been hypothesised as playing a major role in the symbiosis. Within the nematode, pathways associated with its development and sexual differentiation, as well as the autophagy pathway, were upregulated during the Day 11 and 14 time-points, which have previously been shown to control *Wolbachia* populations. As such this study demonstrates important changes occurring within the *Wolbachia* transcriptome at discrete time-points that may be related to population growth/control or energy metabolism requirements for either the *Wolbachia* endosymbiont or the nematode host. Such information will be useful to understand the basic biology that underpins a complex and devastating group of diseases.

10:15 (15 mins)

Drug selection and CRISPR-Cas for schistosome transgenesis - *A17500*

Presenter: **Dr Gabriel Rinaldi**, *Senior Staff Scientist, Wellcome Sanger Institute*

G Sankaranarayanan[1]; A Coghlan[1]; M E Lotkowska[1]; P Driguez[1]; N Holroyd[1]; M Berriman[1]; **G Rinaldi**[1];
[1] Wellcome Sanger Institute, UK

Schistosomiasis is a neglected tropical disease affecting >200 million people worldwide. Genome sequences for several *Schistosoma* species are available, including a high-quality annotated reference for *Schistosoma mansoni.* There is an urgent need to develop a functional toolkit to translate these data into new biological insights and

targets for intervention. The eggs of *S. mansoni* can be transduced using mammalian retroviruses. Transgenes can be stably integrated into chromosomes and transmitted through the germline as stable transgenic lines. However, in the absence of a robust selection protocol for transgenic parasites, transgenic organisms become diluted among non-transformed parasites and eventually lost in successive generations. We have previously shown that the antibiotic aminoglycoside G418 (geneticin) can be employed to enrich for retrovirustransfected schistosomes expressing NeoR. However, the eggs, gateway for germline transgenesis, seem to be naturally resistant to this antibiotic. Puromycin treatment of PuroR-expressing schistosomes might be a promising alternative, given that this aminonucleoside antibiotic indeed kills eggs in a concentration-dependent manner. In addition to antibiotic selection anthelmintic drugs with schistosomicidal activity could be employed as mutations in a sulfotransferase (ST) were identified as causing resistance to oxamniquine (OXA). We have targeted the ST locus using CRISPR-Cas 9 and introduce transgenes in to the germ line of *S. mansoni*, aiming to obtain stable transgenic lines resistant to OXA. Sensitivity to OXA was analysed in eggs, miracidia and sporocysts. In addition, different developmental stages, including adult worms, eggs, miracidia and sporocysts were transfected with CRISPR-Cas9, gRNA against ST and DNA donor molecules to drive the knock-in of transgenes in the ST locus via Homology Directed Repair (HDR). Miracidia from these transfected eggs were screened for the presence of the knocked-in transgene and employed to infect snails aiming to obtain transgenic cercariae and derive a stable line. Drug selection coupled with genome editing technologies promises exciting opportunities for functional genomics of this neglected tropical disease parasite.

Cell Biology - III - (Renold C2)

16-April-2019, at 11:00 to 12:30

11:00 (30 mins)

On the expansion of an exported kinase family in virulent malaria - *A16562*

Presenter: **Dr Heledd Davies**, *Francis Crick Institute*

M Treeck[1];
[1] Francis Crick Institute, UK

How do intracellular parasites, such as *Plasmodium falciparum* and *Toxoplasma*, establish their niche in a host cell and in the host? Both parasites secrete a number of effector proteins into the vacuole that physically separates them from the host cell cytoplasm, while some proteins are further transported into the host cell. This leads to changes of the infected cell itself, which enables the colonisation of the host and escape from the immune system. Here I will concentrate on most recent findings on host cell modulation by the malaria parasite Plasmodium falciparum, and the role of an expanded and exported kinase family in this process.

11:30 (15 mins)

A membrane component of the apical annuli structures in *Toxoplasma gondii* is essential for parasite survival and replication - *A17307*

Presenter: **Miss Huiling KE**, *PhD student, University of Cambridge*

H Ke[1]; L Koreny[1]; K Barylyuk[1]; R F Waller[1];
[1] University of Cambridge, Department of Biochemistry, UK

Apicomplexan parasites including *Toxoplasma gondii* possess specialized cell features such as the apical complex that enable the parasite invasion, and a highly organized cell pellicle consisting of the outer plasma membrane and

the inner double-layered Inner Membrane Complex (IMC). The IMC is connected with the parasite cytoskeleton and is composed of multiple rectangular alveolar vesicles that are sutured together, and one continuous conical plate covering the apical portion of the cell (the apical cap). A peripheral ring of about 6 annuli has been identified at the lower boundary of the apical cap in *Toxoplasma gondii* by centrin2 localization. All the known annuli proteins so far lack transmembrane domains and are considered to be cytoskeleton components. The function of these mysterious annuli structures remains unknown. Apical Annuli Protein 6 (TgAAP6), however, is the first integral membrane protein located exclusively at the apical annuli. Super-resolution 3D- structured illumination microscopy (3D-SIM) revealed that TgAAP6 is localised specifically at the intersection points of the longitudinal IMC sutures and the lower edge of the apical cap. We showed that the C-terminus of TgAAP6 was underneath the plasma membrane and in the alveolar space between the plasma membrane and IMC membrane by co-localisation with GAP45 and other pellicle markers. The annuli staining of TgAAP6 was only found in the mature tachyzoites and not in the replicating daughter cells, suggesting that recruitment of the plasma membrane is required for its location. Conditional knockdown of TgAAP6 caused significant growth and replication defects. We are currently investigating the cellular and molecular function of the protein. TgAAP6 contains two putative lipid-binding domains that are implicated in endocytosis and possess lipid-binding ability. Further investigations of TgAAP6 in lipid binding and uptake may contribute to the understanding of the nutrients acquisition mechanism and are currently under way.

11:45 (15 mins)

The effect of formulation and radiation – a quantitative imaging-based analysis of sporozoite motility - *A17297*

Presenter: **Ms Clarize de Korne**, *PhD, Leiden University Medical Center*

C M de Korne[1]; B M Winkel[1]; M N van Oosterom[1]; L T Lageschaar[1]; D B Staphorst[1]; S C Chavelley[1]; E Baalbergen[1]; K J Dechering[2]; A H Velders[3]; B M Franke-Fayard[1]; F W van Leeuwen[1]; M Roestenberg[1];
[1] Leiden University Medical Center, Netherlands, Netherlands; [2] TropiQ, Netherlands; [3] Wageningen University and Resarch Centre, Netherlands

Introduction: An effective malaria vaccine has the potential to prevent around half a million deaths each year. Live attenuated malaria parasites (sporozoites; spz) are considered the most promising vaccine candidates, however their efficacy critically depends on the spz potential to migrate in the human host. Key components of the spz motility machinery have been identified, however the regulation of this machinery is an unknown process. Moreover, (life attenuated) spz migration in human tissue (e.g. skin) remains wholly uncharacterized to date. We have developed the quantitative analysis tool SMOOT which enabled us to study spz motility *in vitro* and in human skin. Using this tool, we assessed how formulation and radiation affects sporozoite motility. Methods: Fluorescence confocal microscopy was used to image *Plasmodium berghei* spz *in vitro* in nine different formulations to investigate the regulation of spz motility by the different components available in solution. Also, movies were obtained of wild type and radiation attenuated *Plasmodium falciparum* spz migrating in human skin explants to study spz migrating behaviour in the human host and to investigate how this is affected by radiation attenuation. SMOOT enabled the quantitative analysis of key spz motility features: their adherence capacity, movement pattern, directionality and velocity during forward locomotion. Results: Image analysis revealed that spz motility is highly dependent on the environment. *In vitro* spz displayed primarily (98%) counter clockwise circular movement. Albumin acted as an essential supplement to induce parasite attachment and movement. Glucose, salts and other whole serum components further increased the attachment rate and regulated the velocity of the movement. In human skin, the physical constraints asserted by the tissue morphology slowed down the spz and yielded more complex directional migration patterns; spz movement alternated between turning (either CW and CCW) and linear patterns. Head-to-head comparison revealed that radiation attenuation impaired the capacity of sporozoites to vary

their movement angle and velocity, promoting less refined movement patterns. Conclusion: We created a tool which enabled quantitative analysis of spz motility both *in vitro* and in human skin. We revealed that a complex interplay of albumin, glucose and certain salts and amino acids regulates parasite motility. Moreover, we showed that radiation attenuation altered spz migration behaviour. Insights in how parasite motility is regulated by formulation and affected by radiation attenuation will potentially contribute to the development of an efficacious live attenuated parasite based malaria vaccine.

12:00 (15 mins)

RH5-basigin binding tropisms within the *Laverania* reveal a key event in the origin of Plasmodium falciparum malaria - *A17291*

Presenter: **Dr Gavin Wright**, *Senior Group Leader, Wellcome Sanger Institute*

F Galaway[2]; R Yu[2]; A Constantinou[2]; F Prugnolle[1]; **G J Wright**[2];
[1] Univeristy of Montellier, France; [2] Wellcome Sanger Institute, UK

Many human infectious diseases originate as zoonoses including *Plasmodium falciparum* malaria which is a major global health problem. *P. falciparum* belongs to the *Laverania*, a subgenus of parasites that infect African great apes and which exhibit strict host tropism in the wild. One factor that could restrict *P. falciparum* to humans is the specific binding tropism between the parasite ligand reticulocyte-binding protein homologue 5 (RH5) and its host erythrocyte receptor, basigin. Genome comparisons within the *Laverania* revealed the introgression of a region encoding RH5 between a gorilla-restricted parasite and the ancestor of *P. falciparum*, which was probably a crucial event for the zoonotic transfer to humans but how the transfer of *rh5* between parasites breached host tropisms to permit human infection is unknown. By comparing the host basigin receptor binding properties of extant and calculated ancestral sequences of the RH5 invasion complex within the *Laverania* subgenus, we show that a crucial property of the introgressed RH5 was the remarkable ability to bind both gorilla and human basigin receptors. We further demonstrate that the subsequent restriction of *P. falciparum* to humans can be explained by mutation of a single residue in RH5 that has become fixed in all sequenced *P. falciparum* isolates. These findings reveal molecular events for the origin of human *P. Falciparum* malaria and may inform molecular surveillance to predict future zoonoses.

12:15 (15 mins)

New insights into the drug susceptibility of the primate malaria parasite *P. knowlesi in vitro* and *in vivo* - *A17515*

Presenter: **Dr Colin Sutherland**, *Parasitologist, London School of Hygiene & Tropical Medicine*

C J Sutherland[1]; D A van Schalkwyk[1]; I N Lubis[1];
[1] London School of Hygiene & Tropical Medicine, UK

We have been exploiting the availability of the human erythrocyte-adapted A1-H.1 line of *Plasmodium knowlesi* to compare the *in vitro* susceptibility of this species to a variety of established and investigational antimalarial compounds, relative to that of *P. falciparum*. We have found particularly striking evidence of higher *P. knowlesi* susceptibility to DHFR inhibitors such as cycloguanil and pyrimethamine and to the new drug KAF 156, currently entering clinical trials in West Africa. In contrast, the simian species is less susceptible than *P. falciparum* to ATP4 inhibitors such as cipargamin (KAE609) and DODH inhibitors such as DSM1 and DSM265. We are currently testing whether the susceptibility profiles of *P. knowlesi* against each of these drug classes is a good indication of *ex vivo* susceptibility of the other human *Plasmodium* species, including *P. vivax.* Finally, new clinical data from

Indonesia will be presented suggesting that current artemisinin-based combination therapy is wholly effective against *P. knowlesi* and *P. vivax,* but not *P. malariae* or *P. falciparum,* in North Sumatera province.

12:30 (20 mins)

Proline, a “metabolic penknife” for the dangerous lifestyle of Trypanosoma cruzi

Presenter: **Pro Areil Silber**, *Parasitologist, Institute of Biomedical Sciences, University of São Paulo*

Silber AM [1]
[1]Laboratory of Biochemistry of Tryps – LaBTryps, Department of Parasitology, Institute of Biomedical Sciences, University of São Paulo, São Paulo – Brazil

Trypanosoma cruzi, the causative agent for Chagas disease, has a complex life cycle alternating among two different types of hosts: reduviid insects and mammals. Inside each host, the parasite faces different environments: the different parts of the digestive tube in the insect host, and the bloodstream, and the cytoplasm of different cells in different tissues inside each species of mammalian host that can be infected by this parasite. The parasite must survive to the conditions that are predominant in such different environments. Significant variations rely among others on redox and nutritional stress. It has been shown by our group and others that proline and its metabolic intermediate P5C play different roles in the cell bioenergetics, differentiation processes, and survival to redox and severe nutritional stresses, and contributes to the metabolic flexibility of T. cruzi. Additionally, other amino acids such as histidine, glutamine, and alanine, which are metabolically related to proline, are also able to participate in the interplay between redox and bioenergetics metabolism in this parasite. Summarizing, the multi-functionality of proline and other amino acids as well as their intermediate metabolites is critical for T. cruzi survival in the challenging environments this parasite transits during its life cycle.

Special Lecture - (Renold C16)

16-April-2019, at 14:00 to 14:30

14:00 (30 mins)

Reducing the time from Innovation to Impact for infectious disease prevention *- A17009*

Presenter: **Prof Janet Hemingway**, *Director of the Liverpool School of Tropical Medicine, Liverpool School of Tropical Medicine*

J Hemingway[1];
[1] Liverpool School of Tropical Medicine, UK

The pipeline of new products to prevent and control infectious diseases in many cases needs to be refreshed. With resistance to drugs and insecticides spreading rapidly these products cannot come to market at the glacial speed of their predecessors. Re-engaging industry is only part of the problem, to achieve impact products need to be accepted by disease endemic countries and used at scale in appropriate settings. There are numerous problems along this pathway. The journey over the last decade for new vector control products for malaria and NTDs will be described, alongside lessons learned. The talk spans establishing a new product development partnership, mapping out the route to market and culminates in a new model for randomised control trials embedded in a

countrywide operational implementation, to generate epidemiological impact data. Adopting this new model of working should reduce the time for bringing new products from innovation to impact by up to 15 years.

Wright Medal Lecture - (Renold C16)

16-April-2019, at 16:00 to 17:00
16:00 (30 mins)

Some personal reflections on Connections, Collaborations and Cross-overs: Three important 'Cs' in a career in schistosomiasis research and control - *A17305*

Presenter: **Prof Russell Stothard**, *Medical Parasitologist, Liverpool School of Tropical Medicine*

R Stothard[1];
[1] Liverpool School of Tropical Medicine, UK

I am personally delighted to receive this honour from the BSP, foremost as Dr Chris Wright's research legacy on flukes and snails is a longstanding stimulus on my own. Having worked at the Natural History Museum, in the very section he first established and with many of the same staff he recruited, Chris's publications and influences have continued to fascinate me. In this presentation, I would like to reflect a little on how key individuals inspire us and how the BSP has provided me with many fruitful connections during my academic career. Several of these connections have led to international collaborations and I make specific mention to three large-scale projects, CONTRAST (2006-2010), SIMI (2008-2012) and COUNTDOWN (2014-2019). Each was tasked with conducting applied research on the control of schistosomiasis and discovered something fascinating – ex Africa semper aliquid novi. Uptake of such findings has led to incremental improvement in WHO policies, either facilitating much needed access to praziquantel treatment or strategies in appropriate environmental modification, inclusive of snail control. As a parasitologist (actually a malacologist), a key lesson is to develop the skill to cross-over disciplines and address new questions. A skill learned, perhaps, from our greatest educators, the parasites themselves, who jump between many different worlds so adroitly.

Presidents Lecture - (Renold C16)

16-April-2019, at 17:30 to 18:00
17:30 (15 mins)

Cryptosporidium, a genetically tractable parasite - *A17325*

Presenter: **Dr Mattie Pawlowic**, *Principal Investigator, Lecturer, University of Dundee*

M Pawlowic[1];
[1] University of Dundee, UK

Diarrheal disease is responsible for 10% of the deaths of children under five years of age, of which cryptosporidiosis is the second leading cause. There are no vaccines available, and the only drug approved to treat cryptosporidiosis is not effective in immunocompromised patients—the group that needs drug therapy the most. Inability to continuously culture this parasite in the lab and difficult animal models have hindered both our basic understanding of its biology as well as drug discovery efforts. As a postdoctoral researcher in Prof. Boris Striepen's lab, Dr. Pawlowic was part of the group that developed genetic tools and an *in vivo* animal model for *Cryptosporidium parvum*. These genetic tools allow us for the first time to directly explore parasite biology. The

Pawlowic lab at the University of Dundee is using molecular and biochemical approaches to dissect the function of genes involved in construction of the oocyst wall, the life cycle stage important for transmission of *Cryptosporidium*.

Host-Pathogen interactions - II - (Renold C16)

16-April-2019, at 09:00 to 10:30

09:00 (30 mins)

Leishmania-myeloid cell interactions at the tissue level - *A16554*

Presenter: **Prof Paul Kaye**, *University of York*

P Kaye[1];
[1] University of York, UK

Leishmania are obligate intracellular parasites, that reside within cells of the myeloid lineage, including monocytes, macrophages, dendritic cells and neutrophils. Although the interaction between *Leishmania* and these varied host cell types has been studied extensively *in vitro* and *ex vivo*, much less is known about how infection modifies the behaviour of these different host cells in the context of the rapidly changing microenvironments associated with inflammation and tissue remodeling. This talk will review what is known about these interactions, using *Leishmania donovani* infection as a representative system, and drawing on data from both experimental models of infection and human disease. The application of new highly multiplexed techniques in pathology such as digital spatial profiling will be highlighted and challenges for future research discussed

09:30 (30 mins)

Full development of tsetse-transmitted trypanosomes in advanced human skin tissue models - *A17361*

Presenter: **Mr Markus Engstler**, *Professor, Julius-Maximilians-Universität Würzburg*

M Engstler[1];
[1] Julius-Maximilians-Universität Würzburg, Germany

African trypanosomes are transmitted by the tsetse fly through deposition of the infective metayclic stage parasites into the mammalian skin. Our knowledge about the early stages of human trypanosome infection at the site of the insect's bite remains limited. Therefore, we propose bioartificial human skin as versatile model system for the investigation of tsetse-borne trypanosome infections. We have developed novel primary human skin equivalents with improved mechanical properties. Our skin model resembles native human skin in its histological architecture and distinctive physiology. We have used tsetse flies to successfully simulate the natural infection process by direct transmission of trypanosomes to our artificial skin models. High-end 4D imaging of the injection site revealed an unexpected complexity of the skin lesions, with direct implications on the early dissemination of the trypanosomes within the host dermis. Most importantly, the parasites complete their natural developmental progamme within the human skin model. We found a very rapid transition from the transmitted quiescent metacyclic trypanosomes to proliferative slender bloodstream forms, and further differentiation to fly-transmissible stumpy forms. We have also documented the interaction of trypanosomes with dermal fibroblasts, and have embarked on an extensive dual RNA-Seq analysis of trypanosome infections of primary human skin models.

10:00 (15 mins)

Investigating the role of eosinophils in barrier function in infection - *A17487*

Presenter: **Miss Sheila Macharia**, *PhD Student, University of Manchester*

S Macharia[1]; S Cruickshank[1]; K J Else[1]; R Forman[1];
[1] University of Manchester, UK

Eosinophils are fully-differentiated granulated cells that are found in the gut during homeostasis and inflammation. Despite their abundance in the gut, little is known about their function. Indeed, previous data has shown that while their numbers increase during inflammatory conditions, their roles, particularly in the context of worm infections, are not clear. Even under homeostasis, the role that eosinophils play is not well defined. However, previous research suggests that a loss of eosinophils leads to gut dysfunction and increased permeability. Therefore, studying how eosinophils specifically interact with the gut barrier is important in determining their role.

We have studied the role of eosinophils in gut barrier function in C57BL/6 and eosinophil-deficient (ΔdblGATA-1) littermate mice, infected with *Trichinella spiralis.* Although there were no differences in gut morphology, we did observe a significant increase in the number of eosinophils located close to epithelial cells at day 8 post infection. Additionally, we also observed an eosinophil granule protein, major basic protein (MBP), in the lumen, suggesting that the eosinophils are activated and releasing their contents. Collectively, these data suggest that activated eosinophils are interacting with epithelial cells and influencing gut barrier function. We now aim to investigate barrier integrity by assessment of tight junction proteins, markers of gut permeability such as calprotectin as well as additional eosinophil markers.

10:15 (15 mins)

Assessing the role of neutrophils in vector-transmitted *Trypanosoma brucei* infections - *A17273*

Presenter: **Dorien Mabille**, *PhD student, University of Antwerp*

D Mabille[1]; L Maes[1]; G Caljon[1];
[1] Laboratory of Microbiology, Parasitology and Hygiene (LMPH), University of Antwerp, Belgium

Introduction: Human African Trypanosomiasis (HAT), also known as sleeping sickness, is a tsetse fly transmitted parasitic disease indigenous for the African continent. Trypanosome transmission occurs during the blood feeding of infected flies, resulting in the inoculation of parasites in the skin. The drugs that are currently available to treat this disease all have their limitations and to date an effective vaccine is lacking, endorsing the need for novel treatment strategies. Instead of focusing on the parasite, strategies to prevent parasite transmission are gaining interest as they are not subject to drug resistance. Insight into the early immunological events upon the bite of infected tsetse flies is required as a scientific basis for the development of such transmission-blocking approaches. Results: Neutrophils are rapidly recruited to the dermal infection site but their role in vector-transmitted *Trypanosoma* infections is largely unknown. Therefore, the response of neutrophils to a range of parasitic stimuli was evaluated. These experiments showed that exposure of human neutrophils to naive tsetse fly saliva and live bloodstream form (BSF) parasites significantly prolonged neutrophil survival *in vitro*. The prolonged survival induced by tsetse fly saliva was shown to be mediated by TLR4 activation. Additionally, BSF parasites induced neutrophil extracellular trap (NET) formation and degranulation of azurophilic granules. Trypanosomes are thus responsible for neutrophil activation, however limited cell death in the presence of neutrophils and low levels of parasite phagocytosis show that the parasite is not hampered by activated neutrophils. Neutrophil depletion experiments in various genetically modified mouse models (Genista, TNF -/- and MPO -/- mice) in combination with bioluminescent imaging showed an impact on dissemination and systemic parasite levels, suggesting that

neutrophils regulate parasite retention at the site of infection and affect systemic propagation and/or immune control.

Host-Pathogen interactions - III - (Renold C16)

16-April-2019, at 11:00 to 12:30

11:00 (30 mins)

Chronic infection and virulence: a role for the *Plasmodium pir* gene family? - - *A16549*

Presenter: **Prof Jean Langhorne**, *Francis Crick Institute*

J Langhorne[1];
[1] Francis Crick Institute, UK

Plasmodium proteins, particularly those encoded by subtelomeric multigene families are thought to contribute to virulence and chronicity of blood-stage malaria. We study the *pir* (*Plasmodium* interspersed repeat) family, which is related to the *rif*/*stevor* gene families of *P. falciparum*. The presence of *pir* genes in the genomes of *Plasmodium* species infecting rodents allows the investigation of this gene family *in vivo*, with direct relevance to the majority of *Plasmodium* species including the important human pathogens *P. falciparum* and *P. vivax*. Mosquito transmission of *P. chabaudi* increases expression of a large subset of *pir* genes in acute blood-stage infection, which is associated with reduced virulence of the infection. By contrast, parasites from chronic infections or from serially blood-passaged parasites express fewer and different *pirs*, and are more virulent when injected into naïve mice. Our data suggest a causal link between *pir* expression and virulence, and with the ability of the host to establish chronic infections. The changes in *pir* expression in acute and chronic infections occurs in other rodent malarias and in infections in the natural host, the thicket rat, suggesting this may represent an important event for parasite survival in the blood. Mosquito-transmitted *P. chabaudi* infections elicit a very different early host response from that induced by infections initiated by serially blood-passaged parasites, which may be responsible for the reduced virulence. Our next tasks will be to elucidate the relationship between *pir* gene expression and virulence, and the mechanisms by which virulence is altered. Understanding the role of this *Plasmodium*-wide gene family is critical to the understanding of the basic biology of these infections and in engendering new research directions that could inform new interventions to combat malaria.

11:30 (15 mins)

Disparate education of inflammatory and patrolling monocytes underpins tissue-specific immunity during gastrointestinal infection. - *A17281*

Presenter: **Miss Kelly Wemyss**, *PhD Student, University of Manchester*

K Wemyss[2]; L Webb[1]; H M Bridgeman[2]; I E Prise[2]; A S MacDonald[2]; J S Cavet[2]; J E Konkel[2]; K J Else[2]; J R Grainger[2];
[1] Baker Institute for Animal Health, United States; [2] University of Manchester, UK

Gastrointestinal inflammation has dramatic effects on systemic health. Two keystone mechanisms by which this can occur are through impacts on circulating innate cell output and function, and through altered lymphocyte polarisation and trafficking in distal tissues. Both of these mechanisms can influence protection against heterologous inflammatory stimuli, but how these two distinct mechanisms of systemic immune modulation are integrated to promote host survival following inflammation has not been explored. Here we show that, following

infection with the gut helminth *Heligmosomoides polygyrus bakeri*, distinct tissues acquire distinct immune profiles. This tissue-specific training is dependent upon specific recirculation of T cells. Type 2 cells infiltrate mucosal tissues providing a local type 2 training environment, but are absent from major sites of monocyte haematopoiesis, where type 1 educating signals dominate. In combination with this tissue-specific training, circulating Ly6C^{low} monocytes, which remain in the bloodstream during infection, rapidly take on an unappreciated IFN-γ educated state whilst Ly6C^{hi} monocytes, destined to leave the bloodstream and move into distal tissues, remain largely unaltered, retaining uncompromised plasticity to polarising signals upon tissue entry. Such compartmentalised bloodstream monocyte education is achieved via an exquisite sensitivity of Ly6C^{low} cells to IFN-γ and is functionally important. Thus, strategic education of innate immune cells results in a capacity for the host to be protected at mucosal surfaces from secondary worm infection, whilst simultaneously protected against systemic secondary bacterial infection at the early stages of parasite infection.

11:45 (15 mins)

Filarial-associated pathological lymphatic remodelling is rapidly induced post-larval infection and is mediated by both interleukin 4 receptor alpha-dependent adaptive immune responses as well as recruited inflammatory CCR2+ monocytes. - *A17306*

Presenter: **Mr Julio Furlong-Silva**, *PhD Student, Liverpool School of Tropical Medicine*

J Furlong-Silva[1]; S D Cross[1]; N Pionnier[1]; A E Marriott[1]; A Steven[1]; J Archer[1]; M J Taylor[1]; J D Turner[1];
[1] Centre for Drugs and Diagnostics Research Department of Tropical Disease Biology, Liverpool School of Tropical Medicine, UK

Lymphatic Filariasis (LF) related morbidity (lymphoedema and elephantiasis) affects 40 million patients globally and is a leading cause of global disability. Current recommended treatment is limited to symptom management with novel strategies to ameliorate, or even reverse, LF pathology urgently required. A novel murine *Brugia malayi* L3 (*Bm*L3) infection model, utilising near infrared intravital imaging, was developed to longitudinally track changes to the lymphatic architecture following infection. Immunophenotyping of local skin draining lymphoid tissues and associated afferent infected lymphatic collecting vessels, use of immunodeficient mouse strains and targeted ablations of CCR2 or phagocytic cells were utilised in the model to investigate mechanisms of filarial-associated lymphatic remodelling. Lymphatic remodelling, dilation and impaired drainage (lymphatic insufficiency) were observed as early as 6 days following *Bm*L3 infection concomitant with lymphoid/lymphatic tissue expansions of: IL-4$^+$ and IL-13$^+$ CD4$^+$T-cells, CD11b$^+$Ly6C$^+$CCR2$^+$ monocytes and CD11b$^+$MHCII$^+$F480$^+$ macrophages with an inflammatory-recruited, alternative activation phenotype (RELM-α$^+$CD206$^+$MHCII$^+$Tim4$^-$). *Bm*L3 infected Severe Combined Immunodeficient (SCID) and IL-4rα knockout mice demonstrated significant amelioration of lymphatic remodelling and insufficiency compared to wild type (WT) counterparts. Additionally, ablation of inflammatory monocytes or macrophages in *Bm*L3 infected WT mice resulted in significantly reduced lymphatic insufficiency. The data demonstrates a novel role for host adaptive Th2 responses and recruited inflammatory monocytes as mediators of *Bm*L3 driven pathological lymphatic remodelling. Targeting this pathway may represent a novel therapeutic strategy to prevent, or even reverse development of later LF related morbidity.

12:00 (15 mins)

The unexpected role of Natural Killer cells in the anti-filarial nematode innate immune response - *A17495*

Presenter: **Dr Nicolas Pionnier**, *PostDoc, Liverpool School of Tropical Medicine*

N Pionnier[1]; J Furlong-Silva[1]; H Sjoberg[1]; H Metuge[2]; V Chunda[2]; A Steven[1]; S Wanji[2]; M Taylor[1]; J D Turner[1];
[1] Centre for Drugs and Diagnostics Research Department of Tropical Disease Biology, Liverpool School of Tropical Medicine, UK; [2] Research Foundation for Tropical Diseases and Environment, Buea, Cameroon

Lymphatic filariasis and onchocerciasis are major neglected tropical diseases affecting over 140 million people worldwide with painful and profoundly disfiguring pathologies (such as lymphedema or blindness). Despite crucial roles of granulocytes and alternatively activated macrophages in controlling the early stages of the parasitic infection, little is known about the induction of the innate immune response at the infection site. As innate lymphoid cells (ILCs) are known to play important roles in the initiation of the inflammation, we therefore investigated comparative ILC1, ILC2 and natural killer (NK) cell population expansion during Th2 driven *Brugia malayi* and *Onchocerca ochengi* peritoneal filarial infections using either immunocompetent (BALB/c) or immunodeficient (NOD.SCID and RAG2 being deficient in functional lymphocyte responses; NOD.SCID.γ and RAG2$^{-/-}$γc$^{-/-}$ being moreover deficient in ILC populations due to an absence of IL-2 gamma chain signaling) mice.
Pilot studies performed on BALB/c immunocompetent animals infected with *B. malayi* revealed that a 10-fold NK cell population expansion was evident at the site of infection within 3 days post-infection (p.i.) and that NK cells constitutively represent over 90% of the ILC populations on site within the first 7 days p.i., shedding light on those commonly Th1-associated cells.
Those surprising results were confirmed using BALB/c, NOD.SCID and RAG2 mice either infected with *B. malayi* larvae or implanted with *O.ochengi* adults. In this configuration, once again an expansion of NK cells at the site of filarial parasitism was evident in those mice whilst ILC1 and ILC2 cell populations did not expand at any time point examined post-infection
In addition, profound NK cells impairment in NOD.SCID.γ and RAG2$^{-/-}$γc$^{-/-}$ was linked to increased susceptibility in both infection models as well as a significantly altered granulocyte recruitment local to the site of infection. While peritoneal macrophage and neutrophil numbers were not particularly impacted, eosinophil recruitment was significantly impaired in ILC-deficient mice during filarial infection, indicating a potential novel role for NK cells in regulating eosinophil granulocyte filaricidal activity.
Finally, as this IL-2 γ chain impairment also affects other ILC populations development, we selectively depleted NK cells in mice using anti-NKp46 or asialo GM1 antibodies injections. Data showed that RAG2 and NOD.SCID mice susceptibility to *B. malayi* infection was 1.5- to 3-fold increased, again directing this body of evidence towards a role for NK cells in the innate control of filarial infection.
In follow-up experiments we are addressing expansions of NK subsets in tissues distal to the site of infection, providing more insights to the innate immune mechanisms involved in the regulation of disease pathogenesis.

12:15 (15 mins)

Neuropathogenic schistosomes in the spinal cord: does the peripheral immunity register the infection? - *A17355*

Presenter: **Mr Martin Majer**, *Research Assistant, Charles University, Faculty of Science, Department of Parasitology*

M Majer[1]; T Macháček[1]; L Súkeníková[2]; J Hrdý[2]; P Horák[1];
[1] Charles University, Faculty of Science, Prague, Czech Republic; [2] Charles University, First Faculty of Medicine & General University Hospital, Prague, Czech Republic

Migration of parasitic helminths through the central nervous system (CNS) is a phenomenon which attracts parasitologists as well as immunologists. Since the CNS is sensitive to any damage, the local immune response is closely regulated. Formerly, the CNS was even regarded as an immunologically privileged site. Here we examined

the CNS inflammation during the infection of mice with the avian neuropathogenic schistosome *Trichobilharzia regenti*. In mice (accidental hosts), most parasites are entrapped and killed in the skin within a few days after penetration. However, some of them escape and migrate through the CNS where they are eliminated after 2–3 weeks. Since the impact of the ongoing CNS inflammation on the peripheral immune response is unknown, we also investigated the polarization of T cell subpopulations in the spleen and the skin- or CNS-draining lymph nodes.

First, we characterized the dynamics of immune cells present in the CNS of mice at several time-points after infection. The tissue inflammation, particularly infiltration of granulocytes and T-lymphocytes into the injured spinal cord, peaked 14 days post infection (dpi). Microglia, the resident CNS macrophages, also expanded during the infection and represented the major MHC II+ population. Unexpectedly, granulocytes and T-lymphocytes also infiltrated the brain 21 dpi, although it was virtually free from parasite DNA.

To elucidate the peripheral immune response, we harvested cells from the spleen and skin- or CNS-draining lymph nodes. In all these samples, T-bet+ and GATA3+ T helper (Th) cells were prominent 7 dpi suggesting mixed Th1/Th2 response as a consequence of the skin inflammation triggered by parasite penetration. Later, the ratio of T-bet+ and GATA3+ T cell populations decreased (even in the CNS draining lymph nodes) being probably unaffected by the parasite-killing CNS inflammation 14 and 21 dpi. Indeed, there were less T-bet+ and also RORγt+ T cells than in uninfected animals, but this was not correlated with increase of Foxp3+ regulatory T cells, amount of which barely changed during the infection.

Taken together, the invasion by *T. regenti* of the mouse CNS induces a significant nervous tissue inflammation which leads to parasite clearance. However, it likely does not influence the peripheral immune response in terms of Th polarization, which is rather affected by the initial inflammation in the skin. Characterization of serum cytokine milieu and phenotype changes in bone marrow-derived dendritic cells after exposure to parasite antigens might reveal further details of how *T. regenti* influences host immune response.

Poster Pitches HP III - (Renold C16)

16-April-2019, at 12:30 to 13:00

Bioavailability improvement of Artemisinin through cocrystal approach: in-vivo and in vitro studies (Manreet Kaur)

Miltefosine restores the infectivity of miltefosine resistant Leishmania parasites by attenuating the innate immune response (Dimitri Bulté)

Evaluating the effect of hen age on poultry red mite feeding and mortality (Francesca Nunn)

Inferring clearance and reinfection dynamics of Schistosoma mansoni from Kato-Katz and circulating cathodic antigen-based diagnostics. (Jessica Clark)

A library of Schistosoma mansoni cell surface and secreted proteins for the identification of vaccine candidates and early serological markers of infection (Cecile Crosnier)

Small RNAs with a role in parasitism by Strongyloides nematodes (Vicky Hunt)

Spatial patterns of geo-helminths in soil environment at the Adankolo campus of Federal University Lokoja, an endemic area in North Central Nigeria (Patrick Amidu Audu)

Diagnosis of intestinal schistosomiasis by POC-CCA. A new field applicable approach to quantify score intensities. (Miriam Casacuberta Partal**)**

Novel cystatin of Trichinella spiralis inhibits inflammation mediated by bone marrow-derived macrophages (Porntida Kobpornchai)

The role played by B cells in supporting protective immunity against Trichuris muris infection is dependent on host genetic background and is independent of antibody (Rinal Sahputra)

Ecology and Ecosystems - I - (Renold C9)

16-April-2019, at 09:00 to 10:30

09:00 (30 mins)

Theory and practice of parasite management in multi-host systems - *A16552*

Presenter: **Dr Josephine Walker**, *University of Bristol*

J Walker[1];
[1] University of Bristol, UK

Humans, wildlife, domesticated animals, and parasites exist as part of complex socio-ecological systems. However, approaches to understand disease transmission have historically focused on the interactions between a single host and single disease agent. Where disease systems exhibit complexity that is not captured by current models, management strategies for that disease may fail to account for important drivers of transmission. In particular, host-generalism of parasites will impact transmission and therefore effective management strategies within a host species of interest. I will introduce my work on nematodes infecting ungulate hosts in Botswana, and draw on other studies from the literature in order to discuss methods for quantifying host-generalism and its impact on transmission through statistical and mathematical models. I will then discuss how these models have been used to make parasite management strategies more robust to the presence of additional host species through seasonal and individual targeting of treatment.

09:30 (15 mins)

Survival costs of reproduction are mediated by immune responses and parasites in wild Soay sheep - *A17254*

Presenter: **Dr Adam Hayward**, *Research Scientist, Moredun Research Institute*

A D Hayward[2]; J Leivesley[4]; [5]; L Bussiere[4]; [5]; K A Watt[3]; J M Pemberton[3]; J Pilkington[3]; T N McNeilly[2]; K Wilson[1];
[1] Lancaster University, UK; [2] Moredun Research institute, UK; [3] University of Edinburgh, UK; [4] University of Stirling, Canada; [5] University of Stirling, UK

A cornerstone of life-history theory is that reproduction is expected to be costly, such that allocation of resources to current reproduction diminishes future reproductive potential. Parasites are thought to play a key role in mediating this trade-off: reproduction is associated with less effective immune defence against parasites, and thus, reduced survival and future reproduction. A considerable number of both experimental and observational studies have tested these hypotheses in wild populations and have found that increased reproductive effort is often associated with greater parasite burden or diminished immune responses. Further, the link between infection or parasite burden and reduced survival is well established in many wild host-parasite systems. However, few systems are able to explicitly link reproductive effort, parasite-specific immune responses and future survival due to a lack of immunological tools capable of measuring responses to ecologically relevant parasites, or the inability to reliably monitor the survival of known individuals. The wild Soay sheep population of St Kilda has been intensively monitored for over 30 years, with data on reproduction, survival and gastrointestinal nematode (GIN) faecal egg counts (FEC) routinely collected. Immunological tools developed by veterinary science also enable measurement of the effectors of defence against GIN such as nematode-specific antibody responses. Using data collected during

the lambing seasons of 1991-2008, we found that animals of all ages and sexes experience an increase and then decrease in FEC, a phenomenon commonly observed in domestic sheep and referred to as the peri-parturient rise (PPR). The PPR was particularly pronounced in young animals, but among one- and two-year-olds, reproductive effort had no effect on the severity of the PPR. Among fully-grown adults, production of lambs, and particularly the successful suckling of lambs through to weaning, was associated with a more pronounced PPR. Structural equation models (SEM) revealed that reproduction in spring influences subsequent winter survival through pathways linking reproduction with FEC and body weight: reproducing females have higher FEC, lower body weight, and ultimately lower survival. Further, we collected data on FEC and faecal levels of nematode-specific antibodies throughout the lambing season of 2016. Analyses revealed that females bearing heavier litters showed increased FEC and weaker antibody responses than females bearing lighter lambs. Further, females mounting stronger parasite-specific IgG responses had lower FEC. Thus, it appears that increased reproductive effort is associated with a less effective parasite-specific immune response, with consequences for parasite FEC. Overall, these two studies provide explicit support for the hypothesis that the future fitness costs of reproduction can be mediated by effects of reproduction on parasite-specific immune responses and parasite infection.

09:45 (15 mins)

Patterns of genetic variation in the parasitic nematode *Strongyloides ratti*. - *A17112*

Presenter: **Miss Rebecca Cole**, *PhD Student, University of Bristol*

R Cole[1]; M Viney[2];
[1] School of Biological Sciences, University of Bristol, UK; [2] University of Liverpool, UK

We have investigated the population genetics of *Strongyloides ratti*, a nematode that infects brown rats (*Rattus norvegicus*). Population genetics can have important consequences for a parasites' population dynamics, infection dynamics, and response to selection pressures. The life history of *Strongyloides* spp. is dominated by repeated cycles of mitotic parthenogenesis, with facultative sexual reproduction. The frequency of sexual reproduction is highly variable among genotypes, and is believed to be extremely rare or absent in the studied populations. Mitotic parthenogenesis is unusual in nematodes and may strongly affect a species' population genetics. We have sequenced the whole genomes of more than 50 individual *S. ratti*, sampled non-destructively from three wild rat populations in the southern UK. When the whole genome is considered, individuals do not group according to sampling site but instead form two genetically distinct clusters with a range of intermediate genotypes. Each of these clusters may represent clonal descendants from a single individual, with intermediate genotypes arising from occasional sexual reproduction between these clusters. Some genomic regions show high concentrations of loci at which allele frequency is correlated with sampling site, at odds with the pattern of the genome as a whole. These genomic regions may be under differential selection at different sampling sites. Loci putatively associated with the parasitic lifestyle have been detected in *S. ratti*, and the variation in these is being investigated. Furthermore, we have compared the population genetics of *S. ratti* with that of the rat hosts, assessed by microsatellite genotyping. This has shed light on previously unclear aspects of *S. ratti* ecology. This work represents the first whole genome analysis of a parasitic nematode on this scale, and is illuminating new population genetic patterns in a species with an unusual mode of reproduction.

10:00 (15 mins)

A non-invasive sampling coupled with high-throughput sequencing for helminth characterisation from cetacean faecal samples - *A17308*

Presenter: **Dr Natalia Fraija-Fernández**, *Postdoctoral researcher, The Natural History Museum*

N Fraija-Fernández[1]; M Papaiakovou[1]; A G Briscoe[1]; R Misra[1]; K James[1]; T Littlewood[1];
[1] Natural History Museum, UK

Cetaceans hold a unique, taxonomically diverse and highly specific helminth fauna. At present, there are *ca*. 174 helminths species reported in cetaceans, including nematodes (62 spp.), digeneans (54 spp.), cestodes (38 spp.) and acanthocephalans (20 spp.). Sampling occurs after necropsies, making this methodology conditional on the availability of recently stranded cetaceans. Also, species diagnostic characteristics might be affected by the level of decomposition of host, interfering in accurate morphological identifications. Alternative methods for data collection (e.g. non-invasive sampling) and data processing (e.g. high-throughput sequencing) offer novel approximations to study and to characterise cetacean helminth communities. For this study we have established a proof-of-concept to characterise the helminth fauna found in cetaceans by applying amplicon sequencing (i.e. metabarcoding) and shotgun sequencing (i.e. metagenomics) on faecal samples collected from bottlenose dolphin *Tursiops truncatus* (n=1), sei whale *Balaenoptera borealis* (n=2) and sperm whale *Physeter macrocephalus* (n=2). Genomic DNA from each sample was extracted and, shotgun sequenced and subject to PCR amplification of the V9 region of the 18S rRNA gene using universal eukaryote primers. Libraries were prepared and sequenced on an Illumina MiSeq. Data were inspected to remove short low quality reads and chimaeras. Metabarcoding results were processed using *mothur*, and sequences were clustered into Operational Taxonomic Units (OTUs), whilst shotgun sequencing results were processed in *metaxa*, which taxonomically assign reads according to small subunit ribosomal sequences of nuclear eukaryote origin. We compared the results obtained from the two metagenomic approaches applied in order to detect helminths in cetacean faeces. We highlight the need for a dedicated bioinformatic pipeline and the importance of a properly curated database for a taxonomy-dependent classification of reads, fundamental for diagnostic metagenomics. Our study informs the development of a toolkit for helminth diagnosis from non-invasive sampling, as an alternative to study host-parasite associations when direct host sampling is problematic.

10:15 (15 mins)

Exploring trophic niches and parasite communities of sympatric Arctic charr and brown trout populations of southern Norway - *A17484*

Presenter: **Dr Rachel Paterson**, *Research Fellow, Cardiff University*

R Paterson[1]; J Nefjodova[1]; R K Salis[3]; R Knudsen[2];
[1] Cardiff School of Biosciences, Cardiff University, UK; [2] Department of Arctic and Marine Biology, Faculty of Biosciences, Fisheries and Economics, UiT The Arctic University of Norway, Tromsø, Norway; [3] University Duisburg-Essen, Germany

Catchment-scale variation between lake habitats has the potential to simultaneously influence the trophic niche and parasite community of fish hosts. Here we investigated the trophic niche and parasite community of sympatric Arctic charr *Salvelinus alpinus* and brown trout *Salmo trutta* populations from two inter-connected southern Norwegian lakes at different altitudes. Arctic charr and brown trout occupied profundal and littoral habitats in each lake respectively, whereas brown trout replaced Arctic charr in pelagic habitats of the lower altitude lake. Distinct between-lake differences in diet and parasite community composition were noted for brown trout, however both fish species showed highly overlapping trophically transmitted parasite communities regardless of the habitats each species used. Our results suggest that environmental differences over relatively limited geographical distances have the potential to influence fish habitat use and parasite community structure.

Ecology and Ecosystems - II - (Renold C9)

16-April-2019, at 11:00 to 12:30

11:00 (30 mins)

Environmental impacts on host susceptibility in mesocosms for This Wormy World - *- A16545*

Presenter: **Prof Andrea Graham**, *Associate Professor, Princeton University*

A Graham[1];
[1] Princeton University, United States

Why do hosts vary so much in worm burden, even under identical exposure conditions? My group is interested in how host genotype and environment interact to determine the establishment, growth and survival of nematodes within the gastrointestinal tract. To investigate this, we study nematodes in mice of selected genotypes under semi-natural environmental variation, in experimental mesocosms. Our findings reveal strong effects of environment: While C57BL/6 mice are resistant to high doses of *Trichuris muris* eggs under laboratory conditions, mice released outdoors for just 2 weeks harbored greatly increased worm burdens and worm biomass. We discovered enhanced microbial diversity and specific bacterial taxa predictive of nematode burden in outdoor mice. We also observed decreased type 2 immune responses in lamina propria and mesenteric lymph node cells from infected mice outdoors. These results suggest that a more natural environment rapidly changes gut microbial communities and mucosal responses to nematode infection. We are developing our mesocosm system to characterize behavioral and nutritional mechanisms by which hosts in natural populations may compensate for costs of parasitism and defense. This system provides a unique bridge between controlled laboratory immunoparasitology and host-parasite interactions in nature.

11:30 (15 mins)

Single nucleotide polymorphism linkage groups define population structure in *Cryptosporidium hominis* - *A17509*

Presenter: **Dr Anna Paziewska-Harris**, *Research Fellow, Cardiff University*

A Paziewska-Harris[1];
[1] Cardiff University, UK

Cryptosporidium hominis is a human-specific pathogen responsible for major outbreaks of cryptosporidiosis in the developed world (e.g. Milwaukee, USA, 1993; Östersund, Sweden, 2010) and for extensive mortality of infants in the developing world. While zoonotic *C. parvum* shows population substructuring into distinct clades, the population structure of *C. hominis* appears at first sight to be flat, with little variation between isolates. Comparing single nucleotide polymorphisms (SNPs) within genes across 55 *C. hominis* genomes available within public databases we find compelling evidence for the existence of two SNP linkage groups which characterise two distinct sets of *C. hominis* isolates. SNPs providing evidence of these two groups occur at a frequency of c. 1 SNP per 5kb within the gene space of the *C. hominis* genome. A complicating feature is that the two available genome sequences of the 'reference' *C. hominis* genome (TU502, an African isolate) are examples from each of the two linkage groups, suggesting that at some point in the more than 10 years between collection of samples for genome sequencing, one *C. hominis* isolate had replaced another, and there is no evidence supporting the hypothesis that the isolate had evolved between the two dates. Both *C. hominis* linkage groups include both plesiomorphic and apomorphic alleles, indicating that they are evolving from a common ancestor, rather than one being derived from the other. While most isolates can be attributed to one linkage group (TU502_resequence, UKH1, UKH3, UKH5,

30974, 37, SWEH08-13) or the other (TU502_original, UKH4, Bangladeshi isolates, SWEH01-07), there is evidence of recombination between the two groups, and the Colombian CHUDEA isolate appears to be of hybrid origin. This set of SNPs provides important markers for studying the epidemiology of *C. hominis* and can be especially useful for establishing the extent of panmixis in the species. This project has received funding from the European Union's Horizon 2020 research and innovation programme under the Marie Skłodowska-Curie grant agreement No 663830 and National Centre for 3Rs grant No NC/R000913/1.

11:45 (15 mins)

Epidemiology of "neglected" tick-borne infections in Nigeria: A (hopefully) early quest of USALTI-Afrique - *A17507*

Presenter: **Prof Richard Birtles**, *Chair in Biomedicine, University of Salford*

R J Birtles[5];V Lorusso[2]; B Adam[6]; H M Adamu[5]; I A Alozor[5]; A G Dogo[3]; [4]; M Wijnveld[1]; K Bown[6];
[1] Centre for Pathophysiology, Infectiology and Immunology, Medical University of Vienna, Austria, UK; [2]Global Research & Medical Division, Vetoquinol, Paris, France, UK; [3] University of Jos, Nigeria; [4] University of Jos, UK; [5] University of Salford, UK; [6] University of Salford Tick Infections (USALTI) Group, School of Environment and Life Sciences, University of Salford, UK

Although it is widely accepted that ticks and tick-borne infections (TBIs) majorly undermine livestock health, welfare and productivity in sub-Saharan Africa (SSA), control efforts, and research to underpin these efforts, have long centred on East Coast fever (ECF) caused by *Theileria parva*. This focus is understandable given the veterinary importance of ECF, but it has perhaps resulted in the impact of other TBIs, particularly those that compromise livestock productivity through parasitism rather than provoking acute disease, being overlooked. To disregard these other TBIs would be foolhardy, particularly at a time when factors such as vaccination, acaricide resistance and climate change are reshaping TBI epidemiology in SSA. The University of Salford Tick Infection (USALTI)-*Afrique* group was established in 2016 to provide research, educational and capacity building opportunities to students, scientists and laboratory personnel, focusing on ticks and TBIs. Our initial aim has been to gather data on the epidemiology and impact of ticks/TBIs in livestock species across SSA with an ultimate goal of guiding the design and roll-out of evidence-based strategic control interventions. Here, we present data on the diversity and epidemiology of tick infestations and TBIs in cattle, sheep and goats farmed in Nigeria, and evidence of how these might be impacting on livestock health. We demonstrate the presence of tick species not previously recorded in the country and report new TBIs. Of particular concern is the presence of *Theileria annulata*, the agent of tropical theileriosis, in north-western Nigeria. Tropical theileriosis is of great veterinary importance in northern Africa and across the middle East and southern Asia, but *T. annulata* has not previously been encountered in SSA.

12:00 (15 mins)

Freshwater snails of biomedical importance in the Niger River Valley, *Bulinus* spp., *Biomphalaria pfeifferi* and *Radix natalensis*: a longitudinal survey reveals evidence of spatial and temporal patterns in abundance and distribution. - *A17505*

Presenter: **Ms Muriel Rabone**, *SCAN data manager, Natural History Museum*

F Allan[2]; A Gouvras[1]; **M Rabone**[2]; T Pennance[2]; A Garba[3]; A E Emery[2]; B Webster[2]; A Garba[3]; D Rollinson[2];
[1] Global Schistosomiasis Alliance, UK; [2] Natural History Museum, UK; [3] RISEAL (Reseau International Schistosomoses Environnements Amenagements et Lutte), Niger

Sound knowledge of freshwater intermediate snail host distribution and abundance is critical to understanding schistosomiasis transmission, however such data are often lacking. A longitudinal field survey of freshwater snails of biomedical importance was undertaken in the Niger River Valley (NRV) between July 2011 and February 2016, targeting *Bulinus* spp. and *Biomphalaria pfeifferi*; intermediate hosts for *Schistosoma* spp., and *Radix natalensis*, intermediate host of *Fasciola*. Monthly surveys of snails were undertaken in 97 sites, representing intensive sampling effort. High abundance was associated with extensive irrigation in all species, with highest numbers of *Bulinus* spp. and *R. natalensis* in irrigation canals and *Bi. pfeifferi* only evident in this site type. Key findings were evidence of significant seasonality in abundance in all species, with snail numbers highest in the middle of the dry season (February-March) and lowest in the rainy season (July- October, particularly August) with evidence of a negative association of abundance with precipitation. All snails were investigated for infection with *Schistosoma* spp. For *B. truncatus,* seasonality of infection was also evident with highest prevalence in the middle of the dry season, and lowest in the rainy season. Both *B. truncatus* and *B. forskalii*, prevalence was relatively higher in pond habitats rather than irrigation canals, suggesting the former may potentially have higher transmission. *Bi. pfeifferi* in contrast had relatively higher prevalence than *Bulinus* spp., in particular in tertiary rather than secondary canals with peaks in June/July and again in November/Dec, however this species was only evident in two localities (reflecting its recent colonisation in the upper NRV). Our findings relating to seasonality have implications for both monitoring snails of biomedical importance, and potentially for interrupting transmission of *Schistosoma* spp., in the NRV.

12:15 (15 mins)

Totiviruses in *Leishmania* - *A17508*

Presenter: **Mr Ahmad Garziz**, *PhD, Bangor University*

A A Garziz[1];
[1] Bangor University, School of Biological Sciences, UK

Totiviridae are unsegmented, icosahedral dsRNA viruses which display a fascinating diversity of hosts, a disparity of host effects, and a divergence of transmission strategies. Hosts include human parasites like *Giardia*, plant parasitic oomycetes, fungi and yeasts, red macroalgae (seaweed), terrestrial crustaceans like woodlice, insects like flies, mosquitoes, ants and wasps, marine crustaceans like shrimp, but also fish, fresh water snails that are intermediate hosts to parasites, and plants like papaya, notoginseng, maize, and wild petunias. In *Leishmania* and *Trichomonas*, the viruses increase the virulence of the parasites (hypervirulence), while in Victoria blight of oats it reduces the virulence of the fungus (hypovirulence). In salmon, smelt, and shrimp, it causes myocarditis and myonecrosis, in golden shiners it is asymptomatic. In *Leishmania* and many fungi and some plants, it is non-infectious and vertically transmitted, while in *Giardia*, fish, shrimps, and papaya, it is horizontally transmitted. Using the RNA-dependent RNA polymerase gene of the virus, we are trying to explore the taxonomic boundaries of the vertically transmitted viruses in parasites to estimate the evolutionary age of first infection, the virulence in *Giardia*, and the evolutionary origin of dsRNA viruses in arthropods, especially sand flies, which are vectors of *Leishmania*. Exploring *Leishmania* species of the Old and New World, new viruses paint a clearer picture of the history of dissemination and loss over evolutionary time for human and animal species.

Poster Pitches EE II - (Renold C9)

16-April-2019, at 12:30 to 13:00

Assessing selective pressure in Fasciola hepatica: challenges and relevance to drug and vaccine gene targets
(Olukayode Daramola)

Out of sight: do eye flukes alter predator-prey interactions? (Meg Huggins)
A plan to sequence the genomes of all parasite species from the British Isles (Adam Reid)
The metabolic energy budget of the nymphs (Ixodes ricinus) (Saeed Alasmari)
Regulatory influence of Procambarus clarkii, Girad (Decapoda: Cambaridae) on schistosome-transmitting snails in lotic habitats within the River Athi Basin, Kenya (Geoffrey Maina)
Host specificity of bat flies in South-Eastern Europe (Áron Péter)
Speaking with a forked tongue: pentastomid parasites in man's best friend (Shokoofeh Shamsi)
T. b. gambiense; evidence of absence in NW Uganda (Lucas Cunningham)
Revising the transmission biology of schistosomiasis in Zanzibar (Tom Pennance)

Day 3 Orals

Cell Biology - IV - (Renold C2)

17-April-2019, at 09:00 to 10:30
09:00 (30 mins)

The Delivery and Activity of late blight effector proteins that suppress plant immunity *- A16564*

Presenter: **Prof Paul Birch**, *James Hutton Institute*

P Birch[1];
[1] James Hutton Institute, UK

The oomycete *Phytophthora infestans* causes late blight, the most significant disease of potato and tomato. As such, it is a threat to food security. It has been shown to secrete so-called effector proteins to suppress the host immune system. Some of these effectors, notably the RXLR class, are delivered (or translocated) inside plant cells where they interact with host proteins, manipulating their function to promote disease. The RXLR motif is similar in sequence and relative position to the PEXEL motif in *Plasmodium* effector proteins. Like the PEXEL motif, it appears to be a site for proteolytic cleavage and to act as a secretion sorting signal. I will review our current knowledge on how the RXLR effectors are translocated into host cells from finger-like structures called haustoria that are formed by the pathogen during the early stages of infection. We have found that some of these RXLR effectors target and suppress the activity of plant proteins that are positive regulators of immunity. In contrast, other RXLRs target negative regulators of immunity, presumably supporting or promoting their activity to create a susceptible environment. This presentation will review both classes of RXLR effector activity, and where this occurs within the plant cell.

Divergent roles of the RH5 complex components, CyRPA and RIPR in human-infective malaria parasites *- A17215*

Presenter: **Dr Ellen Knuepfer**, *Research Scientist, The Francis Crick Institute*

E Knuepfer[3]; K E Wright[1]; S Kumar Prajapati[2]; S Howell[3]; A P Snijders[3]; A Rosanas-Urgell[2]; M K Higgins[4]; J Baum[1]; T Holder[3];
[1] Imperial College London, UK; [2] Institute of Tropical Medicine, Antwerp, Belgium; [3] The Francis Crick Institute, UK; [4] University of Oxford, UK

Malaria is caused by *Plasmodium* parasites, which invade and replicate in erythrocytes. *Plasmodium falciparum* causes the most severe form of malaria in humans. *Plasmodium* parasites use multiple receptor-ligand interactions to gain entry into the host erythrocyte. Most of these pathways are dispensable and this redundancy allows the use of alternative invasion pathways to guarantee successful proliferation. Achieving the inhibition of these receptor-ligand interactions is the aim of a blood-stage malaria vaccine strategy. However, this redundancy in invasion ligand usage, together with extensive sequence polymorphisms in these ligands between parasite strains, has hindered the successful development of effective malaria vaccines. Recently a novel, highly conserved ligand, RH5, was identified, which binds to basigin on the host erythrocyte. This interaction constitutes an essential invasion pathway and thus RH5 is now the leading vaccine candidate for blood stage *Plasmodium falciparum* caused malaria.
RH5 forms a trimeric protein complex together with RH5-interacting protein (RIPR) and cysteine-rich protective antigen (CyRPA). The complex first binds to basigin on the host cell but is described to then integrate into the erythrocyte membrane. The current model postulates that a multimeric RIPR- RH5 complex inserted into the erythrocyte membrane results together with unknown proteins in the formation of a pore which ultimately mediates Ca^{2+} signalling in the host cell. This step is believed to prepare the erythrocyte for invasion. One would think that such a fundamental step in the invasion process is likely conserved in other human malaria parasite species. However, RH5 is only found in species of the *Laverania* subgenus, whereas RIPR and CyRPA are conserved more widely across the genus.
Here, using CRISPR-Cas9-mediated gene modifications and the inducible DiCre recombinase system we have studied the functions of RIPR and CyRPA and the role of basigin as a host receptor for other human malaria parasites. We show that both RIPR and CyRPA are essential in *P. knowlesi* but in the absence of RH5 these proteins do not form a complex. We have instead identified a new protein complex involving RIPR and show that this complex plays an essential role during invasion. We also show that amongst the human malaria-causing parasites, *P. knowlesi*, *P. vivax* and *P. falciparum,* only the latter is reliant on basigin for invasion, consistent with the absence of RH5 in the other parasite species. We further elaborate on the crucial but independent roles of PkRIPR and PkCyRPA for parasite proliferation.

09:45 (15 mins)

Using CRISPR-Cas9 genome-editing to study *Plasmodium falciparum var* genes *- A17323*

Presenter: **Prof Alex Rowe**, *Professor of Molecular Medicine, University of Edinburgh*

H Abkallo[1]; H Stawarz[1]; **J A Rowe**[1];
[1] Centre for Immunity, Infection and Evolution, Institute of Immunology and Infection Research, School of Biological Sciences, University of Edinburgh, UK

Malaria parasites undergo antigenic variation to avoid host antibody responses and prolong infection. The main family of variant surface antigens that undergo switching are the *var* gene family, encoding PfEMP1 expressed on the surface of infected red cells (1). Recent work suggests that parasites have a predictable switching hierarchy (2), but it is unknown whether changes in the host environment affect switching rates or patterns. *Var* gene switching can be studied *in vitro*, but parasite cultures usually transcribe multiple different *var* genes, making experimental design problematic. We have used CRISPR-Cas9 genome-editing to create a *Plasmodium falciparum* parasite line that transcribes a single *var* gene *in vitro* when under drug selection. This was done by linking a drug resistance gene (Blasticidin-S Deaminase) to a specific rosette-mediating *var* gene, joined by a 2A peptide to ensure co-translation. When under drug pressure, only parasites expressing that single *var* gene can survive. This allows us to generate a parasite line in which 100% of infected erythrocytes are transcribing the same

var gene and form rosettes. When blasticidin is removed, the parasites start to switch spontaneously to other *var* genes, and the frequency of switching can be monitored over time by monitoring the change in rosette frequency and by using real-time quantitative Reverse Transcriptase-PCR (qRT-pCR). We used this 'single variant' parasite line to investigate the hypothesis that environmental factors influence parasite *var* gene switching patterns. The results generated following parasite exposure to environmental factors associated with severe malaria including low glucose, high lactate, low pH, high cytokine levels and antibodies to PfEMP1, will be presented.
References: 1. Deitsch KW, Dzikowski R. Annu Rev Microbiol. 2017doi: 10.1146/annurev-micro-090816-093841 2. Noble R, Christodoulou Z, Kyes S, Pinches R, Newbold CI, Recker M. Elife. 2013;2:e01074. doi: 10.7554/eLife.01074.

10:00 (15 mins)

Tailored CRISPR screening in *Toxoplasma gondii* identifies novel virulence factors *in vivo* - *A17501*

Presenter: **Dr Joanna Young**, *Postoctoral researcher, The Francis Crick Institute*

J Young[1]; C Dominicus[1]; X Ye[1]; J Wagener[1]; S Butterworth[1]; G Kelly[1]; A Stewart[1]; M Treeck[1];
[1] The Francis Crick Institute, UK

Genome wide CRISPR screening is a powerful tool in identifying genes required for survival or growth in certain conditions. However, the inherent large scale of genome wide screens requires large amounts of starting material and importantly hampers *in vivo* analyses, where the animal would succumb to high infectious doses. To address host-pathogen interactions during *in vivo* infections, a more versatile screening method was required. We have set up a tailored CRISPR screening system in *Toxoplasma gondii*, a natural mouse pathogen. We have generated an arrayed gRNA library for single step cloning of gRNA pools in to a custom CRISPR/Cas9 vector. This system allows the pool size, the genes targeted and the controls to be customised to the experimental question. This versatility means libraries of gene subsets, e.g. transcription factors, kinases, or secreted proteins, can be rapidly generated in a single cloning step. To test the system *in vivo*, we selected a pool size of 1000 gRNA to be compatible with mouse infections while providing sufficient coverage at the gRNA level. Assaying pooled *T. gondii* mutants through mice recapitulated expected phenotypes of known virulence factors, and importantly identified novel genes that are required for infection. Interestingly, some previously reported virulence factors are essential for *Toxoplasma* survival in the murine host while others appear to be non-essential if part of a larger pool. This may separate virulence factors based on their role in the innate immune response.

10:15 (15 mins)

Inhibition of fatty acid oxidation: a new treatment strategy for Primary Amoebic Meningoencephalitis? - *A17248*

Presenter: **Mr Maarten Sarink**, *PhD-student, Erasmus MC*

M J Sarink[1]; M L Bexkens[1]; A G Tielens[2]; J J van Hellemond[1];
[1] Erasmus MC University Medical Center Rotterdam, Netherlands; [2] Utrecht University, Netherlands

Background. The free-living amoeba *Naegleria fowleri* causes Primary Amoebic Meningoencephalitis (PAM), a rapidly fatal disease of the central nervous system (CNS). This brain-eating parasite can enter the CNS by migrating from the nasal epithelium along the nasal nerve to the olfactory bulb. Symptoms include severe headache, fever and seizures, with deterioration into coma and eventually death. Current treatment consists of a wide range of antifungals and antibiotics. However, despite this extensive treatment, prognosis is extremely poor

with a fatality rate of over 95% within 2 weeks of symptom onset. Previous experiments performed in our laboratory showed that *Naegleria gruberi*, a non-pathogenic close relative of *N. fowleri*, prefers fatty acids as a food source. This could provide a new treatment strategy against PAM. Methods. *N. gruberi* ATCC 30224 was used to evaluate the effects of several fatty acid oxidation inhibitors in comparison to the current treatment. A high throughput *N. gruberi* growth monitoring assay using optical density was developed to evaluate inhibitory effect of compounds on growth. Compounds were tested on their own as well as in combinations. In addition to growth inhibition, the killing capacity of the compounds was assessed by analysis of regrowth after washing away the compounds. Results. Several inhibitors of fatty acid oxidation restricted *in vitro* growth (Valproic acid (VPA), Orlistat (ORL), Thioridazine (TDZ)) and some also prevented regrowth (Perhexiline (PHX), Etomoxir (ETO)). Current treatment (Amphotericin B (AmB) and Miltefosine) was shown to be effective as well, which validates our high throughput assay. Additive effects were observed when VPA was combined with any of the other fatty acid oxidation inhibitors. Furthermore, killing was achieved when VPA, ETO or PHX was combined with AmB, while single used drugs did not show killing capacity.

. Repurposing drugs is the only way to obtain new treatment options for PAM, as the rapid fatal nature of the disease does not allow randomized controlled trials to be performed. Using an hypothesis-driven approach, we identified several currently used drugs that inhibit amoebal growth. Two of these (VPA and TDZ) showed effectivity at concentrations attainable in the human brain, in contrast with current therapy (AmB and MIL), which cannot reach therapeutic concentrations at the site of infection. Furthermore, VPA and TDZ showed an additive effect on growth inhibition when these drugs were combined. As the primary effect of VPA also relieves one of the symptoms of PAM, we believe this *in vitro* research can be rapidly applied in the clinic.

Cell Biology - V - (Renold C2)

17-April-2019, at 11:00 to 13:00

11:00 (30 mins)

Mutually Assured Destruction - *Wolbachia* and the role of host autophagy in population control, antibiotic mode of action and viral protection - *A16561*

Presenter: **Prof Mark Taylor**, *Head of Department, Parasitology, Liverpool School of Tropical Medicine*

M Taylor[1];
[1] Liverpool School of Tropical Medicine, UK

Wolbachia are widespread and abundant endosymbionts, ranging from mutualists with filarial nematodes to reproductive parasites of arthropods. Across their diverse host range the bacterium is recognised by host autophagy, which regulates *Wolbachia* population levels. Even where they have evolved a mutualistic relationship, as with filarial nematodes, the host still 'see' them as pathogens – a process which the bacterium has to evade to survive and grow. I will discuss evidence that the interaction of *Wolbachia* with host autophagy extends beyond population control and underpins two of the key public health benefits of targeting *Wolbachia*. Firstly, I will show how antibiotics that are effective in delivering potent macrofilaricidal therapy rely on autophagy as part of their mode-of-action and, secondly, show how *Wolbachia's* subversion of autophagy and its impact on lipid biosynthesis renders cells refractory to arboviruses, which depend on the autophagic machinery for their replication.

11:30 (30 mins)

Flagellum length control during the trypanosome life cycle - *A16565*

Presenter: **Prof Philippe Bastin**, *Director of Research, Institute Pasteur*

P Bastin[1];
[1] Institute Pasteur, France

During its complex life cycle, *Trypanosoma brucei* encounters highly variable environments: the gut and the salivary glands of the tsetse fly, the skin and the blood in mammalian hosts. It adapts to these changing conditions by modifications in cell surface composition, metabolism and morphogenesis. One of the most striking features is the length of the flagellum that fluctuates from 3 to 30 µm. This organelle is essential for parasite survival. This talk will discuss the different mechanisms trypanosome use to modulate the length of their flagellum, with studies in parasites in culture and during the infection of tsetse flies.

12:00 (15 mins)

Trafficking itinerary of aquaglyceroporin 2 in *T. brucei*: new insights into the mode of action of pentamidine. *- A17013*

Presenter: **Dr Juan Quintana**, *Postdoctoral Research Associate, University of Dundee*

J Quintana[1]; M C Field[1];
[1] University of Dundee, UK

In *T. brucei,* intracellular trafficking of surface proteins is essential for the mode of action of several trypanocidal compounds. One clear example is involvement of several components of the endocytic machinery in susceptibility to suramin and ubiquitin-mediated internalisation of ISG75. However, the role of endocytosis in susceptibility to other trypanocidal compounds remains to be further elucidated. Here we demonstrate that *T. Brucei* aquaglyceroporin 2 (TbAQP2), a type III transmembrane domain protein, also undergoes ubiquitin-mediated internalisation in the bloodstream form of *T. brucei*. As previously reported for the type I transmembrane protein ISG75, TbAQP2 is post-translationally modified by ubiquitin. Moreover, TbAQP2 forms high molecular weight complexes (~500 kDa), is a short-lived protein(~1-3h), and degradation seems to be dependent on lysosomal function. Interestingly, there is an overall impairment to lysosomal acidification when cells were exposed to pentamidine, similar to the phenotype observed following Bafilomycin A1 treatment. Furthermore, a concomitant impairment on lysosomal-dependent protein degradation was also observed in pentamidine-treated cells, indicating that pentamidine is likely to disrupt lysosomal function. We conclude that internalisation of TbAQP2 follows a similar, but also distinct, intracellular trafficking itinerary to that of ISG75, leading to lysosomal degradation. We propose a model whereby TbAQP2 internalisation, mediated by direct ubiquitination as reported for other membrane proteins, leads to an accumulation of pentamidine in the lysosome, impairing its function. Our study shows a potential interplay between different intracellular organelles during pentamidine exposure and, in addition to the effects previously reported for loss of mitochondrial membrane potential, provides further insights into the mode of action of pentamidine.

12:15 (15 mins)

In vitro activity of chitosan and derivatives against *Leishmania major* and *Leishmania mexicana* *- A16975*

Presenter: **Mr Alaa Riezk**, *PhD student, London School of Hygiene and Tropical Medicine*

A Riezk[1]; J G Raynes[1]; V YARDLEY[1]; S Murdan[2]; S L Croft[1];
[1] London School of Hygiene & Tropical Medicine, UK; [2] UCL , School Of Pharmacy, UK

Background: Leishmaniasis is a vector-borne neglected tropical disease caused by over 20 species of the protozoan *Leishmania* parasite. Cutaneous leishmaniasis (CL) affects approximately 12 million people worldwide. Currently available drugs are not ideal due to high cost, toxicity, and variable cure rates. There is an urgent need for short, safe, efficacious, affordable and field-adapted drugs against *Leishmania* parasites that cause CL. Chitosan is a biocompatible and biodegradable cationic polysaccharide previously reported with antimicrobial, antileishmanial and immunostimulatory activities. In this study we aimed to determine: (i) the in *vitro* anti-leishmanial activity of chitosan and its derivatives against *L. major* and *L. mexicana* promastigotes and intracellular amastigotes at different pH values, (ii) immunostimulation by high molecular weight chitosan (HMW) via investigation into the production of nitric oxide (NO), reactive oxygen species (ROS) and tumour necrosis factor (TNF-α) by host cells, and (iii) the route of uptake of HMW chitosan by infected macrophages.
Methods: The antileishmanial activity of chitosan was confirmed in *vitro* against promastigotes by a colorimetric assay and against intracellular amastigotes by microscopical counting of number of infected and uninfected cells per 100 macrophages compared to the control. *In vitro* immunostimulatory effects on bone marrow macrophages (BMMs) were evaluated by measuring NO, ROS and TNF-α production. Confocal microscopy and endocytic inhibitors were used to demonstrate the route of uptake of chitosan (rhodamine labelled) by macrophages.
Results: Medium pH was shown to play a critical role in the *in vitro* activity of chitosan and its derivatives against both *Leishmania* promastigotes and amastigotes. Chitosan was approximately 20 times more active in RPMI at pH≈6.5 than in RPMI at pH≈7.5. HMW Chitosan was significantly more active than other types of chitosan against both *Leishmania* promastigotes and intracellular amastigotes. HMW Chitosan had immunostimulatory effects on macrophages, stimulating the production of both NO and ROS in a time and dose dependent manner at pH ≈ 6.5. The inhibition of chitosan uptake by macropinocytosis with reduction in drug activity, indicated strongly the direct anti-leishmanial effect of this molecule. Confocal studies of the uptake of rhodamine-labelled chitosan showed accumulation in the parasitophorous vacuole.
Conclusions: The data indicates that pH had significant effects on the anti-leishmanial activity of chitosan. In the macrophage model, the anti-leishmanial activity of chitosan was not due to immune stimulation but related to direct uptake of chitosan into the parasitophorous vacuole.

12:30 (15 mins)

Trypanosomal peptidases-promising targets for point of care animal African trypanosomiasis diagnostics - *A17303*

Presenter: **Prof Theresa Coetzer**, *Research Professor, University of KwaZulu-Natal*

L E Eyssen[1]; J Viljoen[1]; R Peter[2]; P Büscher[3]; **T Coetzer**[1];
[1] Biochemistry, University of KwaZulu-Natal, South Africa; [2] Global Alliance for Livestock Veterinary Medicine, UK;
[3] Institute of Tropical Medicine Antwerp, Belgium

Tsetse-transmitted haemoprotozoan parasites, *Trypanosoma congolense* and *T. vivax*, cause African animal trypanosomiasis (nagana), a wasting disease of cattle and small ruminants. Current tsetse control methods are not effective and drug resistance has been reported in 17 African countries. No new drugs have been developed for nagana in the past 60 years. The variable surface glycoprotein coat of the parasite makes vaccine development unlikely. A further impediment to nagana surveillance and control is the lack of a simple, rapid and cost-effective diagnostic test for use in resource poor endemic settings. Current diagnostic tests are either based on detecting parasites in the blood of infected animals using microscopy, serodiagnostics using parasite lysates to detect antibodies or by amplifying parasite specific DNA; all of which lack specificity and are costly. We identified cysteine and serine peptidases, which are released by trypanosomes in the host bloodstream, that have potential as diagnostic targets. Recognition of recombinantly expressed cathepsin L-like peptidases from *T. congolense* and *T. vivax* (*Tc*CATL and *Tv*CATL) and oligopeptidase B *Tc*OPB and *Tv*OPB by sera of experimentally infected cattle

was tested in an indirect ELISA. The best performing peptidase antigens were adapted to a penside/dipstick test format to detect antibodies in *T. congolense* and *T. vivax* infected cattle sera. Since antibody-detection tests cannot distinguish between current and past infections, an antigen detection test was devised based on OPB-specific single chain variable fragment (scFv) antibodies identified from the *Nkuku*® phagemid library. This OPB-specific scFv recognises a conserved peptide in the *T. congolense* and *T. vivax* OPB homologs, and detected native OPB in a western blot. An antigen detection ELISA using this scFv as capture antibody and rabbit-anti-OPB IgG-HRPO antibody showed that OPB levels fluctuated with parasitaemia in sera from *T. congolense* infected cattle.

12:45 (15 mins)

Developmental competence and surface antigen switch frequency can be uncoupled in *Trypanosoma brucei* - *A17198*

Presenter: **Prof Keith Matthews**, *Professor, University of Edinburgh*

K R Matthews[2]; K McWilliam[1]; M Mugnier[3]; L Morrison[4];
[1] Institute for Immunology and Infection Research, University of Edinburgh, UK; [2] Institute of Immunology and Infection Research, University of Edinburgh, UK; [3] Johns Hopkins Bloomberg School of Public Health, Baltimore, MD, United States; [4] Roslin Institute, Easter Bush, University of Edinburgh, UK

African trypanosomes use an extreme form of antigenic variation to evade host immunity. This involves the switching of expressed variant surface glycoproteins, antigen exchange being a stochastic and parasite intrinsic process. Parasite development in the mammalian host is another feature of the infection dynamic, with trypanosomes undergoing quorum sensing-dependent differentiation between proliferative slender form and arrested, transmissible, stumpy forms within each parasitaemic wave. Longstanding experimental studies have suggested that the frequency of antigenic variation and transmissibility may be linked, antigen switching being higher in fly-transmissible, developmentally competent, parasites and lower in serially passaged lines. Here, we have directly tested this tenet of the infection dynamic by, firstly, generating lines that inducibly lose developmental capacity through RNAi mediated silencing of components of the stumpy induction signalling cascade ('inducible monomorphs'). Secondly, we have derived *de novo* lines that have lost the capacity for stumpy formation by serial passage ('selected monomorphs') and analysed their antigenic variation in comparison to isogenic pre-selected populations. Analysis of both inducible and selected monomorphs by *in vitro* flow-cytometry based VSG switch assays and VSGseq has established that antigen switch frequency does not change regardless of the method used to prevent parasite development. We conclude that changes in antigen switch frequency and developmental capacity can be uncoupled, these independently selected traits being important contributors to the parasite infection dynamic.

Host-Pathogen interactions - IV - (Renold C16)

17-April-2019, at 09:00 to 10:30

09:00 (30 mins)

Heligmosomoides polygyrus secretes multiple immunomodulators of early innate immune responses - - *A16548*

Presenter: **Prof Henry McSorley**, *University of Edinburgh*

H McSorley[1];
[1] University of Edinburgh, UK

IL-33 is a potent initiator of type 2 immune responses, and is released rapidly on damage to epithelial barriers. It therefore represents an upstream target for prevention of type 2 immune responses which both cause allergic disease and are responsible for parasite ejection. The intestinal nematode *Heligmosomoides polygyrus* forms chronic infections in mice, due to its ability to effectively modulate the host immune response. Functional studies of the secreted products of *H. polygyrus* led us to identify a series of suppressors of the IL-33 pathway, the first of which, the *H. polygyrus* Alarmin Release Inhibitor (HpARI) binds directly to both IL-33 and to DNA within necrotic cells. This dual functionality of HpARI gives it the unique ability to "tether" IL-33 within necrotic epithelial cells, preventing IL-33 release, and blocking its activity. We believe that HpARI is the first of many such parasite-derived suppressors of early innate type 2 immune responses, which could have potential for use as therapeutic agents in human allergic diseases.

09:30 (15 mins)

TGF-β bioactivity in *Trichuris muris* can induce Foxp3+ T regulatory cells and inhibit Th1 and Th2 polarisation. *- A17181*

Presenter: **Mrs Adefunke Ogunkanbi**, *PhD student, University of Manchester*

A Ogunkanbi[3]; B Eldakhakhny[2]; J L Pennock[3]; P J Cooper[1];
[1] Centro de Investigacion en Enfermedades Infecciosas, Pontificia Universidad Catolica del Ecuador, Quito, Ecuador, Ecuador; [2] King Abdulaziz University, Saudi Arabia; [3] University of Manchester, UK

Gut dwelling nematodes infect nearly 2 billion people worldwide with children being the most affected. Chronic infection with helminths is associated with immune hyporesponsiveness; inflammation is regulated by the induction of cytokines such as IL-10 and TGF-β. Evidence to date demonstrates that helminths can encode TGF-β-like ligands to modulate the immune response and enhance their survival, although little is known about *Trichuris spp*. Given the potential for *Trichuris* as a therapeutic, we were interested to better understand the observed immunoregulation by these helminths *in vivo.*
Using a reporter cell line for TGF-β bioactivity, we showed that *Trichuris muris* excretory-secretory product and homogenate have significant dose dependent TGF-β bioactivity when activated at low pH. This activity was seen across all the life cycle stages as well as in both male and female parasites. Other helminth species such as *Trichuris trichiura, Ascaris lumbricoides, Heligmosomoides polygyrus, and Trichinella spiralis* also showed significant homology and TGF-β bioactivity after activation. Importantly, TGF-β activity was abrogated in the presence of pan-vertebrate anti–TGF-β blocking antibody (1D11; known to interact with mammalian TGF-β1, 2, and 3) as well as anti-mouse TGF-β receptor 1 and 2 antibody. Functionally, activated worm homogenate promotes significant Foxp3 induction *ex vivo* in a dose dependent manner and inhibits Th1 and Th2 polarisation. Finally we explore possible activation mechanisms of the worm TGF-β activity *in vitro*. Our data support the paradigm that worms have evolved common mechanisms to potentiate their survival. These data complement and extend our current understanding of helminth immunoregulation, demonstrating that helminth species possess as yet unidentified latent TGF- β activity that can potentially be activated *in vivo.*

09:45 (15 mins)

The major secreted protein of the whipworm parasite tethers to matrix and inhibits interleukin-13 function *- A17108*

Presenter: **Dr Allison Bancroft**, *Research Associate, University of Manchester*

A J Bancroft[1]; C W Levy[1]; T A Jowitt[1]; K S Hayes[1]; S Thompson[1]; E A Mckenzie[1]; B Bellina[1]; S L Brown[1]; P C Cook[1]; A S MacDonald[1]; D J Thornton[1]; R K Grencis[1];
[1] University of Manchester, UK

Infection by soil transmitted parasitic helminths e.g. *Trichuris* spp are ubiquitous in man and animals but mechanisms determining persistence of chronic infection are poorly understood. We show that p43, the single most abundant protein in *T. muris* excretions/secretions, is non-immunogenic during infection and has an unusual sequence and structure containing thrombospondin type 1 subdomain homology to interleukin (IL)-13 Receptor alpha 2. Binding of p43 to IL-13, the key effector cytokine responsible for *T. muris* expulsion, inhibited IL-13 function both *in vitro* and *in vivo*. Tethering of p43 to matrix proteoglycans presents a bound source of p43 to facilitate interaction with IL-13, which may underpin chronic intestinal infection. Exploiting the biology of p43may open up new approaches to modulating IL-13 function and control of *Trichuris* infection.

10:00 (15 mins)

3D X-ray microscopy (XRM) for investigating host-parasite interactions and helminth biology reveals a potential novel behavioural-based survival strategy *- A17239*

Presenter: **Mr James O'Sullivan**, *PhD student, The University of Manchester*

J O'Sullivan[1]; K J Else[1]; S Cruickshank[1]; P Withers[1];
[1] University of Manchester, UK

The whipworm *Trichuris muris* is estimated to infect half a billion people worldwide, causing considerable morbidity and economic damage. The Trichurid lifecycle is unusual as worms spend most of their lives partly embedded within a tunnel of host intestinal epithelial cells. Despite decades of study of *Trichuris muris,* a murine model of Trichuriasis, the formation, function and maintenance of this "epithelial tunnel" during chronic infection remain poorly understood. We have taken a new approach to address these issues by using **X-ray microscopy (XRM)** to view the complex attachment site of whole worms, the inherently 3D nature of which makes it difficult to study by traditional sectioning. Uniquely, XRM was able to capture key architectural features of the gut, as well as the internal morphology of whole worms and their attachment sites. A new behavioural feature of *Trichuris* was identified, namely a "crypt-seeking" behaviour in adult worms. Here, the anterior-most portion of the worm was consistently positioned close to the bases of crypts. Interestingly, crypt-seeking behaviour was less prominent in Severe Combined Immunodeficient (SCID) mice with similar burdens of *Trichuris muris*. In addition, development of a brand new purpose-built 3D mucosa measuring tool has revealed that the increased crypt-seeking behaviour is accompanied by crypt hypertrophy which is less prevalent in SCID mice. The crypt-seeking behaviour and crypt hypertrophy are suggested to represent a novel survival strategy, being indicative of avoidance of the epithelial escalator effector mechanism of the host. These results represent a first in using 3D XRM to understand the *Trichuris muris* niche. Beyond these insights, we illustrate the efficacy and novel unique application of XRM in finding rare features, surveying enteric morphology accurately in 3D and providing new opportunities for more sophisticated, site-specific morphometry of a variety of soft tissues which will be of interest to a broad range of parasitologists.

10:15 (15 mins)

Towards the development of a novel vaccine for *Trichuris trichiura* *- A17205*

Presenter: **Mrs Ayat Zawawi**, *PhD student, The University of Manchester*

A Zawawi[1];
[1] The University of Manchester, UK

Trichuris trichiura (whipworm) is a soil-transmitted helminth parasite that affects around 500 million people worldwide, resulting in disability and poor child development, especially in areas of poor hygiene and sanitation. The ideal vaccine to protect against *T. trichiura* in humans would include protein epitopes that elicit a protective T helper cell type 2 immune response. Herein, we used bioinformatics tools to identify candidate histocompatibility complex class II (MHC-II) molecule T cell epitopes from known *Trichuris muris* proteins selected using inclusion and exclusion criteria. *T. muris* is the murine whipworm that is closely related to the human pathogen making it a relevant model parasite. A number of prediction tools are available for the identification of peptides that bind to MHC II molecules. The lack of standardised methodology and the difficulty of MHC II epitope prediction make the selection of an appropriate prediction tool difficult. This study reports a systematic review to choose the most appropriate tools to predict MHC II epitopes. Subsequently, up to fifteen epitopes were predicted, from the selected *T. muris* proteins and expressed on Hepatitis B core antigen virus-like particles VLP (HBc-Ag). VLPs expressing *Trichuris* MHC II T cell epitopes were tested *in vitro* to address whether they could activate and be taken up by antigen presenting cells (APCs).VLPs expressing T cell epitopes efficiently stimulated both antigen presenting cells (dendritic cells and macrophages) to produce a broad range of pro-inflammatory and anti-inflammatory cytokines and were internalised and well co-localized in the lysosomes of both APCs. We also immunised mice with VLP+T cell epitopes prior to infection with *T. muris* to test the protective immune response *in vivo*. Notably, upon challenge infection, vaccinated mice with VLP+T cell epitopes showed significantly reduced worm burden in the caecum and colon. Immunisation of mice with VLPs+T cell epitopes followed by infection induced *T. muris*-specific IgM and IgG2a antibody responses. High levels of VLPs+T cell epitopes-specific IgM, IgG1 and IgG2a, were also induced after challenge infections. The protection of mice by VLPs+T cell epitopes was also characterised by the production of MLN-derived Th2 cytokines. The predicted epitopes identified using the right combination of immunoinformatics and immunogenicity screening tools have the potential to bring *T. trichiura* to vaccine trial.

Host-Pathogen interactions - V - (Renold C16)

17-April-2019, at 11:00 to 13:00

11:00 (30 mins)

Immune-driven control of *Toxoplasma gondii* in human cells - *A16547*

Presenter: **Dr Eva Frickel**, *Group Leader, Francis Crick Institute*

E Frickel[1];
[1] Francis Crick Institute, UK

Toxoplasma gondii is an important pathogen of man with 30% of the world's population infected. Immunocompetent people generally control the infection. However, *Toxoplasma* infection can lead to congenital abnormalities, ocular disease and health problems in the immunocompromised. People contract *Toxoplasma* by ingesting contaminated food or water or by eating undercooked meat from infected livestock. As a unicellular eukaryote *Toxoplasma* can invade any nucleated cell and reside inside the cell in a parasitophorous vacuole. The vacuole shields the parasite from intracellular defence mechanisms in the absence of the immune system. To date, even though we know that the cytokine interferon gamma can elicit cellular defences against *Toxoplasma*, we do not know the fate of the *Toxoplasma* vacuole in human cells. As the parasite is controlled in immunocompetent people, it is our goal to define molecular mechanisms of how *Toxoplasma* is restricted in IFN-γ stimulated human cells. I will share our latest findings of how different human cell types combat *Toxoplasma*. The common theme is

the recognition of the vacuole by host defence proteins, such as ubiquitin and large GTPases, the guanylate binding proteins (GBPs). The mechanisms of parasite destruction inside the vacuole in non-phagocytic and phagocytic cells is seemingly different. This leads to divergent consequences for the host cells, with a large proportion of infected macrophages undergoing apoptosis. The parasite is thus depleted of its critical host, hence curbing *Toxoplasma* replication. In summary, human host cells employ novel yet undefined pathways to control *Toxoplasma* and cannot always be compared to the murine anti-*Toxoplasma* response.

11:30 (30 mins)

Adopting helminth-induced regulatory strategies: who is exploiting who? - *A16551*

Presenter: **Prof Hermelijn Smits**, *Leiden University*

H Smits[1];
[1] Leiden University, Netherlands

Helminths like *Schistosoma mansoni* are master regulators of the host immune system. They can manipulate and suppress host immune responses directed against the worms. Consequently, worm pairs can live up to ten years in the host without being expelled. The suppression of the host immune system by helminths can have a beneficial 'side-effect': in field studies, a reverse association was found in children between helminth infections and allergies or asthma. This might be explained by a proper and beneficial education of the immature immune system of young children. The strongest evidence that helminth infections protect against allergic respiratory inflammation comes from animal models, where is shown that infections with various helminth species prevent the onset of allergic airway inflammation in a prophylactic fashion and worm-induced regulatory immune cell populations are responsible for this effect. This makes it interesting to investigate host-helminth interactions and to study communication strategies by helminths that are responsible for these beneficial effects. These molecular mechanisms could be adopted to develop new drugs for inflammatory diseases and to take advantage of the therapeutic effects of the worms without the downsides of chronic infections.

12:00 (15 mins)

A controlled human *Schistosoma mansoni* infection model to accelerate the development of novel medicine, vaccines and diagnostics. - *A17231*

Presenter: **Mrs Marijke C C Langenberg**, *PhD student, LUMC*

M C Langenberg[1]; M A Hoogerwerf[1]; J P Koopman[1]; J J Janse[1]; L van Lieshout[1]; A Van Diepen[1]; P L Corstjens[1]; G J van Dam[1]; C H Hokke[1]; M Yazdanbakhsh[1]; L G Visser[1]; M Roestenberg[1];
[1] Leiden University Medical Center, Netherlands, Netherlands

Background: Controlled human infections (CHI) provide a platform to accelerate the development of novel drugs and vaccines for infectious diseases and reduce the risk of failure in downstream clinical development. For schistosomiasis, no such model exists. Previously we established a method to produce single-sex *Schistosoma mansoni (Sm)* cercariae according to regulatory requirements for human use, as a perquisite for the development of a CHI model for schistosomiasis. Infections with single-sex worms do not lead to the deposition of eggs and therefore pathology is avoided. Methods: We performed a dose-escalating clinical trial in 17 healthy volunteers to assess the safety, tolerability and infectivity of an experimental infection with male *Sm* cercariae. Groups of three to eight volunteers were each exposed to 10, 20 or 30 *Sm* cercariae. Results: No serious adverse events occurred. Exposure to 10 male *Sm* cercariae was well tolerated with mild adverse events mainly related to the skin penetration of the parasites. All three volunteers exposed to 30 cercariae reported severe adverse events, of which one volunteer developed a prolonged Katayama syndrome. Subsequent exposure of 11 volunteers to 20 cercariae

was well tolerated. Serum circulating anodic antigen (SCAA) levels peaked at 6-8 weeks following exposure, giving an 82% parasitological infection rate in the 20 cercariae group. All volunteers showed adult worm IgM seroconversion (week 4-6) and adult worm antigen (AWA) specific IgG1 seroconversion (week 16). Symptoms at week 3-5 after exposure are likely due to (juvenile) worm-induced immune responses at this timepoint. All volunteers were cured with one or two regimens of praziquantel. Conclusions: Controlled infection with 20 male *Sm* is safe, well tolerated and gives highly (82%) efficient infection rates. This innovative model paves the way for fast-track cost-effective vaccine and drug testing in the future. Trial registration number: clinicaltrials.gov number NCT02755324

12:15 (15 mins)

The diagnostic potential of glycan specific antibodies in schistosomiasis assessed by glycan microarrays *- A17493*

Presenter: **Dr Anna Kildemoes**, *Postdoc, Leiden University Medical Centre*

A O Kildemoes[1]; Y Y Yang[1]; L Nguyen[1]; T Veldhuizen[1]; G J van Dam[1]; M Yazdanbakhsh[1]; M Roestenberg[1]; A Van Diepen[1]; C H Hokke[1];
[1] Leiden University Medical Center, Netherlands, Netherlands

During *Schistosoma* infections, antibodies are raised against numerous antigens expressed by parasite larvae, adult worms and eggs. A large proportion of these antibodies are directed against antigenic glycans that are part of the parasite's glycoprotein and glycolipid repertoire. If and how anti-glycan antibodies play a role in immunity to schistosomiasis remains poorly understood. However, it is clear that antibodies in sera to defined schistosome glycans may constitute valuable parameters for detection of and distinction between schistosome exposure or infection. Such additional tools would be useful for monitoring treatment efficacy and in schistosomiasis control/ elimination programs.
During detailed glycomics analysis of *Schistosoma mansoni* cercariae, schistosomula, adult male and female worms and eggs, we have isolated and identified hundreds of glycans from the parasite. These native parasite glycans in combination with a number of synthetic glycans related to schistosomes and other helminths were used to construct glycan microarrays covering a large portion of the potential glycan antigen repertoire of schistosomes. As such, the arrays contain glycans uniquely present in schistosomes as well as glycan antigens cross-reactive with other helminths, microbes, vectors, food, or the environment in general. These microarrays were used to analyse sera from experimentally infected animals, as well as cross-sectional human cohorts from *S. mansoni* and *S. haematobium* endemic areas, with respect to IgM, IgG and IgE specific for each glycan motif, and in relation to infection duration, intensity and treatment.
Overall, in human infection cohorts the most pronounced IgM and IgG responses are against a range of highly fucosylated glycans associated with cercarial and egg glycoproteins and glycolipids, while IgE responses appears to be restricted to glycoprotein N-glycan core modifications only. We observed anti-glycan responses in longitudinal experimental schistosome infections in rodents and non-human primates, including during settings of protective immunity. In general anti-glycan IgG is more sustained than IgM, but with clear distinctions in the response dynamics between different glycan antigens groups. Currently, we are investigating the development of glycan-specific antibody responses in a controlled human *S. mansoni* infection model that has been developed at the LUMC. The glycan array data obtained from these natural and experimental schistosome infections will be discussed in view of the diagnostic potential of antibodies to specific glycan antigens, and the possible role(s) in immunity of specific anti-glycan antibodies.

12:30 (15 mins)

Cellular immunological analysis of naïve European and pre-exposed African volunteers infected with *P. falciparum* sporozoites - *A17338*

Presenter: **Mr Mikhael Manurung**, *PhD Student, LUMC*

M Manurung[2]; S de Jong[2]; K Stam[2]; M Roestenberg[2]; P G Kremsner[3]; B Mordmüller[3]; B Lell[1]; M Yazdanbakhsh[2];
[1] Centre de Recherches Médicales de Lambaréné, Gabon; [2] Leiden University Medical Center, Netherlands, Netherlands; [3] University of Tuebingen, Germany

Malaria still causes significant morbidity worldwide. However, a safe and effective vaccine remains elusive. Vaccines that showed promising results in the early phase of trials, which was usually conducted in malaria-naive areas, eventually proved suboptimal when tested in the endemic areas. Coinfections and particularly pre-exposure to malaria are known to dysregulate immune system considerably, which can contribute to the differences in the efficacy of vaccines tested. To address this, we recruited five malaria-naïve Europeans and 20 malaria-preexposed Gabonese for a controlled human malaria infection (CHMI) with *Plasmodium falciparum* sporozoites (PfSPZ) Challenge (Sanaria™) via direct venous inoculation (DVI). Following the CHMI, all Europeans developed parasitaemia, whereas 8/20 (40%) African volunteers did not for the whole study period. This outcome enables the comparison of groups with various degree of antimalarial immunity. We analysed PBMCs from baseline, five and eleven days after DVI and stimulated them with *P. falciparum* infected red blood cells (PfRBC) and controls to analyse antigen-specific cytokine response by flow cytometry. We demonstrate that the Gabonese who were able to control their parasitaemia (TBS-) had a higher percentage of IFN-g-producing CD4 T cells compared to TBS- Africans, who in turn had higher frequencies of these cells compared to the malaria-naïve Europeans. Additionally, we observed higher baseline frequency of Pf-RBC specific CM CD4 T cells in TBS- Africans, whereas TBS+ Africans have a higher frequency of TNF-producing CD8 NKT cells. Distinct patterns of immune responses over time associated with parasite control were also observed, which when supplemented with targeted gene set enrichment analyses, suggests migration of cells into the peripheral tissues to exert antimalarial responses. Our data provide information on the geographic differences in the immune response against malaria as well as the underlying mechanism of naturally-acquired immunity that lead to parasite control.

12:45 (15 mins)

Elucidating the pulmonary immune response in schistosomiasis - *A17512*

Presenter: **Ms Emma Houlder**, *PhD student, University of Manchester*

E Houlder[2]; S L Brown[2]; A R Ridley[2]; J P Koopman[1]; M C Langenberg[1]; B M Winkel[1]; J J Janse[1]; M A Hoogerwerf[1]; P C Cook[2]; M Yazdanbakhsh[1]; M Roestenberg[1]; A S MacDonald[2];
[1] Leiden University Medical Centre, Netherlands; [2] University of Manchester, UK

The parasitic helminth *Schistosoma mansoni* infects more than 200 million people worldwide. Following skin penetration, the parasite migrates through the lung vasculature before maturation in the hepatic portal system. Lung migrating schistosomula are potential vaccine targets, however directed vaccine design is hindered by a lack of understanding of the natural lung immune response. Here, we present the first thorough immune characterisation of mouse and human lung immune responses in *S. mansoni* infection. In a murine lung infection model we have observed lung immune cell influx and cytokine expression characteristic of a low-level type-2 immune response. These findings are complemented by analysis of human sputum - an accessible proxy for lung immune responses - pre and post experimental infection with *S. mansoni*. Despite a low sample size (n≤3), we were able to observe trends for an increase in type-2 immune mediators in sputum post infection, as well as a significant increase in the regulatory cytokine IL-1RA. These novel findings improve basic understanding of the immunology of *S. mansoni* infection. Furthermore they are relevant in vaccine development, as well as potentially

providing mechanistic insight to help explain the impact of *S. mansoni*infection on allergic lung diseases, such as asthma.

Ecology and Ecosystems - III - (Renold C9)

17-April-2019, at 09:00 to 10:30

09:00 (30 mins)

Unravelling the factors that affect immune variability in wild rodents - *A16550*

Presenter: **Prof Jan Bradley**, *University of Nottingham*

J Bradley[1];
[1] University of Nottingham, UK

Much of our understanding of the mechanistic performance of the vertebrate immune system has been based on studies of rodents reared in artificial conditions where variables, both genetic and environmental are minimised. Recently, myself and others are attempting to unravel how variables such as infection, food supply, age and sex combine to determine immune trait development, the outcome of infection and ultimately the health and fitness of animals in the wild. However, 'wild' or 'ecological' immunology, as this field has become known, has been inhibited by our inability to quantify, in non-model animals, their complex immune traits or "immune phenotypes". We have used quantitative qPCR to look at immune gene expression in wood mice and field voles in relation to infection. More recently, we are using conventional immunological assays in wild mouse mice, utilising the immunological toolbox developed for laboratory studies. We are using multi-coloured FACS analysis and cytokine production after stimulation with PAMPS and specific antigens to assess immunological phenotype development in a study of house mice living wild on the Isle of May, Scotland. Mice on this island live wild unaffected by pest control making a longitudinal mark recapture study possible. Results on how food source, microbiome and infections relate to immune expression in both voles and house mice will be presented.

09:30 (15 mins)

The value of museum collections: a case study to investigate the length relationship between cymothoid isopods and their fish hosts. - *A17256*

Presenter: **Dr Wynand Malherbe**, *Subject specialist, North-West University*

W Malherbe[1; 2; 3]; R L Welicky[1; 2; 3]; K A Hadfield[1; 2; 3]; N Smit[1; 2; 3];
[1] Unit for Environmental Sciences and Management, North-West University, South Africa; [2] Unit for Environmental Sciences and Management, North-West University, UK; [3] Unit for Environmental Sciences and Management, North-West University, United States

Cymothoid isopods are a diverse group of ectoparasites of fish species, and are particularly conspicuous as they are large and attach to the body surface, mouth, and gill chamber of fish hosts. These parasites transition from juvenile to male to female, and how their size changes with ontogeny and correlates with host size is not well understood. To better understand these relationships, data from field and museum collected samples of South Africa were combined to test for the associations between host and parasite length for three mouth and one gill chamber-infesting genera (*Ceratothoa*, *Cinusa*, *Cymothoa*, and *Mothocya* respectively). Generally, the number of parasites collected from 90 hours of museum surveying was similar to that of seven, one-week long field collections. For two of the three mouth-infesting parasites, parasite and host size were significantly and positively correlated for males and females, but not juveniles. For gill chamber-infesting parasites, female and male parasite

sizes were weakly and not significantly correlated with host size. These results provide the first morphometric data and growth relationship data for African cymothoid species and their fish hosts, and demonstrate the value and efficiency of using museum collections in ecological research.

09:45 (15 mins)

Semi-field evaluation of wAlbB *Wolbachia* potential for population replacement of dengue vector *Ae. aegypti* from Lahore, Pakistan - *A17175*

Presenter: **Prof Nusrat Jahan**, *Professor in Zoology, Govt College University*

N Jahan[1]; A Q Sajid[1]; M S Sarwar[1];
[1] Govt College University, Pakistan

Dengue is a vector-borne disease that lack vaccine or effective drug, resulting in vector control being the primary disease control strategy. *Wolbachia* is an intracellular bacterium that can spread through vector population via cytoplasmic incompatibility (CI). It has been shown to inhibit the transmission of a number of the human pathogens such as dengue, chikungunya viruses and filarial nematode in mosquitoes. In order to utilize *Wolbachia* to block the transmission of pathogens to the humans, a more efficient vector population replacement strategy is required. The main objective of the current study was to evaluate the potential of wAlbB *Wolbachia* to invade wild population of *Ae. aegypti* with high frequency of infection through various release ratios. For this purpose three experimental (1,2,3) and two control (4-5) groups with constant number of wild males and females (1:1) were designed under semi-field conditions. In group 1-4 *Wolbachia* infected females (Wcl♀) were remained constant (20) while *Wolbachia* infected males (Wcl♂) varied with 1:1, 1:2, 1:4 & 1:0 (20, 40, 80 & 0) ratios while negative control (5) did not have any *Wolbachia* infected male and female. After one week of 1st release, *Wolbachia* infected population was released again in 2nd release with fixed ratio (05 Wcl♀ constant X Wcl♂ 10, 20, 40) to boost the replacement strategy. Presence of *Wolbachia* was confirmed by PCR in each successive generation using wsp *Wolbachia* specific primers. The results indicated that the release of additional infected males (group 3) into the population can accelerate the population replacement by increasing the frequency of incompatible mating and results in decline of uninfected population. *Wolbachia* invasion was evaluated on three parameters; oviposition count, eggs hatch rate and *Wolbachia* induced population replacement frequency in successive generations. There was no significant difference ($p > 0.05$) in egg laying capacity of females of various experimental groups compared with control at 1-4 generations. However, significantly lower ($p \leq 0.05$) hatch rate (48%) was observed in release ratio 1:4 of *Wolbachia* infected females X males (group 3) at generation 1. In addition highest average population replacement was also observed in group 3 and group 2 (100%± 0.00) at generation 3 (F3) and generation 4 (F4) respectively. There is a direct correlation between an increased ratios of infected males released with the increase rate of population replacement. In conclusion 100% *Wolbachia* infected population replacement occurred in group 3 with maximum *Wolbachia* infected males as rapid as within 3-4 months period. There is a dire need for further research on mass rearing of *Wolbachia* infected males to use in the field trials in specific localities for dengue vector population replacement and suppression in Pakistan to control the disease.

10:00 (15 mins)

Human schistosomiasis in the Senegal River Basin: does wildlife matter? - *A17183*

Presenter: **Mr Stefano Catalano**, *PhD student, Stefano Catalano*

S Catalano[3]; E Léger[3]; C B Fall[4]; A M Borlase[3]; N D Diouf[1]; M Sène[5]; K Bâ[2]; J P Webster[3];
[1] IFSAR Bambey, Universite de Thies, Senegal; [2] Institut de Recherche pour le Développement, Senegal; [3]Royal

Veterinary College, University of London, UK; [4] Universite Cheikh Anta Diop de Dakar, Senegal; [5]Universite Gaston Berger de Saint Louis, Senegal

Schistosomiasis is a neglected tropical disease of profound medical and veterinary importance caused by dioecious trematodes of the genus *Schistosoma*. This disease affects over 240 million people globally, with the highest burden in sub-Saharan Africa. *Schistosoma* parasites are characterized by complex multi-host dynamics and interspecific interactions leading, under certain conditions, to viable hybridizations between human and animal schistosomes with subsequent zoonotic transmission. Anthropogenic land-use changes and the progressive loss of ecological barriers may have also favoured interactions between different *Schistosoma* species. Our study elucidated the role of wild rodents as potential reservoirs of zoonotic *Schistosoma* species and hybrids in the Senegal River Basin, a region subject to dramatic anthropogenic change. Between May 2016 and November 2017, we trapped, humanely euthanized and necropsied small mammals from sites around Lake Guiers and the town of Richard Toll, Senegal, applying a multi-locus molecular analysis to identify the isolated *Schistosoma* spp. and estimate local prevalence. A total of 671 small mammals were captured over 4,149 trap nights. *Schistosoma mansoni*, occasionally coupled with zoonotic *Schistosoma haematobium*/*Schistosoma bovis* hybrids, and *S. bovis* were isolated in the portal system and/or mesenteric vessels of 24 out of 367 *Mastomys huberti* mice (prevalence 6.6%; intensity range 2-64) and 6 out of 257 *Arvicanthis niloticus* rats (prevalence 2.3%; intensity range 1-44). Infection prevalence was highly focal among study sites, with rates up to 52.6% and 28.6% in the villages of Gueo and Temey, respectively. Our findings emphasize the role of *M. huberti* and *A. niloticus* as important zoonotic reservoirs of *Schistosoma* species and hybrids, potentially amplifying transmission to humans. In the Senegal River Basin, as in many other endemic areas of sub-Saharan Africa, the breakdown of ecological barriers warrants the application of a One Health, multi-host framework to better tailor setting-specific schistosomiasis control programmes, enhancing public health interventions.

10:15 (15 mins)

The sweet spot between the lab and the real world - detailed analysis of the immune response against *T. muris* in a wild house mouse population

- A17337 *- A17337*

Presenter: **Dr Iris Mair**, *Postdoc, University of Manchester*

I Mair[1]; A Wolfenden[2]; A Lowe[2]; J Brookfield[2]; A MacColl[2]; K J Else[1]; J Bradley[2];
[1] University of Manchester, UK; [2] University of Nottingham, UK

The intestinal nematode *Trichuris trichiura* is one of the most common worm infections worldwide and affects around 500 million people. Studies on laboratory mice – using high dose, low dose, or trickle infection with the murine species of *Trichuris, Trichuris muris* (*T. muris*) in highly controlled conditions – have been immensely useful to understand the immunological processes involved in susceptibility and resistance to infection. However, humans are invariably exposed to a variety of environmental factors, present co-infections, and are genetically diverse; these will all influence the intensity and quality of the immune response mounted against *Trichuris*. How these factors combine to alter the *Trichuris*-specific immune response is poorly understood, as human longitudinal and in-depth studies are challenging and laboratory-based models do not encompass natural variation.
The Isle of May (Scotland) is home to a highly tractable wild house mouse population with a lack of terrestrial predators and only few predatory birds, allowing for longitudinal tracking of the mice. This population has a high prevalence of *T. muris* infection (~80%), which allows us to assess *T. muris*-specific immunity over time via collection of repeated serum samples, tracking worm presence via faecal egg count, and performing in-depth analysis of the immune state at cull. We also record detailed ecological measurements at each capture and collect genetic material, allowing us to see associations between environmental or genetic factors and the immune

response against *T. muris*. We have collected in-depth cull data from 85 animals over the past year, of which 52 have been captured at least once before, providing longitudinal data.
Our results show that the distribution of infection in the Isle of May mice is over-dispersed, mimicking that of human populations with the majority of individuals harbouring low worm burdens, a few individuals with very high worm burdens and a few individuals that are seropositive but worm-free. Serum levels of anti-*T. muris* IgG1 and IgG2 were highly variable between individuals and across time, and re-stimulation of cells from mesenteric lymph nodes with *T. muris* excretory-secretory product yielded a diverse pattern of cytokine production, even across animals with comparable worm burden, indicating that other factors influence the *T. muris*-specific immune response in this study population. These data, together with flow cytometric cellular analysis of spleen, mesenteric lymph nodes and peritoneal exudate cells, are currently being correlated with ecological data including sex, age, weight, trap location, and co-infection status, and will give a first detailed insight into which factors influence the immune response against *T. muris* in a wild mammal population.

Human Interventions - II - (Renold C9)

17-April-2019, at 11:00 to 13:00

Chair - Prof Guy Caljon

11:00 (30 mins)

Challenges for academia to sustain innovative drug discovery against neglected tropical diseases: focus on Leishmaniasis - *A16559*

Presenter: **Prof Louis Maes**, *University of Antwerp*

L Maes[1]; S Hendrickx[1]; G Caljon[1];

[1] Laboratory of Microbiology, Parasitology and Hygiene (LMPH), University of Antwerp, Belgium
Being a neglected tropical disease (NTD), drug R&D against the different clinical forms of leishmaniasis has become a prime responsibility of academia and public private partnerships related to the limited involvement of the pharmaceutical industry, particularly in the early discovery phases (target identification, drug screening, lead optimization) and exploratory preclinical development (PK-PD and toxicology). Recognizing that the logistic and budgetary means are generally quite limited, it is pivotal that the proper assays, benchmarks for activity, essential minimal study package for proof-of-concept (POC) and go - no-go criteria are clearly defined. A pragmatic overview will be given of the minimal study package that is generally needed to advance from drug screening to lead development, enabling to deliver a strong POC that may convince public and/or private partners to become involved. While focus here is given to *Leishmania*, the basic principles may also be applied to other NTD's and other infectious diseases.

11:30 (30 mins)

Is host specificity beneficial to mosquitoes? – the case of the *Anopheles gambiae* complex - *A16567*

Presenter: **Prof Willem Takken**, *Wageningen University*

W Takken[1];
[1] Wageningen University, Netherlands

Female mosquitoes acquire food from plants and vertebrates. Plant nectar is used for metabolic energy, while vertebrate blood is needed for egg development. While many mosquito species are opportunistic in their food choice, having no specific host association, a few species have developed a strong selective trait for host specificity. Several of this selective group of mosquitoes feed preferentially on humans, and have become the world's most effective vectors of pathogenic agents. The *Anopheles gambiae* complex counts amongst the world's most effective malaria vectors, mostly because of the high degree of anthropophily of several siblings, while other siblings within the complex express a more generalistic host choice. These behavioural traits affect the persistence of malaria in tropical Africa. It will be discussed how these, and other behavioural characters, affect interventions aimed at disease control.

12:00 (15 mins)

Anthelmintic resistance in sheep farms using pasture in Quebec, Canada - *A17362*

Presenter: **Prof Roger Prichard**, *Professor, McGill University*

R K Prichard[2]; L Urdaneta-Marquez[2]; D Belanger[4]; V Barrere[4]; G Rioux[1]; A Leboeuf[3]; K Keller[2]; C Fernandez-Prada[4];
[1] Centre d'Expertise en Production Ovine du Québec, Canada; [2] McGill University, Canada; [3] Ministère de l'Agriculture, des Pêcheries et de l'Alimentation du Québec, Canada; [4] Universite de Montreal, Canada

A study was conducted on 22 sheep farms in Quebec, Canada, which graze sheep on pasture during the summer and autumn. The objective was to determine the extent of anthelmintic resistance to benzimidazoles (BZ) and ivermectin (IVM), administered at recommended dose rates, by the estimation of reduction in egg counts and by molecular diagnostics for early detection and surveillance of anthelmintic resistance. On each farm, 45 animals grazing together in July and August were randomly allocated to three groups of 15 sheep. Group 1 sheep were treated with fenbendazole (FBZ), Group 2 with IVM oral and Group 3 sheep were left untreated. Fecal samples were individually collected from each sheep immediately prior to anthelmintic treatment, and 14 days post-treatment for establishing the fecal egg count reductions (FECR). The proportion of *Haemonchus contortus* eggs in the samples was estimated by fluorescence. *H. contortus* eggs predominated (≥80%) across all farms. Following flotation, *H. contortus* eggs were separated and DNA extracted. The presence of polymorphisms in codons 167, 198 and 200 in Hco_*β-tubulin* isotype-1 gene (*Hco_β-tub1*), which is associated with BZ resistance in *H. contortus,* and polymorphisms at positions 141, 234 and 438 in the *dyf-7* gene, which have been proposed to be associated with IVM resistance in *H. contortus*, were assessed by pyrosequencing. Based on the reduction due to anthelmintic treatment, estimated by a Bayesian hierarchical model, 13 of 14 farms, which had adequate egg counts prior to treatment, showed FBZ resistance and 12 of 16 farms showed IVM resistance. Widespread BZ resistance was also predicted by the *Hco_β-tub1* genetic analysis and a significant association was detected for the seven farms in which conventional FECRT could be undertaken. The level of polymorphism seen in *dyf-7*was too low to account for the loss of efficacy of IVM estimated by the model, suggesting that other genes are more important for IVM resistance. In conclusion, the study showed widespread BZ and IVM resistances in Quebec sheep flocks, and that molecular analysis could predict the presence or absence of BZ resistance, even when egg counts were low.

12:15 (15 mins)

Screening for antiparasitic leads from a library of natural products from temperate zone plants - *A17296*

Presenter: **Prof Paul Horrocks**, *Professor, Institute for Science and Technology in Medicine*

P Horrocks[2]; H Hameed[1]; K Doleckova[3]; B Bartholomew[4]; S L Berry[6]; R Nash[5]; H Price[2];
[1] Institute for Science and Technology in Medicine, Keele University, UK; [2] Keele University, UK; [3] Keele University, School of Life Sciences, UK; [4] PhtoQuest, UK; [5] PhytoQuest Ltd, UK; [6] School of Life Sciences, Keele University, UK

There is an urgent need to identify and evaluate novel chemical scaffolds to seed the drug discovery pipeline for parasitic diseases. Complementing international efforts to explore the potential of huge commercial chemical libraries, the search for new leads also encompasses the evaluation of natural products. PhytoQuest, a UK-based Industrial Biotechnology small to medium-sized enterprise, has produced a library of approximately 1000 molecules, isolated predominantly from temperate zone plants. As such, this library represents a unique resource for lead discovery of high value chemicals from temperate zone plants against parasitic diseases, with previous studies focusing largely on plants from tropical and subtropical zones. The library comprises a wide range of chemical classes, two thirds of which are novel, and the remaining third not commercially available. Critically, the compounds are pure, overcoming common issues with screening fractions of complex mixes, and have been selected to reflect potential development, with a high degree of functionality and physiochemical properties that match Lipinski's Rule of Five. A subset of approximately 650 compounds have been screened against the intraerythrocytic stages of *Plasmodium falciparum* and axenic amastigotes of *Leishmania mexicana*, with a further screen against *Trypanosoma brucei* now underway. Here I report a characterization of our hits against *P. falciparum* and *L. mexicana*.

12:30 (15 mins)

The action of ivermectin against filarial nematodes; new clues from RNASeq and *C. elegans* genetics - *A17043*

Presenter: **Dr Adrian Wolstenholme**, *Professor, University of Georgia College of Vet Medicine*

A J Wolstenholme[1]; N E Wilson[1]; M J Maclean[1]; E Price[1]; B J Reaves[1];
[1] University of Georgia College of Vet Medicine, United States

Ivermectin is a key component of current mass drug administration (MDA) programs aimed at the elimination of lymphatic filariasis and onchocerciasis. However, aspects of its mode of action against these parasites remain obscure and it has proved difficult to reproduce its clinical potency *in vitro*. We treated gerbils carrying an intraperitoneal infection of *Brugia malayi* with a single dose of ivermectin equivalent to that used in human MDA programmes and isolated RNA from the nematodes 1 day and 7 days after treatment. RNASeq analysis revealed a total of 113 differentially expressed genes (DEG). Gene expression was most affected in microfilariae at 1 day post-treatment and in adult females 7 days post-treatment. 72 of the DEG had clear orthologs in the *C. elegans* genome; strains are available with mutations in 44 of these genes. We hypothesized that the DEG genes might identify novel pathways of anthelmintic action and mutations in them would confer resistance or hypersensitivity to ivermectin. We tested this by measuring the effects of ivermectin on the development of the mutant strains and on their ability to lay eggs. To date, strains carrying mutations in *cey-2*, *wht-4*, *tyr-2*, *inx-14*, *unc-22*, *tap-1*, *hil-1* and *aff-1* were resistant to ivermectin in the egg-lay assay. The *aff-1*mutant was also resistant in the development assay, as was a *che-12* mutant. Mutants in *unc-22*, *lips-7* and *nhl-2*were hypersensitive to ivermectin in this assay. WHT-4 is an ABC transporter and INX-14 is a component of gap junctions; members of both protein families have previously been implicated in ivermectin resistance. AFF-1 is involved in membrane trafficking and cell fusion. Mutation of *unc-22*, which encodes twitchin, has opposite effects on drug sensitivity, depending on the assay used; egg-laying is resistant to the drug in mutant worms, but development from the eggs in hypersensitive. These results identify new mechanisms of ivermectin action against filarial nematodes and may open new avenues for future drug discovery.

12:45 (15 mins)

Exploring cyclic nucleotide phosphodiesterases as drug targets in *Schistosoma mansoni* - *A17315*

Presenter: **Prof Harry De Koning**, *Professor of Parasitology, University of Glasgow*

H P De Koning[4]; J C Munday[4]; S S Botros[6]; M Siderius[3]; C Gil[5]; S Kunz[3]; S Gul[2]; D G Brown[7]; C S Hoffman[1]; R Leurs[3];
[1] Boston College, United States; [2] Fraunhofer Institute, Hamburg, Germany; [3] Free University Amsterdam, Netherlands; [4] Institute of Infection, Immunity and Inflammation, University of Glasgow, UK; [5] Institute of Medicinal; Chemistry, CSIC Madrid, Spain; [6] Theodor Bilharz Research Institute, Cairo, Egypt; [7] University of Kent, Canterbury, UK

The EU/FP7-funded consortium PDE4NPD has initiated an effort to develop a platform for evaluating cyclic nucleotide phosphodiesterases (PDEs) of *Trypanosoma brucei*, *Trypanosoma cruzi*, *Leishmania* spp and *Schistosoma mansoni* as drug targets. As part of the effort, 265 potential PDE inhibitors were tested for *in vitro* effects against *S. mansoni*, with a high percentage impacting on worm survival and/or egg production; worm killing almost completely restricted to males. Three of the compounds, as well as the human PDE4 inhibitor roflumilast, were selected for tests in a mouse model of schistosomiasis, alone and in combination with praziquantel, leading to outcomes of reduced worm and egg burdens and reduced inflammatory hepatic granuloma. While this work proved that some PDE inhibitors have *in vitro* and *in vivo* antischistosomal activity, it is necessary to identify which one(s) of the 11 SmPDEs should be targeted for a systematic inhibitor development campaign. Thus, 9 of the 11 PDEs were (to date) successfully cloned, sequenced, and named according to accepted classifications. Various approaches were employed to verify that these were functional PDEs with catalytic activity towards cAMP and/or cGMP, mostly through functional complementation in specialised cell lines of *Trypanosoma brucei*, *Saccharomyces cerevisiae* and *Schizosaccharomyces pombe*. Catalytic activity was also probed for some PDEs with heterologously produced purified enzyme or cell extracts. Both a virtual library screen using an *in silico* model of SmPDE4A and a preliminary inhibitor screen with recombinant SmPDE4A with the PDE4NPD toolbox of inhibitors were performed. Overall, we conclude that PDE inhibitors have potential as anti-schistosomal agents but that much work is yet required to establish which of the PDEs would make the best target.

Science Communications - (Renold C16)

17-April-2019, at 14:00 to 15:20

14:00 (50 mins)

The science communication imperative - - *A16546*

Presenter: **Prof Andy Miah**, *University of Salford*

A Miah[1];
1 University of Salford, UK

This presentation examines the rise of science communication over the last decade, arguing that there are crucial social, cultural, political, and economic factors which explain the need for science to be more publicly present. Central to these transformations is a radical reconfiguring of the relationship between the science industries and society, whereby key areas of concern include public anxieties about expertise and truth, threats toward academic independence, the democratization of media technologies, loss of trust in journalism, the rise of fake news, the

expansion of informal learning environments, and a growing public expectation for science to be accountable and transparent. Together, these facets of contemporary culture provide the context to a moral framework for science communication, which describes its centrality to the business of science more broadly and its location within the wider ambitions of science as a project of human society.

14:50 (30 mins)

Increasing awareness and dialogue around the themes of Infection and Immunology in non-native English Speakers - *A16555*

Presenter: **Prof Sheena Cruickshank**, *Professor of biomedical sciences and public engagement, University of Manchester*

S Cruickshank[1];
[1] University of Manchester, UK

Our previous work with immigrant communities identified a lack of awareness of NTDs and a lack of English language skills around medical and scientific terms. People from minority ethnic and linguistic backgrounds participate significantly less in public engagement with science practices or informal science learning activities. We suggest this may be in part due to their lack of language skills around scientific English. To address these issues of scientific language accessibility, we developed a bespoke set of English and science lessons that dealt with the theme of infection aimed at non-native English speakers. These lessons have been running for several years and will be launched on line this year for open access use. All students who have participated in the lessons so far have reported they feel the lessons are invaluable to them in their everyday lives. We propose that developing programmes of this nature represent a potentially fruitful avenue for more-accessible public engagement with research and health education practices. Indeed, resources and learning from these lessons are now being applied in field work in Madagascar to address issues around Schistosoma transmission

Awards and Close - (Renold C16)

17-April-2019, at 16:00 to 16:30

Posters

Poster 1 : Genetic diversity patterns of *Haemonchus contortus* isolated from sheep and goats in Bangladesh

Presenter: **Dr Mohammad Zahangir Alam**, *Teaching and Research at University, Bangladesh Agricultural University*

M Alam[1]; A Dey[1]; N Begum[1];
[1] Bangladesh Agricultural University, Bangladesh

Haemonchus contortus is the most prevalent parasitic nematode among the Trichostrongylids causing severe health hazards leading to production losses in small ruminants around the world. This study was conducted to explore genetic variation within and among *H. contortus* populations from seven topographic zones of Bangladesh in small ruminants using second internal transcribed spacer (ITS-2) of nuclear ribosomal DNA and the mitochondrial nicotinamide dehydrogenase subunit 4 (*nad4*) genes. To do this, a total of 95 adult *H. contortus* were collected from abomasa of slaughtered sheep and goats from seven different geographic zones of Bangladesh. After the extraction of DNA, ITS-2 of nuclear ribosomal DNA and partial region of the mitochondrial *nad4* genes were amplified and sequenced for 95 and 85 worms, respectively. After editing and alignment, sequences were employed for analysis to determine sequence variation, genetic diversity and population genetic structure. Genetic analysis defined 19 distinct ITS-2 genotypes and 77 unique *nad4* haplotypes among the *H. contorts* isolates. The nucleotide diversities were 0.0098 and 0.025 for ITS-2 and *nad4*gene, respectively. Phylogenetic analysis (neighbor joining, maximum likelihood and maximum parsimony) of haplotypes indicated the existence of two populations without marked specification of host and locations within *H. contortus* populations in Bangladesh. By population genetic analysis, 93.67% of genetic variance was partitioned within the population. Very low genetic differentiation but high gene flow was observed among different populations of *H. contortus* in Bangladesh. This is the first study on genetic variability of *H. contortus* isolates of small ruminants in Bangladesh. Our study could be the basis for further molecular epidemiological studies, using more discriminative markers and tracing possible changes in the population structure of *H. contortus*.

Poster 2 : Web resource for investigation of Schistosoma mansoni long non-coding RNAs and their expression correlation to protein-coding genes.

Presenter: **Dr Elton Vasconcelos**, *Bioinformatics Research Officer, University of Leeds*

E Vasconcelos[3]; V C Mesel[1]; L F daSilva[1]; D S Pires[2]; G M Lavezzo[1]; A S Pereira[1]; M S Amaral[2]; S Verjovski-Almeida[1];
[1] Departamento de Bioquímica, Instituto de Química, Universidade de São Paulo, Brazil; [2] Laboratório de Expressão Gênica em Eucariotos, Instituto Butantan, Brazil; [3] University of Leeds, UK

Long non-coding RNAs (lncRNAs) have been widely discovered in several organisms with the help of high-throughput RNA sequencing. LncRNAs are over 200 nt-long transcripts that do not have protein-coding (PC) potential, having been reported in model organisms to act mainly on the overall control of PC gene expression. Little is known about the functionality of lncRNAs in evolutionarily ancient non-model metazoan organisms, like

Schistosoma mansoni, the parasite that causes schistosomiasis, one of the most prevalent infectious-parasitic diseases worldwide. In a recent transcriptomics effort, we identified thousands of S. mansoni lncRNAs predicted to be functional along the course of parasite development. Here, we present an online catalog of each of the S. mansoni lncRNAs whose expression is correlated to PC genes along the parasite life-cycle, which can be conveniently browsed and downloaded through a new web resource http://verjolab.usp.br/folders/smLincs/. We also provide access now to navigation on the co-expression networks disclosed in our previous publication, where we correlated mRNAs and lncRNAs transcriptional patterns across five life-cycle stages/forms, pinpointing biological processes where lncRNAs might act upo

Poster 3 : Killing quickly – validation of an improved Rate-of-Kill assay to support antimalarial discovery.

Presenter: **Mrs Maria van Veelen**, *Medical Student, Keele University School of Medicine*

M van Veelen[3]; M Famodimu[2]; P D Horrocks[1];
[1] Institute for Science and Technology in Medicine, Keele University, UK; [2] Keele University, UK; [3] Keele University School of Medicine, UK

The emergence of *Plasmodium falciparum* resistant to current front-line antimalarials provides an impetus to develop and deliver new and innovative *in vitro* screening assays in the support of antimalarial drug discovery. New antimalarials are needed that are both potent as well as capable of affecting a high rate of initial cytocidal kill. Using a novel Bioluminescence Relative Rate-of-Kill (BRRoK) assay, an open source library of antimalarial drug development targets (Malaria Box) was previously screened for compounds with high RoK. Recognising some limitations with the BRRoK assay, subsequent development work utilised a modified BRRoK assay to explore RoK and potency together in a format much more amenable to a high throughput approach. This modified assay was applied to 13,000 antimalarial development targets from the Tres Cantos Antimalarial Set (TCAMS library) provided by GlaxoSmithKline. However, hits predicted from the modified assay need to be confirmed both in terms of their potency and initial cytocidal action to validate the screening approach.
The aim of this project was to validate the potency and RoK for hits identified in the modified BRRoK assay of the TCAMS library. The specific aims of this project were to (i) review the EC_{50} data of 24 TCAMS compounds on 3D7 parasite strain, (ii) use the EC_{50} data to determine their initial RoK, (iii) validate the predictions of RoK made from the modified BRRoK assay of TCAMS by repeating the RoK assessment using the standard BRRoK assay, (iv) determine the RoK in two genetic backgrounds of *P. falciparum* with distinct antimalarial drug resistant phenotypes. Twenty-four TCAMS compounds were screened in two different parasite strains; $Dd2^{Luc}$ and NF54. There were seven compounds predicted to be rapidly cytocidal, 12 compounds predicted to be intermediate, and five compounds predicted to be slow. Standardised BRRoK assays confirmed their relative RoK; providing data that validates the new high throughput approach when compared against a range of standard antimalarial benchmark compounds. Several compounds, however, did show some differences in RoK between the $Dd2^{Luc}$ and NF54 strains used. Interestingly, examination of the structure of these compounds reveals a quinolone moiety, potentially affecting these different RoK in what are chloroquine resistant and sensitive parasite strains, respectively.
This data supports validation of an improved *in vitro* assay that screens compounds in terms of both their antiplasmodial potency but also their initial cytocidal activity – both critical aspects of the Target Product Profile for new antimalarial drugs. The BRRoK assay can now be readily scaled to screen massive (>100,000– multi-million) compound libraries to support the discovery of new antimalarial drugs.

Poster 4 : Epidemiology of intestinal helminthiasis among patients visiting the out-patient unit of the University of Abuja Teaching Hospital, Gwagwalada, Abuja.

Presenter: **Mr Lazarus Ezekiel Dabuwaat**, *Chief Lecturer, Plateau State Polytechnic, Barkin Ladi*

L Dabuwaat[2]; **G G Deme**[1];
[1] Federal University Lafia, Nigeria; [2] Plateau State Polytechnic, Barkin Ladi, Nigeria

The prevalence of intestinal helminths infection was carried out among patients visiting the out-patient unit of University of Abuja Teaching Hospital Gwagwalada, Abuja from June to October, 2010. A total of 500 patients were examined for stool. The stools were analyzed for intestinal helminths using formol-ether concentration technique. Out of 500 samples collected and examined, 100 (20.00%) were positive for different intestinal helminths. *Ascaris* 65.50% had the highest prevalence rate of in intestinal helminth infection. Intestinal helminth infection was more in males than females with a significant difference (P≤0.05). Based on age, the younger age 16-25 had more intestinal helmiths than the older 66-above with a significant difference (P≤0.05). This study underscores the implications of these infections among the populace.
Keywords: Intestinal-helminth, Patients, University of Abuja Teaching Hospital.

Poster 5 : *In vitro* antiparasitic activity of camel milk against *Blastocystis* sp.

Presenter: **Mr Rowaida Bakri**, *Assistant professor , Umm-Al- Qura University*

R Bakri[1];
[1] Umm-Al- Qura University , Saudi Arabia

Blastocystis sp. is an enteric protozoa infecting humans as well as many animals. It is considered as a parasitic organism even though its pathogenic potential continues to be debatable. Anti-pathogenic properties of milk from different animals have been already reported *in vitro* and *in vivo*. We investigated *in vitro* anti-protozoal activity of camel, cow, and goat milks against three *Blastocystis* sp. strains isolated from symptomatic patients, identified as subtype ST3 by PCR using SSUrDNA sequence-tagged-site primers. A significant *in vitro* killing effect was obtained with camel milk at minimal concentration of 62.5µl/2ml culture media compared to cow milk (P>0.007) and goat milk (P>0.002). Both, cow and goat raw milk did not show a noticeable in-vitro killing effect at the highest dose of 500ul/2ml. *In vitro* antiprotozoal propriety of camel milk against *Blastocystis* sp.ST3 strains observed in this study opens a promising perspective for its use for the control of this wide spread gastrointestinal parasite both in humans and livestock. Further investigations are needed to explore most effective antiprotozoal components of camel milk.

Poster 5 : African schistosomes; inter species interactions and hybridisation.

Presenter: **Dr. Bonnie Webster** , *Parasitologist, Natural History Museum,*

B Webster[1];

[1] Natural History Museum, UK

Schistosomes are parasitic trematodes that cause Schistosomiasis, the most important water-borne Neglected Tropical Disease burdening and inflicting unnecessary suffering on many poor rural communities. 206.4 million

people require treatment in 78 tropical and sub-tropical developing countries. Schistosomiasis is also a major disease of animals, affecting large numbers of domestic livestock worldwide.
There are 25 described schistosome species. Their two-host lifecycle includes an asexual stage in certain species of fresh water snails, governing their geographical distribution, and a sexual stage living in the blood vessels of species specific/preferred mammalian hosts. Asian schistosomiasis is highly zoonotic complicating control, whereas in Africa species specific host preferences exist. However, hybridisation between schistosome species is now frequently being reported across Africa, with the hybridisation between human and animal schistosomes raising.

Poster 6 : Impact of wild mammals' ectoparasites on transmission of different pathogens

Presenter: **Ms Indre Lipatova**, *lecturer, researcher, Vytautas Magnus University*

I Lipatova[1]; J Radzijevskaja[1]; A Paulauskas[1];
[1] Vytautas Magnus University, Lithuania

Wild mammals are associated with vector-borne (tick, flea, mite, lice) pathogens that is causing infectious diseases worldwide. Ectoparasites of wild mammals can transmit different pathogens such as *Bartonella*, *Rickettsia*, *Borrelia* and other bacteria or viruses. Human outdoor activities in parks and suburban forests are increasing and providing excellent conditions for contact between wild mammals, vectors and human or domestic animals. Thus, in order to assess risks of infection, is important to know what pathogens can be detected in wild mammals' ectoparasites. For that purpose, we used real-time PCR, nested-PCR, multiplex PCR and vector-borne bacteria flow chip for different pathogens detection. A total 118 ectoparasites were collected (110 ticks and 8 fleas) from road kill wild mammals (*Lepus europaeus, Mustela putorius, Nyctereutes procyonoides, Meles meles, Vulpes vulpes*). We identified two tick species (*Ixodes ricinus* and *Dermocentor reticulatus*) and two flea species (*Chaetopsylla globiceps* and *Ctenocephalides canis*). Genus of *Bartonella, Rickettsia, Borrelia* and *Anaplasma* were detected. *Rickettsia* DNA were found in 23.1% *D. reticulatus* ticks and 13.4% *I. ricinus* ticks, as well in 12.5% fleas of *C. globiceps* species. Sequence analysis of the 17 kDa protein coding gene fragment sequinces showed that sequences are similar to *R. helvetica* and *R. raoultii*species. A total 3.39% tested ectoparasites were infected with the *Bartonella* pathogen. Sequence analysis of the 16S-23S rRNR ITS region fragment sequences showed that fleas were infected with *B.hensellae* and ticks with *B. schoenbuchensis* species. *Borrelia* spp. and *Anaplasma* spp. were found in 27.1% and 56.8% tested ectoparasites respectively. *Borrelia* DNA were found in 37.5% fleas and 26.4% ticks. *Anaplasma* DNA were found in 59.1% ticks and 25% fleas.

Poster 7 : A review on parasites of Australian cormorants

Presenter: **Dr Shokoofeh Shamsi**, *Senior Research Fellow, Charles Sturt University*

S Shamsi[1];
[1] Charles Sturt University, Australia

Cormorants have been subject of many studies due to their impacts on recreational fisheries, aquaculture, vegetation and habitat, other bird species and spread of diseases. However few studies dealt with their parasites and their impacts on above mentioned areas. In Australia, our knowledge regarding the parasitism of Australian cormorant species is poor. In this presentation, results of examining several species of Australian cormorants for parasite infections are presented followed by a review of parasites reported from Australian cormorants by other

workers. We discuss the importance and potential impacts of parasites found in cormorants for both the aquaculture industry and fish health and in a broader sense.

Poster 8 : The effect of a single dose of oral ivermectin on human volunteers

Presenter: **Dr Adrian Wolstenholme**, *Professor, University of Georgia College of Vet Medicine*

N E Wilson[2]; B J Reaves[2]; J Murrow[1]; A J Wolstenholme[2];
[1] University of Georgia, United States; [2] University of Georgia College of Vet Medicine, United States

Ivermectin is widely used in human medicine to treat and prevent parasite nematode infections. It has been suggested that its mode of action requires the host immune system, as it is difficult to reproduce its clinical efficacy *in vitro*. We therefore studied the effects of a single dose of ivermectin (Stromectol – 0.15 mg/kg) on cytokine levels and immune cell gene expression in human volunteers. This dose reduces bloodstream microfilariae rapidly and for several months when given in mass drug administration programmes. Healthy volunteers with no travel history to endemic regions of Africa were given 3-4 tablets, depending on their weight, of either ivermectin or a placebo. Blood samples were drawn immediately prior to administration, 4 hrs and 24 hrs afterwards, and complete blood counts performed. Serum levels of 41 cytokines and chemokines were measured using Luminex and expression levels of 770 myeloid-related genes determined using Nanostring. No significant differences were observed in CBC or cytokine levels at either time point between people given ivermectin vs placebo. Some small changes in gene expression were measured; 10 genes showed a significant change in expression in PBMC after ivermectin was given. Leukocytes isolated from those participants given ivermectin showed no difference in their ability to recognize and kill *B. malayi* microfilariae in vitro. Overall, our data do not support a direct effect of ivermectin on these central players of the human immune system as the mechanism of its antifilarial activity.

Poster 9* :Assessing selective pressure in *Fasciola hepatica*: challenges and relevance to drug and vaccine gene targets

Presenter: **Mr Olukayode Daramola**, *Selective Pressure in Fasciola, Institute of Integrative Biology*

O Daramola[2]; J Hodgkinson[1]; S Paterson[2];
[1] Institute of Infection and Global Health, University of Liverpool, UK; [2] Institute of Integrative Biology, University of Liverpool, UK

This study investigates the evolutionary pressures acting on genes of *Fasciola hepatica*, a zoonotic trematode parasite of huge economic importance in livestock. In the last decade, a big challenge facing the control of the liver fluke has been the increasing reports of resistance to triclabendazole; the drug of choice effective against all stages of the parasite. Drug resistance has been reported in farms across Europe, and more importantly in the UK. Significant progress in genomic studies on *Fasciola* spp was the publication of a draft genome of *F. hepatica*, which revealed a large genome of 1.2Gb, as well as other related species especially *F. gigantica* (a genome assembly of which was recently published). Here we utilize these genomes, with the aim of investigating adaptive evolutionary changes in gene families of interest in these trematodes, particularly in *F. hepatica* to identify potential drug and vaccine targets. In our studies, we have been using annotated gene models from our group, and from other trematodes available on WormBase Parasite and NCBI to validate *F. hepatica* gene models, identify candidate gene families to screen for evidence of positive selective pressure. Using various bioinformatics such as codeml in PAML, ETEtookit pipeline, Orthomcl, and a few more tools; selective pressures are been assessed in coding genes sequences of gene families of interest. We have assessed selective pressures in alpha and beta tubulins in *F. hepatica* and trematode orthologues, as well as in glutathione transferases, and some other selected

genes. Here, a brief overview of these analyses is provided, including methods and findings so far, as well as challenges associated with these studies. These studies provide more insights into the genome of *F. hepatica*, in relation to the biology of the parasite.

Poster 10 : Tick-borne pathogens in passerine migratory birds in Lithuania

Presenter: **Mrs Vesta Matulaitytė**, *PhD, Vytautas Magnus University*

V Matulaitytė[2]; J Radzijevskaja[2]; A Petraitis[1]; A Paulauskas[2];
[1] Klaipeda University, Lithuania; [2] Vytautas Magnus University, Lithuania

Migratory passerine birds are increasingly considered to be important in the global dispersal of tick-borne pathogens. It is known that migratory bird caries ticks which is infected with *Rickettsia* spp, *Borrelia* spp, *Anaplasma phagocytophilum* and other tick-borne pathogens, but only a few studies are done to detect tick-borne infections in migratory birds. The aim of this study was to investigate tick-borne pathogens in migratory birds. A total, 104 dead migratory birds belonged to 17 different species were collected from 2016 to 2018 years migrations in various Lithuania districts. For analysis heart, liver, Spleen and brain samples from each individual were collected. Two multiplex real-time PCR assays were performed for detection of *Anaplasmaphagocytophilum, Borrelia* spp, *Babesia* spp., *Rickettsia* spp. *Bartonella* spp. using as targets *msp2*, *23S rRNA*, *18S rRNA, gltA* and *ssrA* genes, respectively. Tick-borne pathogens were detected in different tissue of 9 bird species: Eurasian jay (*Garrulusglandarius*), Goldcrest (*Regulus regulus*), Great tit (*Parus major*), Coal tit (*Parus ater*), Song thrush (*Turdus philomelos*), Blackbird (*Turdus merula*), Yellowhammer (*Emberizacitronela*), European greenfinch (*Chloris chloris*) and Icterine warbler (*Hippolais icterina*). Only three pathogens *A. phagocytophilum*, *Borrelia* spp and *Rickettsia* spp. DNA were detected in 31% (33/104), 7.6% (8/104) and 7.6 % (8/104) examined birds, respectively. Coinfections with *Anaplasma* spp. and *Borrelia* spp. pathogens were found in 5.7% (6/104) individuals. These findings highlight the importance of migratory birds in circulation of tick-borne pathogens in Baltic region.

Poster 11 : Molecular, biochemical and functional analysis of LmxKin29 kinesin in *Leishmania mexicana*.

Presenter: **Mr Suad Al Kufi**, *PhD, Strathclyde University*

S Al-Kufi[1];
[1] Strathclyde Institute of Pharmacy and Biomedical Sciences, UK

Kinesins are motor proteins that convert the energy from ATP hydrolysis into mechanical work to drive cargo along microtubules in a variety of cellular processes, organelle transport and cell division. Disruption of the normal function of these proteins has been shown to lead to many pathologies, including ciliopathy, neurodegenerative diseases and cancers. The current study presents a comprehensive biochemical and cell biological analysis of a kinesin thought to be associated with flagellum formation. Initially the cloning, mapping, and expression of a novel kinesin LmxKin29 were achieved. LmxKin29 is expressed is expressed in both the amastigote and promastigote life stages of *L. mexicana*. LmxKin29 was assigned to the “orphan” kinesin family. To assess the function of LmxKin29 in *L. mexicana* single and double allele mutants were generated. Morphological analysis of promastigotes displayed no obvious phenotypic differences comparing the mutants with wild type cells. Localisation studies using GFP-tagged LmxKin29 revealed that it is predominantly found in between the nucleus and the flagellar pocket, while in dividing cells LmxKin29 was found at the anterior and posterior ends of the cells. Hence, LmxKin29 might play a role in cytokinesis. Female Balb/c mice infected with ΔLmxKin29-/- did not show a footpad lesion, whereas LmxKin29 add-back clones and single allele knockout clones caused the disease similar

to wild type parasites. It was confirmed by ELISA that the serum of mice infected with *L. mexicana* wild type, single allele mutants and add-back mutants showed increased levels of IgG1 and IgG2a. However, the LmxKin29 null mutant scored very low similar to the level of uninfected mice serving as a negative control. The inability to cause lesions in the infected animal suggests that LmxKin29 is a potential drug target against leishmaniasis. On the other hand, the absence of an immune response against the LmxKin29 null mutant clearly rules out these mutant parasites as an attenuated live vaccine. Biochemical analysis has been applied. It has been found, the MAP kinase homologue LmxMPK3 can phosphorylate a peptide derived from LmxKin29 encompassing serine 551 and serine 554 (Rosenqvist, H. 2011; Emmerson, 2014). A full-length GST-fusion protein of wild type LmxKin29 and five different mutants with substitutions of the putative serine or threonine phosphorylation sites, by alanine or aspartate, namely LmxKin29SA, LmxKin29SD, LmxKin29A2, LmxKin29A4 and LmxKin29554A. Using these mutants, it was possible to narrow down the site that is phosphorylated by activated His-LmxMPK3 as serine 554.

Poster 12* :The metabolic energy budget of the tick *Ixodes ricinus*: effects of season and temperature

Presenter: **Mr Saeed Alasmari**, *Lecturer, Bristol University*

S Alasmari[1];
[1] Bristol University , UK

The spread of tick-borne diseases in many parts of the world represents a significant health challenge for livestock and companion animals despite many advancements in the understanding of tick biology. Of crucial importance to the success of a tick species to reproduce and thrive in its specific environmental niche is the ability to efficiently obtain, store and metabolise the key bio-nutrients from their blood meal. Neither the metabolic requirements of developing ticks nor the allocation of resources to development have been studied extensively. Therefore, many aspects of tick physiology remain unclear. In the present work, a range of biochemical assays were used to estimate the seasonal patterns of free sugar (glucose), glycogen, lipid and protein accumulation through the life cycle of ticks in s.w. England. A total of 1,303 nymphs, males and females were analysed over the course of a year. The metabolic patterns observed provide a direct insight into the feeding history and life-history partitioning of resource during tick development.

Poster 13 : Comparison of two commercial ELISA assays for detection of *Strongyloides stercoralis* antibodies

Presenter: **Dr Foekje F. Stelma**, *Medical Microbiologist, MD-PhD, Radboud University Medical Center*

C kleine Tank[2]; E A Lieshout[1]; P Daemen[2]; J de Vries[1]; **F Stelma**[2];
[1] Leiden University Medical Centre, Netherlands; [2] Radboudumc, Netherlands

Background: Infection with the helminth *Strongyloides stercoralis* can persist for many years due to autoinfection and may cause hyperinfection syndrome in immune compromised patients. Screening for antibodies can be used to indicate past exposure to this parasite, which is important in patients prior to immunosuppressive therapy. This study evaluates the diagnostic performance of two commercial immunoassays testing for *S. stercoralis*specific antibodies. Methods: Two sample panels were used to evaluate the NovaLisa *Strongyloides* ELISA (NovaTec Immundiagnostica GmbH, Dietzenbach, Germany) and the Anti-*Strongyloides* IgG ELISA (Euroimmun AG, Lubeck, Germany). The first panel (n≤44) was defined by an LUMC in-house *Strongyloides* ELISA which characterised the samples as being strongly-positive (n≤11) , weakly-positive (n≤5) or negatives (n≤28). Among the negatives, n≤17 were seroreactive to other parasitic worm infections. The second panel (n≤30) was selected

from the Radboudumc serumbank being assumedly seronegative to *strongyloides* spp. of which n≤22 were selected because of seropositivity to common cross-reactive antigens (rheumatoid factor, Epstein Barr virus, HBs antigen and Borrelia spp.) and n≤8 were selected from a panel of Dutch infants between 1 and 2 years. Results: The NovaTec and the Euroimmun assay tested positive in 11 and 12 of the 16 LUMC positive samples, respectively, both missing one of the strongly-positives**.** The NovaTec assay showed false positive reactivity in two *Schistosoma* reactive samples. Both commercial assays remained seronegative when testing the LUMC confirmed *Strongyloides* negative samples and the Radboudumc negative panel. Conclusions: The Euroimmun assay seems the most suitable commercial alternative for an in-house ELISA immunoassays testing for *Strongyloides* specific antibodies.

Poster 14 : First report of *Biomphalaria* in Lake Malawi and emergence of intestinal schistosomiasis in Mangochi District, Malawi

Presenter: **Mr Mohammad Alharbi**, *PhD student, Liverpool School of Tropical Medicine*

M Alharbi[1];
[1] Liverpool school of tropical medicine , UK

Schistosomiasis is a waterborne neglected tropical disease of particular public health importance in Malawi. While urogenital schistosomiasis is endemic to Lake Malawi, local transmission of intestinal schistosomiasis is thought not to occur as *Biomphalaria*, the intermediate snail host of *Schistosoma mansoni*, has never been reported from the lake. However, during general malacological surveys undertaken in November 2017, we encountered *Biomphalaria pfeifferi* at 2 sampling sites along the Mangochi District shoreline. Snail species identity was confirmed by molecular DNA analysis of the mitochondrial cytochrome oxidase sub-unit 1 gene. Subsequently, in May 2018 with additional sites surveyed, *B. pfeifferi* was found at 9 further locations with its presence reconfirmed within the lake. School children (n≤175) from three primary schools located close to known *B. pfeifferi* sites were examined for intestinal schistosomiasis; the prevalence of *S. mansoni* infection was estimated by urine circulating cathodic antigen (CCA) dipsticks to be 46.7%, 25.0% and 9.1%, respectively. Upon faecal sampling and microscopy, several children had egg-patent *S. mansoni* infection. Our surveys provide an excellent example of how malacological surveillance can be used to target with more precision tailored parasitological surveys to pinpoint the focality of intestinal schistosomiasis. These observations are of local and national interest highlighting autochthonous transmission of *S. mansoni* and of international importance for updating travel medicine guidance and advice for the lake. *Biomphalaria*, the intermediate snail host of *Schistosoma mansoni*, has never been reported from the lake. However, during general malacological surveys undertaken in November 2017, we encountered *Biomphalaria pfeifferi* at 2 sampling sites along the Mangochi District shoreline. Snail species identity was confirmed by molecular DNA analysis of the mitochondrial cytochrome oxidase sub-unit 1 gene. Subsequently, in May 2018 with additional sites surveyed, *B. pfeifferi* was found at 9 further locations with its presence reconfirmed within the lake. School children (n≤175) from three primary schools located close to known *B. pfeifferi* sites were examined for intestinal schistosomiasis; the prevalence of *S. mansoni* infection was estimated by urine circulating cathodic antigen (CCA) dipsticks to be 46.7%, 25.0% and 9.1%, respectively. Upon faecal sampling and microscopy, several children had egg-patent *S. mansoni* infection. Our surveys provide an excellent example of how malacological surveillance can be used to target with more precision tailored parasitological surveys to pinpoint the focality of intestinal schistosomiasis. These observations are of local and national interest highlighting autochthonous transmission of *S. mansoni* and of international importance for updating travel medicine guidance and advice for the lake.

Poster 15 : Genome-led reverse vaccinology for visceral leishmaniasis: establishment of a bioluminescent murine infection model and candidate evaluation

Presenter: **Dr Han Ong**, *Postdoctoral Fellow, Sanger Institute*

H B Ong[1]; S Clare[1]; G J Wright[1];
[1] Wellcome Sanger Institute, UK

Visceral leishmaniasis (VL) is an infectious parasitic disease caused by the protozoan parasites *Leishmania donovani* and *Leishmania infantum*. These parasites primarily infect the host liver and spleen macrophages resulting in hepatosplenomegaly and the disease is fatal if left untreated. Currently, the disease is managed by drugs but they are highly toxic causing harmful side effects, and are not widely accessible. A better solution would be an effective vaccine but none exist for VL. To identify potential vaccine candidates, we have assembled a library of 93 *L. donovani* proteins that are predicted to be exposed on the parasite cell surface or secreted by searching the genome for proteins containing features such as signal peptides and transmembrane regions. The entire extracellular regions were expressed as secreted recombinant proteins in HEK293 mammalian cells to increase the chances that structurally critical posttranslational modifications such as disulphide bonds were faithfully added. To evaluate their efficacy as vaccine candidates, we have established a bioluminescent murine infection model of *L. donovani* to quantitatively determine the parameters of infection. Our model allowed us to longitudinally visualise the initial infection of livers and their resolution during the first 4-6 weeks, followed by parasite-dissemination and persistence in the spleens. These observations were consistent with other *L. donovani* murine infection models that relied on impression smears for parasite quantification. Using our model, we have identified five potential candidates that altered infection dynamics of the livers and spleens of infected mice. We have also used our protein library together with sera from infected mice, dogs and humans to identify serological markers of infection. We identified four potential biomarkers that could be developed for diagnostics purposes.

Poster 16 : Diversity of cercariae in Lake Victoria: A confounding factor for environmental monitoring of schistosomiasis?

Presenter: **Dr Fiona Allan**, *Cerc diversity, The Natural History Museum*

F Allan[2]; T Angelo[1]; S Kinung'hi[1]; A E Emery[2];
[1] National Institute for Medical Research, Mwanza, Tanzania; [2] Natural History Museum, UK

Schistosome cercariae shed by freshwater snails are the immediate source of infection for communities at risk of schistosomiasis. Transmission potential can therefore be monitored by collecting snails and identifying infection. Such methods are a component of control monitoring in China but rarely used in Africa, one disadvantage being the considerable work involved in such surveys. Many host snails must be collected and identified since infection prevalence among the snails is usually low.
The advent of environmental DNA (eDNA) methods in molecular ecology has renewed attention on monitoring free-swimming cercariae in water bodies. Field sampling for these methods is simple relative to snail collection, but more investigation is needed before it is possible to say whether they will be useful for identifying location and force of transmission.
One potential drawback of eDNA detection is the potential for false positives caused by cross-reactivity with non-target species. Lake Victoria has a diverse array of digenean cercariae, many of which are very abundant compared to schistosomes. Care must therefore be taken in choice of DNA target as even a small degree of cross-

reactivity could lead to ambiguous results. Here we present a preliminary survey of cercarial diversity in lake Victoria being tested against eDNA methods currently in use.

Poster 17* :M2 macrophage-associated protein Ym1 mediates parasite expulsion in *T. muris* infection

Presenter: **Miss Hannah Smith**, *PhD Student, University of Manchester*

H Smith[1]; T Sutherland[1]; J E Allen[1]; K J Else[1];
[1] University of Manchester, UK

Macrophages represent a spectrum of activation states. At their extremes, these can be pro-inflammatory (M1) or anti-inflammatory (M2). M2-like macrophages are characterised by production of markers such as Ym1. Ym1 has previously been shown to be present in acute injury and act as an adjuvant for the Th2 and Th17 responses in nematode infections. In *Trichuris muris* infection, in a C57BL/6 mouse model, Ym1+ M2 cells appear in the colon from d10 post-infection. We hypothesised that, as a modulator of the immune and repair responses, neutralising Ym1 function in *T. muris* infection will result in increased susceptibility to the parasites and worsened gut pathology. To assess the function of Ym1 in the context of *T. muris* infection in the gut, Ym1 function was inhibited using a neutralising anti-Ym1 antibody both early (d0–d12 p.i.) and late (d12–d21 p.i.) in *T. muris* infection in C57BL/6 mice. Late, but not early, depletion of Ym1 function resulted in enhanced worm expulsion by d21 p.i.. Enhanced worm expulsion was mediated by a heightened Th2 response as indicated by parasite-specific serum antibody levels and cytokine data. Additionally, no difference in gut pathology was detected. These results are contrary to our original hypothesis that Ym1 is an adjuvant for the Th2 response and involved in wound repair, and may give new insight into the role of Ym1 in the context of intestinal inflammation

Poster 18 : Fermentable dietary inulin modulates mucosal immune responses and prevents *Trichuris muris* expulsion

Presenter: **Miss Laura Myhill**, *PhD fellow, University of Copenhagen*

L J Myhill[2]; S Stolzenbach[2]; H Mejer[2]; T Hansen[2]; S Jakobsen[2]; P Nejsum[1]; S Thamsborg[2]; A Williams[2];
[1] Aarhus University, Denmark; [2] University of Copenhagen, Denmark

Fermentable dietary fibres, such as inulin, have been shown to influence mucosal immunity and gut health. In pigs, we have shown that dietary inulin modulated the characteristic Th2-immune response induced by the porcine whipworm, *Trichuris suis*, by synergistically up-regulating the expression of Th2 and mucosal barrier genes (e.g. *IL13*, *TFF3*), and down-regulating inflammatory genes (e.g. *IFNG)*. We have subsequently used the murine whipworm infection model to further explore this novel diet-parasite interaction, where inoculation with either a low (20 eggs) or high (300 eggs) *T. muris* egg dose results in worm persistence or expulsion, respectively, in C57BL/6 mice. Interestingly, dietary inulin enhanced worm numbers and size in both low- and high-dosed mice, and prevented worm expulsion in high-dosed mice typically resistant to infection. In these high-dosed mice, immune responses were markedly skewed towards a Th1-dominant state, as evidenced by increased numbers of T-bet expressing T-cells and *IFNG* and *NOS2* caecal gene expression, and reduced mast cell numbers. Moreover, the inulin-induced persistence of *T. muris* altered gut microbiota profiles, with expansion of Proteobacteria and depletion of 'healthy' microbial phyla, such as Bacteroidetes and Actinobacteria observed. Conversely, in uninfected mice, inulin promoted the growth of Bacteroidetes, Actinobacteria and Verrucomicrobia (mainly *Akkermansia muciniphila*). Our results indicate a profound effect of diet on *T. muris* infection and immune regulation in C57BL/6 mice. Elucidation of the inulin-mediated mechanisms responsible for *T. muris* persistence is

still required, nevertheless these findings have clear implications for the use of diet in regulating helminth infection and host gut health.

Poster 19* :The SUMO protease is important for flagellum biogenesis in *Leishmania mexicana*

Presenter: **Mr Meshal Daalah**, *Phd student, university of the west of Scotland*

M DaalahF HenriquezR Williams
[1] university of the west of Scotland , UK

Leishmaniasis affects 12 million peoples from 88 tropical countries. Protective and curative treatments is impossible and inadequate respectively with currents drugs being toxic and their overuse have selected resistant parasites. This makes the cases for a rational drug discovery programme to identify novel molecular targets to increase drug specificity, reduce toxicity and efficacious against resistant parasites. Genome differences amongst *Leishmania* spp cannot account for the three types of leishmaniasis. This suggests that they are regulated Post-translationally or epigenetically. Our aim is to determine if the **s**mall **u**biquitin-like **mo**difier post translational machinery called SUMOylation is important for parasite development and virulence. We demonstrate that the SUMO protease is situated exclusively in the mitochondria and has conjugating and de-conjugating activities, which are inhibited by selective cysteine protease inhibitors. Overexpression of this protease in aging promastigotes called SUMO-CP produced parasites with retracted flagella, a process which was negated in part, by the cysteine protease inhibitor, N-ETHYLMALEIMIDE (NEM). Generally, parasites with retracted flagellum accumulated sterols in endocytic compartments and are hypersensitive to the sterol inhibitor, ketoconazole. Interestingly, SUMO-CP had equivalent sterol levels as their naïve counterpart and sensitivity to ketoconazole, suggesting that this defect was not due to a defective endocytic trafficking pathway. We now hypothesize that the SUMOylation is vital for flagella biogenesis, the organelle used for attachment, motility, infectivity and preventing macrophages from mounting coordinated attacks to destroy the parasite. We are now generating gene knockout parasites to test if the mutant parasites have disrupted flagella function and elucidate the mechanism through which it occurs. This research has provided new information about the role of the SUMO protease in flagellum biogenesis and virulence, invaluable for the discovery of new anti-leishmanials.

Poster 20 : Studies of the biology of human follicular mites

Presenter: **Mr Edhah Salem M. Alsaeedi**, *PhD student at the University of Reading*

E Alsaeedi[1];
[1] the University of Reading, UK

Follicular mites are members of the Acari, family Demodicidae. They infest the hair follicles of most mammals, including wild and domestic animals. *Demodex* species are some of the most specialised arthropod parasites of mammals. Humans are no exception; two species of follicular mites have been detected in human skin, namely *Demodex folliculorum* (Simon, 1842) and *D. brevis* (Akbulatova, 1963). *D. folliculorum* and *D. brevis* are common intracutaneous parasites of the hair follicles and sebaceous and meibomian glands. They can be found on the face, forehead, chest, neck, eyelids, eyebrows and scalp, as well as in the ear canal. The pathogenesis of human *Demodex* mites is far from being understood. It has been suggested that the development of skin diseases like dermatitis, rosacea and pityriasis *folliculorum* are caused by *Demodex* mites, in addition to scabies-like eruptions, pigmentation on the face, gland dysfunction, hair loss on the scalp and even follicular basal cell carcinoma. Furthermore, it has been proposed that *D. folliculorum* and *D. brevis* are the cause of blepharitis. In contrast,

Demodex species are also inhabiting the skin of healthy individuals; where they are harmless and their presence has an unknown pathogenesis. A species from dogs, *D. canis* has been confirmed as causative of severe mange in young puppies or those with compromised immune system, and have also been detected, although rarely, on humans. *Demodex* mite cross infection between dogs and humans is suspected. We are currently studying the biology of human follicular mites and developing new tools to assist dermatologists in their diagnosis. Methods for microscopic identification of the human *Demodex* species have been revised. A single multiplex PCR reaction for the differentiation between the three most common *Demodex* species*, D. folliculorum, D. brevis* and *D. canis* has also been developed. Their prevalence of on human subjects has been analysed by screening a localised population, and a variety of artificial rearing media are being currently tested.

Poster 21 : Structural Investigation of cyclic nucleotide binding proteins from Trypanosoma cruzi

Presenter: **Mr Gabriel Ferri,** *PhD student,University of Leicester,*

GI Ferri[1], M Edreira[1] and I Campeotto[2]:
1 IQUIBICEN-CONICET, University of Buenos Aires, Argentina
2 Leicester Institute of Structural and Chemical Biology, University of Leicester, Lancaster Road, Leicester, LE1 7RH, United Kingdom

For a targeted therapy of Trypanosomiasis, new antiparasitic drugs should be specifically directed against essential pathways in the parasite life cycle. Among these potential targets are signal transduction pathways, which have remained largely unexplored in Trypanosoma species. Of special interest is cAMP-mediated signaling, since cAMP has been shown to play critical roles in the life cycle of *T. cruzi* and in host cell during invasion. The presented research focuses on the identification and characterisation of novel cAMP response proteins (CARPs) in *T. cruzi* by using a multidisciplinary approach involving the parasitology group of Dr Martin Edreira (University of Buenos Aires, Argentina) and the structural biology group of Dr Ivan Campeotto (University of Leicester, UK). The aim of the project is not only to increase our knowledge about *T. cruzi* biology but also to target CARPs for the design and development of novel therapeutic agents against Chagas disease.

Poster 22* :*Heligmosomoides polygyrus* infection elicits a hepatic immune response marked by spatio-temporally distinct polarisation programmes in infiltrating and resident myeloid populations.

Presenter: **Mr Rufus Daw**, *PhD Student, University of Manchester*

R H Daw[1]; J E Allen[1]; J R Grainger[1];
[1] University of Manchester, UK

The immune response to *Heligmosomoides polygyrus*, an entirely enteric gastrointestinal (GI) nematode infection, is well characterised within the small intestine. Recent investigations into the peritoneal cavity have eluded to the presence of a distal Th2 response during infection, whilst earlier investigations hint at a hepatic response to infection. Here, we wished to understand if, and how, the liver responds to GI nematode infection. This is due to the close anatomical connection between the small intestine and the liver via the hepatic portal vein, and the current notion that the liver responds to gut-derived signals during times of intestinal and microbial perturbation.

Using a series of timepoint studies, here we show the presence of two distinct immune responses at different time points of infection, likely linked to the nematode's lifecycle. Investigation into the initial hepatic response at day 3 is marked by a profound increase in Ly6C^{hi} infiltrating monocytes, and the classical activation of both the monocyte derived and tissue resident macrophage populations (as marked by Sca1 and IL-1b expression). Conversely, on day 7 we observe a Th2 response to nematode infection in the form of eosinophilia, eosinophil Relm-α expression, and the restricted upregulation of factors and pathways associated with the type II immune response. Here, our bulk liver RNA-seq describes the hepatic response at the transcriptional level, both confirming that a Th2 response occurs, and indicating the major markers of this response. Initial immunofluorescence imaging of the liver during *H. polygyrus* infection illustrates that immune cell involvement, and polarisation, is likely mediated by the anatomical structure of the liver. Indeed, such imaging shows that recently infiltrated eosinophils are one of the main immune cells involved in hepatic periportal inflammation during infection. Whilst our time-point, RNA-seq, imaging, and flow cytometry approaches begin to define the hepatic response at different dynamic timepoints, more characterisation of the response, and the role it performs in the eventual expulsion of nematode infection, is required.

Poster 23 : Immunomodulatory properties of *T. muris* antigens

Presenter: **Mrs Munirah Albaqshi**, *PhD student, University of Manchester*

Withdrawn

M Albaqshi[1];
[1] University of Manchester, UK

Poster 24* :Identification of *Trypanosoma congolense* genes with metacyclic stage-specific expression through transcriptomic analysis of wild-caught tsetse flies (*Glossina palpipes*).

Presenter: **Ms Kawira Mathenge**, *Research AS, Institute of Infection and Global Health*

K Mathenge[1]; A P Jackson[2];
[1] Institute of Infection and Global Health, UK; [2] University of Liverpool, UK

Animal African trypanosomiasis is a lethal disease of wild and domestic animals, endemic throughout sub-Saharan Africa and caused by African trypanosomes (Trypanosoma spp.). In Eastern Kenya, *T. congolense* is transmitted

by tsetse flies (*G. palpipes*), when infectious metacyclic-stage parasites that reside within the fly mouthparts are introduced while feeding. To better understand the developmental regulation of parasite genes during the infectious metacyclic stage, we used RNA-seq to estimate transcript abundance in dissected mouthparts, and then DE-seq to identify transcripts preferentially expressed in metacyclic cells. Tsetse flies were caught using baited traps in the Shimba Hills national park, Kenya, and metacyclic trypanosomes were sluiced from dissected mouthparts. Extracted RNA was sequenced on the Illumina Hiseq4000 platform and mapped to the *T. congolense*IL3000 PacBio reference genome. Our analysis has identified 793 genes, transcripts of which are significantly over-represented in metacyclic-stage cells. These include diverse *T. congolense*-specific genes, such as a Variant Surface Glycoprotein (VSG) sequence, that might offer new opportunities for vaccine development, as well as new insights into the molecular host-parasite interactions during the early stages of trypanosome infection following tsetse bite.

Poster 25* : Nucleoside analogues against trypanosomatid parasites: phenotypic screening and mechanism-of-action

Presenter: **Mr Camila Santos**, *PhD student, University of Antwerp*

C Cardoso-Santos[3]; D Mabille[4]; F Hulpia[1]; I Roditi[5]; S Van Calenbergh[1]; M N Correia Soeiro[2]; L Maes[4]; G Caljon[4];
[1] Ghent University, Belgium; [2] Instituto Gonçalo Moniz, Fundação Oswaldo Cruz (FIOCRUZ), Brazil; [3]Instituto Oswaldo Cruz, Rio de Janeiro, Brazil; [4] Laboratory of Microbiology, Parasitology and Hygiene (LMPH), University of Antwerp, Belgium; [5] University of Bern, Switzerland

Chagas disease (CD), human African trypanosomiasis (HAT) and Leishmaniasis are three neglected tropical diseases with a large medical need caused by trypanosomatid parasites. No human vaccines are available and current drugs have significant drawbacks in terms of efficacy, toxicity or development of resistance, justifying the need for alternative chemotherapies. Given that trypanosomatids are purine auxotrophs, focused purine libraries can be a source of antiparasitic agents as described in literature for both *T. cruzi* and *T. brucei*. A new series of nucleoside analogues was evaluated in vitro against a panel of trypanosomatid species, revealing four highly active candidates against *T. cruzi* (IC50 50-200 nM). In vivo proof-of-concept in an acute *T. cruzi* mouse infection model was already obtained for one particular compound (Hulpia et al, J. Med. Chem., 2018, PMID: 30234983). Surprisingly, one of the four compounds showed a broad anti-trypanosomatid potency, with nanomolar activity against *T. brucei* (IC50 < 0.5 µM) and promising activity against *Leishmania infantum* (IC50 2 µM) without cytotoxicity against murine primary macrophages or human fibroblasts (CC50 > 64 µM). This compound proved to be metabolically stable in the presence of rodent and human liver microsomes, which warrants further in vivo evaluation in the various trypanosomatid infection models and mechanism of-action (MOA) studies. Cross-resistance studies revealed a contribution of adenosine kinase (ADKIN) in the MoA whereas compound uptake is independent of the P2 adenosine transporter (AT1). A genome-wide *T. brucei* RNA interference (RNAi) library is currently being used to further scrutinize in an unbiased fashion the MoA of this potent anti-trypanosomatid nucleoside analogue.

Poster 26* :Mechanisms of pyrethroid resistance in *Aedes aegypti* populations from Saudi Arabia

Presenter: **Ms Ashwaq Alnazawi**, *PhD student, Liverpool School of Tropical Medicine*

a alnazawi[1];
[1] Liverpool School of Tropical Medicine, UK

Pyrethroids are regularly used as a control measure for dengue fever in Saudi Arabia. Effectiveness of control may be impacted by resistance but there is lacking information on insecticide resistance in *Ae. aegypti* in the Middle Eastern Region. *Aedes aegypti* from the two primary dengue-endemic areas of Saudi Arabia (Makkah and Jeddah) were assayed for resistance phenotypes; their target site mutations investigated using sequencing and genotyping; and metabolic resistance mechanisms investigated using microarrays technology. Both strains were resistant to multiple insecticides, with especially high deltamethrin resistance in Makkah. Three kdr mutations were detected (F1534C, V1016G, S989P), two of which were previously only identified in Asia. The V1016 and S989P mutations were in perfect linkage disequilibrium (LD) and strongly predicted deltamethrin resistance. Microarray analysis was used to identify genes differentially expressed between two susceptible strains and Saudi Arabian strains from Makkah and Jeddah. Results showed enrichment of P450s, some previously identified as pyrethroid metabolisers. However, the lead candidate gene statistically, CYP9J7 has not previously been functionally-investigated and we investigated its metabolic capacity via in vitro insecticide metabolizm assays. No depletion of permethrin and was noted. Surprisingly, CYP9J7 metabolized the organophosphate malathion. Mosquitoes from Makkah and Jeddah are highly resistant to pyrethroids. The gene expression and target site mutation data propose that the Jeddah strain relies on both metabolic and target site resistance mechanisms, with evidence suggesting the latter may be more prominent at present. Further work is needed to identify whether the organophosphate metabolism detected represents detoxification or activation, which have opposing implications for resistance management.

Poster 27 : A plan to sequence the genomes of all parasite species from the British Isles

Presenter: **Dr Adam Reid**, *Senior Staff Scientist, Wellcome Sanger Institute*

A J Reid[1]; M Berriman[1];
[1] Wellcome Sanger Institute, UK

The Wellcome Sanger Institute and partners including the Earlham Institute, the University of Edinburgh, Royal Botanic Gardens at Kew, European Bioinformatic Institute and the Natural History Museum have announced a plan to sequence all eukaryotic life in the British Isles. This project is called the Darwin Tree of Life and a new Tree of Life programme is being established at the Sanger Institute. As part of this effort we would like to begin a collection of UK parasite DNA. We would particularly like to reach out to researchers interested in the parasites of wildlife and plants, including helminths, protozoa and fungi as well as parasitic lice, mites and plants. We would like to speak with scientists who have access to samples of British parasites and would be interested in helping to assemble a collection for genome sequencing. Our aim is to generate high-quality genome assemblies with gene annotation based on transcriptome sequencing where possible. These data will be made freely available to the wider scientific community.

Poster 28* :Characterising *in vitro* G-Quadruplexes (G4) in *S. mansoni*

Presenter: **Miss Holly M. Craven**, *PhD Student, Aberystwyth Univeristy*

H Craven[1]; R Bonsignore[2]; M Swain[1]; H Whiteland[1]; A Casini[2]; K F Hoffmann[1];
[1] Aberystwyth University, UK; [2] Cardiff University, UK

The parasitic platyhelminth *Schistosoma mansoni* is a causative agent of schistosomiasis, an NTD that affects some 200 million annually. Bioinformatic approaches have highlighted the presence of putative quadruplex sequences (PQS) in *S. mansoni* and the parasite proved sensitive to G-quadruplex (G4) targeting compounds under experimental conditions. Hence, further techniques to assess the viability of PQS folding capacity under*in*

vitro conditionswere employed. We discovered that oligonucleotides, representing PQS present within *Wnt, Fzd* and *Tbx2* genes, folded into stable parallel G4 structures *in vitro* as measured by circular dichroism (CD). Further to this, the *S. mansoni* telomeric tandem repeat (TTAGGG) exhibited an antiparallel hybrid G4 topology when annealed in the presence of K+ measured by CD. To confirm the presence of G4 structures within the parasite, whole mount worms were incubated with the scfv antibody BG4 (a known G4 binding agent). Samples exposed to the antibody displayed diffuse foci staining present across the body, with localisation in cell nuclei. To our knowledge, this is the first confirmation of G4 present in a parasitic worm, and creates a novel area for exploring the functional significance of this DNA structure during schistosome development.

Poster 29 : Three new cymothoid isopods from the fish parasitic genus *Elthusa* Schioedte & Meinert, 1884 (Crustacea, Isopoda, Cymothoidae) from South Africa

Presenter: **Dr Kerry Hadfield Malherbe**, *Senior Lecturer, North-West University*

S van der Wal[1]; N J Smit[1]; **K A Hadfield**[1];
[1] North-West University, Potchefstroom, South Africa

The branchial attaching cymothoid genus, *Elthusa* Schioedte & Meinert, 1884 is widely distributed around the world. There are currently 33 described species from this genus but *Elthusa raynaudii* Milne Edwards, 1840 is the only species that has been recorded from southern Africa. All South African material held at the National Museum of Natural History, Paris, France (MNHN) and the Iziko South African Museum, Cape Town (SAMC) identified as or appearing to belong to *Elthusa* was examined.Four species were identified, *Elthusa raynaudii*and three species that proved to be new to science. *Elthusa xena* sp. n. can be distinguished by an evenly rounded pereonite 1 anterior margin, a roughly rectangular pleotelson and narrowly rounded uropod apices that extend to more than half the length of the pleotelson. *Elthusa acutinasa* sp. n. is identified by the produced and narrowly rounded cephalon anterior margin, acute uropods that are shorter than half the length of the pleotelson and pereonite 1 anterior margin with medial projection. *Elthusa rotunda* sp. n. is characterised by the round body shape, broadly rounded uropod apices and protrusions on the proximal and lateral margins of the merus and carpus of pereopod 7. This brings the total number of *Elthusa* species to 36 and more than doubles the known records of *Elthusa* from this region.

Poster 30* :Nanopore sequencing significantly improves genome assembly of the protozoan parasite *Trypanosoma cruzi*

Presenter: **Miss Florencia Díaz-Viraqué**, *PhD student, Institut Pasteur Montevideo*

F Díaz-Viraqué[2]; G Iraola[1]; S Pita[2]; G Greif[2]; R Cássia Moreira de Souza[3]; **C Robello**[2];
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Chagas disease was described by Carlos Chagas, who first identified the parasite *Trypanosoma cruzi* from a two-year-old girl called Berenice. Many *T. cruzi* sequencing projects based on short reads have demonstrated that genome assembly and downstream comparative analyses are extremely challenging in this species, given that half of its genome is composed of repetitive sequences. Here, we report de novo assemblies, annotation and comparative analyses of the Berenice strain using a combination of Illumina short reads and MinION long reads. Our work demonstrates that Nanopore sequencing improves *T. cruzi* assembly contiguity and increases the assembly size in ~16 Mb. Specifically, we found that assembly improvement also refines the completeness of

coding regions for both single copy genes and repetitive transposable elements. Beyond its historical and epidemiological importance, Berenice constitutes a fundamental resource since it now represents the best-quality assembly available for TcII, a highly prevalent lineage causing human infections in South America. The availability of Berenice genome expands the known genetic diversity of *T. cruzi* and facilitates more comprehensive evolutionary inferences. Our work represents the first report of Nanopore technology used to resolve complex protozoan genomes, supporting its subsequent application for improving trypanosomatid and other highly repetitive genomes.

Poster 31 : Genome-led vaccine target discovery for animal African trypanosomiasis

Presenter: **Dr Gavin Wright**, *Senior Group Leader, Wellcome Sanger Institute*

D Authmeman[2]; C Crosnier[2]; C Brandt[2]; K Harcourt[2]; A Romero Ramirez[1]; S Clare[2]; A P Jackson[1]; **G J Wright**[2];
[1] University of Liverpool, UK; [2] Wellcome Sanger Institute, UK

The livelihoods of millions of people living in Africa are at risk due to infectious diseases that affect the health of livestock animals which provide them with essential food, milk, clothing and draught power. One major livestock disease is animal African trypanosomiasis (AAT) which is primarily caused by two species of blood-dwelling *Trypanosome* parasites: *T. vivax* and *T. congolense* that affect goats, sheep and especially cattle. AAT is endemic in sub-Saharan Africa and is estimated to cause annual productivity losses of up to $600 million, a burden that falls primarily on the poorest. The few drugs that are available to treat AAT are not satisfactory: they cause serious side effects and parasite resistance to these drugs is increasing. There is a widely-held view that vaccinating against these parasites is unachievable due to the presence of a highly abundant parasite cell surface glycoprotein which can serially switch to a large repertoire of antigenically distinct forms that are clonally expressed. We will show using a systematic genome-led reverse vaccinology approach and a murine infection model that vaccinating with non-variant cell surface proteins used as subunit vaccines can attenuate *T. vivax* infection, including one that is capable of eliciting sterile protection. We will present research that describes the discovery of these vaccine candidates and our progress in understanding the immunological mechanisms of protection that are elicited by this vaccine.

Poster 32 : Identification and characterisation of nematode-derived antimicrobial peptides to tackle emerging antimicrobial resistance

Presenter: **Mr Allister Irvine**, *PhD Student, Queen's University Belfast*

A Irvine[1]; S Huws[1]; L Atkinson[1]; A Mousley[1];
[1] Queen's University Belfast, UK

The emergence of antimicrobial resistance (AMR) is a serious threat to the control of disease in human and animals worldwide. As traditional antibiotics fail, the discovery of novel antimicrobials is key to replacing those that have, or soon will, become ineffective. Antimicrobial peptides (AMPs) are natural antimicrobials produced as part of the innate immune response and are appealing contenders in the quest for novel antimicrobials; indeed, a number of AMPs are already in clinical trials underpinning their potential. Invertebrates lack an adaptive immune response and therefore rely on AMPs to combat microbial threats. This is of particular importance to parasitic nematodes which often live in microbial-rich environments, such as the gastrointestinal system of their host. Profiling the AMP armoury of parasitic nematodes may uncover AMPs with therapeutic potential as novel

antimicrobials to tackle AMR. In addition, the role of endogenous AMPs in parasites as the first line of defense against invading pathogens may provide opportunities for the identification of novel anti-worm therapies.
In this study we adopted an *in-silico* approach to the identification and classification of AMPs across phylum Nematoda. Bioinformatics and computational AMP prediction tools were employed to identify >2000 putative AMPs from 96 nematode species. Putative nematode AMPs were categorised into four known AMP families (Defensins, Cecropins, Nemapores and Glycine Rich Secreted Peptides) based on family-specific sequence similarity and motif identity. The Glycine Rich Secreted Peptides (GRSPs) were the most prevalent amongst the Nematoda, followed by the defensins and nemapores. The cecropins were restricted to the order Ascaridida suggesting that they play an Ascarid-specific role. Clade 8 and Clade 2 species displayed a much reduced AMP profile relative to other nematode clades; this was particularly evident in clade 2 *Trichinella* and *Trichuris* species which have both a reduced number and diversity of known AMP families. This may suggest the existence of clade 2 specific AMP families which requires further investigation. The number of putative AMPs in each family varied between species highlighting that the parasite AMP profile is species dependent and is highly adapted to individual lifestyles and lifecycles. Future analysis of nematode AMPs will aim to probe the range of antimicrobial activity displayed by nematode AMPs and investigate the importance of AMPs to nematode biology, exploring tissue-, sex- and life stage- specific AMP expression.

Poster 33 : Functions of the BBSome protein complex in *Leishmania mexicana*

Presenter: **Dr Helen Price**, *Senior Lecturer, Keele University*

S L Berry[2]; S Hart[1]; **H Price**[2];
[1] Institute for Science and Technology in Medicine, Keele University, UK; [2] School of Life Sciences, Keele University, UK

The neglected tropical disease leishmaniasis is caused by infection with the protozoan parasite *Leishmania* spp. With over 1 million new cases per year, this disease is a significant cause of mortality and morbidity in endemic areas. The *Leishmania* parasite cycles between a procyclic promastigote stage in the sandfly vector; a host-infective metacyclic promastigote stage which is transferred from vector to mammalian host during a bloodmeal; and an intracellular amastigote stage which resides inside host macrophages.
The BBSome is a protein complex which is associated with molecular trafficking to/from primary cilia and flagella in other eukaryotes. Previous work (Price *et al* 2013) showed that deletion of one of the subunits, *BBS1,* from *L. major* severely reduces parasite virulence in mice. We hypothesise that the *Leishmania* BBSome is involved in the transportation of macromolecules to the parasite cell surface. We are in the process of testing this hypothesis by analysis of transgenic parasite cell lines with disrupted BBSome function. We have targeted BBS9, a core protein subunit of the BBSome. Our data shows that knocking out the *BBS9* gene in *L. mexicana* causes a significant decrease in cell size, flagellum length and motility in promastigotes. The ability of stationary phase promastigotes to infect THP-1 macrophages is also significantly reduced in *BBS9-/-* mutant lines compared to the parental line. The next steps in this work are to analyse the effect these changes have on the distribution of macromolecules on the cell surface. We are using biotinylation and streptavidin pull down of cell surface proteins, which will be analysed by mass spectrometry for differences in protein levels.

Poster 34* :Prevalence and systematics of *Plasmodium* spp. sampled at Chester Zoo during an avian malaria outbreak among Humboldt Penguins (*Spheniscus humboldti*) in 2017

Presenter: **Miss Merit Gonzalez Olvera**, *PhD student, University of Liverpool*

M Gonzalez Olvera
[1] University of Liverpool, UK

Avian malaria, caused by *Plasmodium* spp., is a major health threat to penguins kept in captivity and possibly in the wild. This disease has produced several outbreaks worldwide and some in the UK, raising the concern about this disease. Nevertheless, many aspects of its epidemiology and genetics remain unknown; thus we carried out a study throughout 2017 collecting mosquitoes and tissue samples from dead birds in Chester Zoo, either belonging to the zoo collection or wild birds found on the premises. Our aim was to determine the presence of *Plasmodium* in the area as avian malaria has never been reported before. We tested all samples for *Plasmodium* by a nested PCR targeting the cytochrome *b* gene; all positive samples were sequenced and then used to build a phylogenetic tree to determine their species. The mosquitoes showed a prevalence of 5% at the beginning of their activity season (May, June) but during the peak of the season (July) the prevalence reached 28%. From the wild birds collected (n≤76) only one blackbird recovered in June was infected. Regarding the birds from the zoo's collection (n≤88), five penguins were infected. The penguins experienced an avian malaria outbreak in September when they were moved from their original exhibit; in October, they started showing disease signs and half of them (n≤21) died by the end of November; from those, 25% were infected with *Plasmodium*. For all bird's samples, only one species of parasite was found, *P. matutinum*. In the mosquitoes, three main species were found, *P. matutinum* (47.1%), *P. vaughni* (33.5%) and *P. relictum* (3.4%). The only species involved in the penguin mortality, *P. matutinum,* is a European species that in general is not considered highly pathogenic and this is the first time that it has been associated with an avian malaria outbreak. On the other hand, *P. relictum*, which was also found in the mosquitoes, is considered as one of the most pathogenic species causing mortalities up to 90%. The composition of the Plasmodium species in the mosquitoes' community and local birds communities can change and shift the species dominance, with implications on the infection and disease risks to susceptible endangered species like penguins. Therefore; constant surveillance could provide valuable information about the pathogenicity of the Plasmodium species, the seasonality of the mosquito vector and the parasite to alert promptly about infections and health status of zoo birds.

Poster 35 : Changes in intestinal permeability and regulatory cell development over the course of murine schistosomiasis

Presenter: **Miss Alice Costain**, *PhD Student, The University of Manchester*

A Costain[1];
[1] The Univeristy of Manchester, UK

As part of the *Schistosome mansoni* lifecycle, schistosome eggs pierce through the intestinal wall. These penetrations likely reduce the integrity of the mucosal barrier and enhance the translocation of gut luminal substances (such as bacteria, antigens, toxins and metabolites) into local tissues and systemic circulation. The permeation of these substances might have major implications for the immune responses observed during schistosomiasis. This includes the expansion of regulatory cell networks (Breg and Tregs) in chronic phases of disease and the subsequent protection against allergy and autoimmune disorders. In this study, we investigated changes in intestinal permeability and regulatory cell expansion over the course of murine schistosomiasis (14 weeks) in mice conventionally infected with egg-laying male and female schistosomes, or as a control, a male-only infection that does not generate eggs. By applying a non-invasive permeability assay (oral gavages with FITC-dextran) we show that intestinal permeability is significantly elevated in conventional mixed-sex infections from weeks 11 onwards, whereas in mice with worm-only infections, permeability remains comparable to naïve for disease duration. In addition, by analysing splenic T cell and B cell populations over the course of infection, we

demonstrate that mixed and single-sex infections are accompanied by the expansion of distinct B and T cell subsets. Importantly, B-cells from mixed-sex infected mice have a greater propensity to secrete IL-10 than B-cells induced by single-sex infections. In conclusion, this work demonstrates impaired mucosal barrier function in egg-producing schistosome infections, and hints that the passage of schistosome eggs across intestinal wall may influence the immunoregulatory landscape observed during schistosomiasis

Poster 36* :In depth analysis of the tubulin family in *Fasciola hepatica*: A combined bioinformatics and sub-proteomic approach.

Presenter: **Miss Magdalena Wilamska-Chyrczakowska**, *MRes Student, Aberystwyth University*

M K Wilamska- Chyrczakowska[1]; C F Collett[2]; D Cutress[2]; R Stuart[3]; R M Morphew[2];
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The parasitic trematode *Fasciola hepatica* infects many host organisms including sheep, cattle and humans. *F. hepatica* is responsible for major economical and veterinary health losses across the globe and such losses include high costs of drug treatment and farm management strategies, reduction in milk and wool production, growth rates and fertility. Triclabendazole (TCBZ), which targets both juvenile and adult forms of *F. hepatica*, is the current drug of choice, yet resistance to TCBZ has developed causing further control challenges. The mechanism of TCBZ action is currently still unknown which thus prevents monitoring resistance in the field and how it has developed.
A significant body of evidence points towards tubulins as a target of TCBZ action. At present our understanding of the tubulin family is limited to 5 alpha and 6 beta tubulins. The current work aims to comprehensively map the *F. hepatica* tubulin superfamily family using bioinformatics, incorporating the latest genome information, combined with a sub proteomics approach. Both α-tubulins and β-tubulins are expanded from the previously known 5 and 6 isoforms respectively. This includes variations in tubulin profiles for TCBZ resistant and susceptible isolates. Using sub-proteomics we have examined the expressed tubulin isoforms. Finally, we are investigating the role of microtubule-associated proteins (MAPs) and TCBZ mode of action through the purification of native microtubules. MAPs are likely altered following TCBZ exposure and thus warrant investigation to help elucidate TCBZ mode of action.

Poster 37* :Lineage-specific rapid diagnostic tests efficiently resolve *Trypanosoma cruzi* TcII/V/VI ecological and epidemiological associations in the Argentine Gran Chaco

Presenter: **Miss Niamh Murphy**, *PhD Student , London School of Hygiene and Tropical Medicine*

N Murphy[2]; V Cardinal[3]; T Bhattacharyya[2]; N Macchiaverna[3]; P Mertens[1]; N Zeippen[1]; R Gürtler[3]; M A Miles[2];
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Trypanosoma cruzi, the protozoan agent of Chagas disease, is comprised by at least 6 genetic lineages (TcI-TcVI). Their geographical distribution, clinical associations, and reservoir hosts are not fully elucidated, as genotyping is hampered due the difficulty in isolation and culture. Lineage-specific serological techniques may address these issues.
Synthetic peptides representing lineage specific epitopes of the *T. cruzi* trypomastigote small surface antigen (TSSA) were used in ELISA and a TcII/V/VI peptide was used in a novel rapid diagnostic test (RDT) to identify

specific IgG. These assays were performed on human, canine, feline and armadillo sera from the Gran Chaco in Northern Argentina, a region of ongoing transmission cycles.
The novel RDT, using Protein G to detect human and canine IgG, was at least as sensitive as ELISA for TSSApep-II/V/VI. The epitope common to lineages TcII/V/VI was recognised in humans by RDT (242/396), in dogs by RDT (48/73), in cats by specific ELISA (5/19) and in armadillos by RDT (1/7). In humans TSSA-II/V/VI recognition was associated with being in households with another TSSA-II/V/VI reactive householder ($p \leq 0.0428$). For dogs TSSA-II/V/VI recognition was associated with being born before the mass spraying ($p \leq 0.0462$) and Toba household ($p \leq 0.0462$).
This study has shown that this Protein G- based RDT can replace ELISA for TcII/V/VI recognition in humans and dogs, and that this can be detected in cats and armadillos, and revealed statistically significant associations. Furthermore, elsewhere we have reported a significant association between level of TcII/V/VI response and severity of chagasic cardiomyopathy. These results form the basis for more detailed studies, enabling rapid in-the-field surveillance of the distribution and clustering of these lineages among humans and mammalian reservoirs of *T. cruzi* infection.

Poster 38* :Out of sight: do eye flukes alter predator-prey interactions?

Presenter: **Miss Meg Huggins**, *MBiol Biological Sciences, School of Biosciences*

M L Huggins[1]; R A Paterson[1];
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Diplostomum spp. are common and widespread parasites of freshwater fish, with eye and brain infections resulting in lens cataracts, blindness and host mortality. Whilst *Diplostomum* are well known to modify the 'prey' behaviour of their second intermediate fish host to facilitate transmission to their definitive avian host; the effects of *Diplostomum* on the 'predator' behaviour of their fish host has rarely been explored. Here we assessed how *Diplostomum* infections influenced the consumer functional response of three-spined stickleback (*Gasterosteus aculeatus*) towards *Daphnia* prey. Our results indicate the impact of *Diplostomum*infection on the consumer functional response of their fish host may differ with prey size. This suggests *Diplostomum* induced changes in the prey choice of their fish host, leading to preferential selection of large prey species, may release small prey species from the direct impacts of predation. This research highlights a hidden consequence of *Diplostomum* infection on predator-prey interactions in aquatic ecosystems.

Poster 39 : Soil-transmitted helminths of groundnut (*Arachis hypogaea L*); A short survey of Aku, Ede-Oballa and Enugu-Ezike town in Enugu State, Nigeria.

Presenter: **Dr Nkiru E Ekechukwu**, *Lecturer, University of Nigeria, Nsukka.*

N E Ekechukwu[1]; F N Ekeh[1]; M Nnaji[1]; G E Odoh[1];
[1] University of Nigeria, Nigeria

Helminth infection remains a health concern particularly in places where unhygienic practices such as indiscriminate disposal of faecal wastes and the use of human night soil as farm fertilizer still exist. Studies in Nigeria have shown a high prevalence of geohelminths among humans living in an unsanitary environment. Groundnut (*Arachis hypogaea L.*) is a popular travellers' snacks in Nigeria due to its easy farming, readily and quickly consumable methods. The consequences of human infection with soil-transmitted helminths are of major health concern here, since most people especially the local commuters eat groundnuts without caring about how

they are processed and handled. More so, peasant farmers have little understanding of the effects of soil-borne helminths in groundnuts and how parasitic infections of the groundnut pods pose a risk to human health. Here, we carried out a three-month survey of the prevalence and intensity of geohelminths in groundnut plants and groundnut farm soil in Aku, Ede-Oballa and Enugu-Ezike towns. A randomized sampling technique was employed to collect groundnut plant and groundnut farm soil. Overall, 180 samples were collected,60 samples from each town comprising 30 samples of 100g of soil and 30 samples of 100g of groundnut plant (leaf, pod, and root). The geohelminths in the samples were isolated by sedimentation-centrifugation techniques. The research revealed that only soil samples and groundnut pods had geohelminth infections. Six (6) helminths were isolated (largely eggs from the farm soil) and five (5) were identified as parasitic nematodes (*Aphelenchoidides arachidis*, *Dityelenchus spp*., *Ascaris lumbricoides* eggs, *Ancylostoma/Necator* eggs, *Taenia spp* eggs), while one remained unidentified. There was a significant difference in the prevalence of geohelminth in the three locations. In Aku, prevalence was 33 (55.0%), Ede-Oballa 28 (46.7%) and Enugu-Ezike 9 (15.0%), ($P < 0.05$). The prevalence of helminth infections in the study areas was moderately high and significantly dependent on the farm location. The overall mean intensity of helminth parasites in groundnut farm soil was high, Aku recorded 5.66 (95% Cls: 4.58-6.79), Ede-Oballa; 5.96 (4.59-7.44) and Enugu-Ezike; 4.43(2.43-6.86). This high intensity of geohelminth parasites observed calls for immediate health responsiveness. We suggest an extended detailed survey and the need to raise geohelminth epidemiological awareness in the study area.

Poster 40 : Protection against experimental allergic airway inflammation by the *Schistosoma mansoni* glycoprotein Omega-1

Presenter: **Dr Thomas Gasan**, *Post-Doc, LUMC*

T A Gasan[2]; K Obieglo[2]; A Ozir-Fazalalikhan[2]; F Otto[2]; Y van Wijck[2]; A Schots[3]; M Yazdanbakhsh[2]; C H Hokke[2]; C Taube[1]; H H Smits[2];
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Parasitic helminths, such as schistosomes, are proficient regulators of the host's immune response, enabling individual worms to persist within hostile host tissues for decades. Chronic infection with *Schistosoma mansoni* is known protect against allergic airway inflammation (AAI) in mice, and to be associated with reduced Th2 responses to inhaled allergens in humans, despite a robust schistosome-specific Th2 responses. With this naturally occurring immunomodulatory capacity, schistosomes are an attractive source of novel AAI therapeutic molecules. We have previously shown that mice treated with an i.p. injection of intact *Schistosoma mansoni* eggs were protected against a subsequent induction of AAI by ovalbumin (OVA)/alum (Obieglo, 2018). One of the most abundantly secreted egg molecules is the glycoprotein omega-1 (ω1). This molecule has been shown to exhibit immunomodulatory effects: targeting mannose receptor (MR)-expressing dendritic cells via Le^x-glycans and suppressing protein translation via its RNAse activity upon uptake in the cell (Everts, 2012). Here, we aimed to investigate the immunoregulatory properties of the egg-derived glycoprotein ω1 in an AAI mouse model.
Mice treated with two i.p. injections of plant-derived recombinant ω1 (50 µg/mouse – one week apart) were protected against a subsequent induction of AAI by ovalbumin (OVA)/alum, injected 4 and 10 days after the last ω1 administration. Administration of ω1 significantly inhibited pulmonary eosinophilia in response to allergic challenge and dampened local Th2 cytokines (IL-5, IL-13) in the lavage and the mediastinal lymph nodes. In addition, ω1 pre-treatment was linked to a reduced influx of pro-inflammatory, monocyte-derived dendritic cells into lung tissue of allergic mice, combined with lower levels of the monocyte-attractant chemokine CCL2 in the lavage fluid following allergen challenge. The induction of allergic inflammation in the OVA/Alum model critically depends on the trafficking of OVA from the peritoneal cavity (the injection site) into the mediastinal lymph nodes by inflammatory monocytes. To deduce the mechanism of ω1-induced protection in the OVA/Alum model, we

examined what effects pre-treatment with ω1 has on the trafficking and processing of subsequent fluorescent-labelled OVA by inflammatory monocytes.
Pre-treatment with ω1 resulted in a significantly higher number of OVA-positive cells remaining in the peritoneal cavity 24 hours following OVA/alum injection and reduces trafficking of OVA-positive cells into the mediastinal lymph node and bone marrow compartment. Therefore, these data suggest that pre-treatment with ω1 may prevent the induction of an allergic response to OVA by reducing allergen trafficking towards the draining mediastinal lymph nodes. In future experiments we aim to look at what MR-expressing cell types ω1 is targeting and how this influences the function of these cells to inhibit migration of OVA carrying inflammatory monocytes towards the lung draining lymph nodes.

Poster 41 : Characterisation of a novel glycosylated glutathione transferase of *Onchocerca ochengi*, a model organism in the study of onchocerciasis

Presenter: **Dr Clair Rose**, *PDRA, Liverpool School of Tropical Medicine*

C Rose[1]; Z Stead[1]; R Taylor-Leak[2]; S Summers[2]; G Praulins[1]; A Casas-Sanchez[2]; A Acosta-Serrano[1]; B Makepeace[3]; E J Lacourse[2];
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Filarial nematodes possess glutathione transferases (GSTs), ubiquitous enzymes with potential to detoxify xenobiotic and endogenous substrates, and modulate the host immune system, which may aid worm infection establishment, maintenance and survival in the host. Here we have identified and characterised a Sigma class glycosylated GST (OoGST1), from the cattle-infective filarial nematode *Onchocerca ochengi*, which is homologous (99% amino acid identity) to an immunodominant and potential vaccine candidate from the human parasite, *O. volvulus*, (OvGST1b). *O. ochengi* native GSTs were purified using a two-step affinity chromatography approach, resolved by 2D and 1D SDS-PAGE and subjected to enzymic deglycosylation revealing the existence of at least four glycoforms. A combination of lectin-blotting and mass spectrometry (MS) analyses of the released *N*-glycans indicated that OoGST1 contained mainly a paucimannose-type (Man5GlcNAc2) structure, but also complex- and hybrid-type oligosaccharides in a lower proportion. Furthermore, OoGST1 showed prostaglandin synthase activity as confirmed by Liquid Chromatography (LC)/MS following a coupled-enzyme assay. This is only the second ever reported and characterised glycosylated GST and our report highlights its potential for a role in host-parasite interactions and use in the study of human onchocerciasis

Poster 42 : A Global Network for Neglected Tropical Diseases: towards new therapeutic solutions for Chagas disease and Leishmaniasis

Presenter: **Dr Mags Leighton**, *NTD Network project officer, Durham University*

M Leighton[1]; S L Cobb[1]; P Denny[1]; E Pohl[1]; P G Steel[1]; G Sandford[1];
[1] Durham University, UK

Whilst almost everyone has heard of malaria, mention Chagas disease or leishmaniasis and most faces are blank. The GCRF-funded, Global Network for Neglected Tropical Diseases (NTDs), based in Durham and spanning South America, Asia and the UK, has a mandate to find new drug targets for these NTDs. The ~500 million people worldwide considered as 'at risk' from Chagas disease and leishmaniasis is an underestimate. These trypanosome-mediated NTDs are associated with populations in extreme poverty across Asia, Africa and South America, in remote, rural areas where data is under-recorded and clinical resources are limited. Infections are

often symptom-free, persisting undiagnosed for years before their consequences appear as major organ failure (heart and gut tissues are affected by Chagas disease, whilst visceral leishmaniasis attacks the spleen and liver). Infections are now spreading to new areas - including the southern US and Europe. Our current treatments, non-specific chemotherapeutics, are over 40 years old, have limited efficacy, and themselves can be lethal. We lack effective, simple-to-administer alternatives that combat the parasites without harming patients. One reason behind this shortfall is that without parasite-specific molecules to use as targets in screens for new compounds, the costs of drug development are prohibitive. Another factor is that these trypanosomes have an 'odd' physiology, meaning that these organisms lack the molecular machinery needed for many standard genetic and cell biology techniques. Relatively few researchers are available in endemic countries with the advanced skills required to study these organisms, and identify and validate the necessary in-parasite molecular targets. A Global Network for Neglected Tropical Diseases includes parasitologists, chemists, immunologists and structural biologists. Our shared vision is to grow a worldwide collaborative network that harnesses expertise from both academic and industrial sources. We believe this combined approach is vital for attaining a truly sustainable solution to Chagas disease and leishmaniasis. Our NTD Network supports multidisciplinary research collaborations between members via:- 6-month, 'pump priming' projects - 2-year, 'proof of concept' investigations (PDRA funding) - Supported researcher secondments Funding opportunities for partners external to the Network membership include:- 'Seed corn' industrial partnership projects- Industrial-academic 'sandpit' events (for networking and creative thinking)- Training in CRISPR-Cas9 and other skills shortages for early career NTD researchers from endemic countries and the UK-Themed symposia (e.g. as an addition to your specialist meeting)- Travel bursaries for Network-relevant meetings/conference attendance- PhD/PDRA positions For further information and alerts for upcoming opportunities, sign up at https://ntd-network.org/.

Poster 43 : The antimicrobial properties of *Ascaris suum* pseudocoelomic fluid and its microbiome

Presenter: **Miss Sorcha Donnelly**, *PhD Research Student, Queen's University Belfast*

S Donnelly[1]; L Atkinson[1]; A Maule[1]; L Stewart[1]; N J Marks[1]; A Mousley[1];
[1] Queen's University Belfast, UK

Parasitic nematodes are common pathogens of agricultural animals where they live in close association with the host intestinal microbiota. This hostile environment presents challenges to worm health and longevity which are managed through the worm's innate immune system that includes the production of antimicrobial peptides (AMPs). The profile and significance of worm-derived AMPs is currently unknown; in addition to protecting the parasite from pathogen infection, worm-derived AMPs may also play a role in shaping the surrounding microbial community of the host including both commensals and invading bacterial pathogens.
Ascaris suum is an excellent model parasite that can be readily collected from the intestines of pig at local abattoirs. *Ascaris* is large in size and amenable to both tissue-level dissection and body cavity fluid collection. In this study we exploit the experimental tractability of *Ascaris* to evaluate the antimicrobial properties of the pseudocoelomic fluid, and to identify an endogenous microbial community within the body cavity fluid.
Data to date highlight that *Ascaris* PCF displays bactericidal properties against the gram-negative bacilli, *Staphylococcus aureus* and *Bacillis subtilis*. In contrast *Ascaris* PCF did not have any impact the gram positive bacterium, *Staphylococcus epidermidis*, or gram negative species, *Escherichia coli*; indeed *Ascaris* PCF appeared to act as a probiotic when in the presence of *S. epidermis* and *E. coli* enhancing growth of these two species. In addition, an endogenous PCF microbiota was observed following an overnight culture of *Ascaris* PCF in aerobic conditions. These data suggest the *Ascaris* PCF has both bactericidal and probiotic properties that appear to be species selective. The presence of an endogenous microbial community within the PCF offers an opportunity to dissect the dynamic interactions between the microbiome of the PCF and worm-derived AMPs, and how they might

both impact on the diversity of commensals and pathogens within the host. Data generated in this project have the potential to uncover AMPs that have therapeutic potential against key pathogens of livestock. In addition, understanding the importance of nematode-derived AMPs to nematode survival may inform future parasite control options.

Poster 44* :Towards novel control strategies for sand fly vectors through genetic modification of olfaction mediated by CRISPR-Cas9 gene drive.

Presenter: **Mr Rhodri Edwards**, *PhD student, London School of Hygiene and Tropical Medicine*

R Edwards[3]; L Brandner-Garrod[2]; L Thompson[2]; T Walker[2]; M E Rogers[2]; C McMeniman[1]; F Olmo[3];
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Current control strategies for mitigating the impact of Leishmaniasis via vector control do not provide a panacea. New strategies for disease control are required. Consequently a novel method is being explored in the current work, namely CRISPR-Cas9 genetic modification of olfaction and host seeking behaviours. In tandem we aim to incorporate traits into CRIPSR-Cas9 mediated gene drives to enable rapid spread of traits through vector populations.
Historically, different genetic techniques have been developed to manipulate genomes, however they are not reliably precise and are technically laborious. In contrast CRISPR-Cas9 systems have recently been developed which provide almost complete control of the gene editing process. In the context of insects of medical importance CRISPR-Cas9 gene drive systems have been applied to manipulate reproductive capacities and express antimalarial peptides in Anopheline vectors of Malaria, and also applied to vectors of Yellow fever.
The current project has three main goals, the first being to construct a suite of plasmids for *Lutzomyia longipalpis* and *Phlebotomus papatasi* designed to selectively knock out non-lethal targets that illicit a phenotypic response. Secondly, we apply a successful microinjection platform, applied to sand flies, and are also developing a novel non-microinjection plasmid delivery system. Thirdly, orthologues of olfactory gene targets of relevance have been identified in sand flies that are likely involved in the detection of their hosts. Here we apply a rationalisation pipeline to locate genes of interest according to different inclusion and exclusion criteria. Three main gene families have been identified through this pipeline as playing an important role in olfaction and host detection in sand flies. Targets are assessed *in vitro* before eventual incorporation into a scaffold containing gene drive components. The work described has the potential to contribute towards a new approach of interrupting disease transmission, applied to leishmania, and reduce the burden of human suffering.

Poster 45* :Repeated doses of Praziquantel in Schistosomiasis Treatment (RePST) – single versus multiple praziquantel treatments in school-age children in Côte d'Ivoire: a study protocol for an open-label, randomized controlled trial

Presenter: **Miss Miriam Casacuberta Partal**, *PhD student, LUMC*

P T Hoekstra[3]; **M Casacuberta Partal**[3]; A S Amoah[3]; L van Lieshout[3]; P L Corstjens[3]; R K Assare[4]; K D Silue[2]; R Tsonaka[3]; Y K N'Gbesso[1]; M Roestenberg[3]; S Knopp[4]; J Utzinger[4]; J T Coulibaly[2]; G J van Dam[3];
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Large scale administration of the anthelminthic drug praziquantel (PZQ) to at-risk populations is the cornerstone of schistosomiasis control, although persisting high prevalence of infections in some areas and growing concerns of PZQ resistance have revealed the limitations of this strategy. Most studies assessing PZQ efficacy have used relatively insensitive parasitological diagnostics, such as the Kato-Katz (KK) and urine-filtration methods, thereby overestimating cure rates (CRs). This study aims to determine the efficacy of repeated PZQ treatments against *Schistosoma mansoni* infection in school-aged children in Côte d'Ivoire using the traditional KK technique, as well as more sensitive antigen- and DNA-detection methods.
An open-label, randomised controlled trial will be conducted in school-aged children (5 to 18 years) from the region of Taabo, Côte d'Ivoire, an area endemic for *S. mansoni*. This 8-week trial includes four two-weekly standard doses of PZQ in the "intense treatment" intervention group and one standard dose of PZQ in the "standard treatment" control group. The efficacy of PZQ will be evaluated in stool samples using the KK technique and real-time PCR as well as in urine using the point-of-care circulating cathodic antigen test and the up-converting phosphor, lateral flow, circulating anodic antigen assay. The primary outcome of the study will be the difference in CR of intense versus standard treatment with PZQ on individuals with a confirmed *S. mansoni* infection measured by KK. Secondary outcomes include the difference in CR and intensity reduction rate between the intense and standard treatment groups as measured by the other diagnostic tests, as well as the accuracy of the different diagnostic tests, and the safety of PZQ.
This study will provide data on the efficacy of repeated PZQ treatment on the clearance of *S. mansoni* as measured by several diagnostic techniques. These findings will inform future mass drug administration policy and shed light on position of novel diagnostic tools to evaluate schistosomiasis control strategies.

Poster 46* :Expression of antiparasite peptides in Sand flies and Triatomine bugs inducing refractoriness to *Leishmania* and *Trypanosoma cruzi* mediated by CRISPR-Cas9 gene drives.

Presenter: **Mr Luke Brandner-Garrod**, *Research assisstant/PhD student, London School of Hygiene and Tropical Medicine*

L Brandner-Garrod[1]; R Atherton[1]; F Olmo[1]; R Edwards[1]; L Thompson[1]; M E Rogers[1]; T Walker[1]; M Yeo[1];
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Leishamniasis and Chagas disease cause an enormous burden of human suffering. Vector control is difficult, there are no vaccines and drug regimes are not always efficacious. New approaches to control are needed. The recent development of CRISPR-Cas9 systems allows for precise genomic knockout and also insertions of exogenous DNA. In the context of vector-borne diseases two main approaches have been previously applied to Anopheline mosquitoes, namely to reduce reproductive capacity and secondarily to express antimalarial peptides mediated through highly efficient gene drives. Both approaches have achieved remarkable results in laboratory settings.Here we aim to develop a platform to assess, introduce, and express anti-parasitic peptides applied to multiple sand fly and triatomine bug species mediated by CRISPR-Cas9 gene drives. Introduced traits spread rapidly through populations leading to a new approach to interrupt transmission for both Leishmaniasis and Chagas disease Delivery of CRISPR-Cas9 components to insect embryos is difficult. Historically, microinjection has been the main approach for transfecting the embryos of disease vectors, although this has led to a number of potential research bottlenecks. The size and robust structure of triatomine eggs makes high throughput microinjection extremely unlikely. We have developed a non-microinjection delivery method to chemically mediate transgenesis in triatomine embryos, with successful delivery of plasmid constructs to embryos within 10 minutes of administering. In the context of sand flies, we are also able to introduce constructs via traditional microinjection approaches. In tandem, we have developed a suite of CRISPR-Cas9 knockout constructs targeting non-lethal endogenous genes that are

likely to induce a phenotypic effect or impact refractoriness to associated parasites. Transgenic constructs designed for the insertion of exogenous DNA and expression of candidate anti-parasitic peptides, validated through toxicity assays, and preferentially expressed in the midgut are being assessed. Selected peptide targets will be incorporated into constructs towards the development of full gene drive systems.
This approach has the potential to deliver a powerful and novel platform to interrupt disease transmission applied to both *Leishmania* and *Trypanosoma cruzi.*

Poster 47 : Expanded access to praziquantel in three communities around the Weija reservoir, Ghana.

Presenter: **Dr Lucas Cunningham**, *PDRA, LSTM*

L J CunninghamS Campbell[2]; S Armoo[1]; A KouKounari[4]; V WatsonP Selormey[1]; J R StothardE AdamsM Osei-Atweneboana[1];
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Background: The current intention of the WHO is to eradicate schistosomiasis (SCH) in specific regions and selected African countries will likely require expanding treatment access to the wider community. This study reports the findings of the initial baseline survey of a much larger, longitudinal study, that will explore the impact of community wide treatment of SCH.
Method:: Three from the Greater Accra region of Southern Ghana, Tomefa, Torgahkope-Adakope and Manheam. From each of these communities 658 individuals were enrolled into the study via random household selection. Urine and faecal samples were taken and underwent urine filtration and Kato-Katz screening. Parallel to the parasitological survey risk factors were identified using an epidemiological questionnaire.
Results: The prevalence of *S. haematobium* ranged from 3% to 19% and *S. mansoni* ranging from 30% to 78% across the three communities The prevalence of STH across the three sites was negligible at 1.5%. A number of morbidity indicators positively associated with high intensity *S. mansoni* and *S. haematobium*, were identified. Notably blood in stool currently or in the past month and blood in urine either currently or in the last month. Boys were had a higher risk of high intensity SCH infection for both species of schistosome. Between adults and school age children there was no significant difference with regards to *S. mansoni* infections. However, amongst school age children there was a higher risk of *S. haematobium* infection compared to adults. Lower socio-economic status was also tied to likelihood of having schistosomiasis.
Conclusion: The communities targeted by this study showed a range of *Schistosoma* prevalence and intensities, from hypo-endemic through to meso-endemic and hyper-endemic. This range of endemicity will help better understand the impacts a community treatment will have in the control of SCh in different settings. The large numbers of adults and pre-school age children that are infected with either *S. mansoni* and/or *S. haematobium* indicate the importance of expanding access to treatment in order to move on from morbidity control and towards some of the more ambitious golas set by the WHO.

Poster 48* :Glutathione transferases of *Haemonchus contortus*; profiling and responses to ivermectin

Presenter: **Miss Shannan Summers**, *Student, University of Liverpool*

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The most economically important gastrointestinal nematode parasite of sheep is *Haemonchus contortus* (the Barber's Pole Worm). It has become increasingly difficult to control infections of *H. contortus* within the global sheep industry due to the rapid development of widespread anthelmintic resistance against multiple drug classes. There are concerns that the worldwide resistance observed against the macrocyclic lactone ivermectin (IVM) in particular may significantly threaten the feasibility of the sheep industry. The mechanisms for anthelmintic drug resistance are poorly understood and prior studies have focused on a range of potential mechanisms and drug targets. Amongst these potential mechanisms are the glutathione transferases (GSTs), a superfamily of phase II detoxification enzymes which may play a role in aiding nematode survival against anthelmintic drugs. However, the GST-specific proteome or 'GST-ome', and biochemical activity of *H. contortus* GSTs expressed under conditions of IVM exposure has yet to be revealed. In this study the cytosolic GSTs of three isolates of *H. contortus*, differing in susceptibility and resistance to IVM, were identified and compared via two-dimensional gel proteomics and enzymic activity assays following exposure to sub-lethal concentrations of IVM. Glutathione transferase enzyme activity was assayed using 1-chloro-2, 4-dinitrobenzene (CDNB) as a second substrate to reduced glutathione. Purification of GSTs was undertaken using S-hexylglutathione affinity chromatography, before the resolution and visualisation of purified GSTs via two-dimensional gel electrophoresis (2DE). Tandem mass spectrometry (MSMS) and protein database in-silico searches provided identification of GSTs present on 2DE. Comparative enzymic activities and GST identifications revealed class-specific profiles and responses across the three different isolates of *H. contortus* under sub-lethal IVM exposure. Adult stages of ivermectin resistant and susceptible *H. contortus* isolates displayed clear differences in protein expression, evident from protein profiles. These data correlate with previous findings in other anthelmintic resistant parasitic nematodes, including increased production of detoxification proteins in drug resistant isolates. The recombinant expression of GSTs identified in *H. contortus* isolates will aid in exploring the role GSTs may play in the detoxification of IVM. Understanding the mechanism of detoxification of IVM in *H. contortus* will aid in combatting the inevitable development of anthelmintic resistance in parasitic nematodes infecting both livestock and humans.

Poster 49* :Mutagenesis of leucine residues at the cytoplasmic end of the TbAQP2 pore affects the protein's ability to transport pentamidine

Presenter: **Mr Ali Alghamdi**, *PhD student, University Of Glasgow*

A Alghamdi[3],F Svensson[1]; H de Koning[2];
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African trypanosomes cause sleeping sickness in humans, a disease that is typically fatal without chemotherapy. The treatment of HAT is based on just a few drugs: Eflornithine, Pentamidine, Melarsoprol, Nifurtimox and Suramin. The extensive use of the available drugs has led to the emergence of drug resistance. Unfortunately, resistance to some of the drugs has reached alarming levels and appears to be spreading, but our comprehension of the resistance mechanisms remains incomplete.
Aquaporins (AQPs) are integral membrane proteins functioning as the cellular entry pathways for antimony oxides in *Leishmania* species, and more generally are the conduit for glycerol, small sugars and water. In virtually all organisms the regulation of osmotic pressure is an important role of aquaporins. The aquaporins are of different sub-types: in human tissues there are 13 known aquaporin genes, and hundreds have been identified in a multitude of non-human species. In *Trypanosoma brucei*, three aquaporins genes, AQP1-3, have been identified. Recent studies have revealed that there is a genetic link between this gene and susceptibility to some drugs,

leading to the hypothesis that some of the clinical trypanocides, specifically pentamidine and the melaminophenyl arsenicals, enter through these aquaporins. In *T. brucei* aquaporins 2 and 3 genes are found on chromosome 10 in a tandem array and share 83% sequence identity. Specifically, TbAQP2 was found to be a highly efficient transporter for pentamidine and melarsoprol and introduction of this gene into *Leishmania mexicana* made these parasites more than 1000-fold more sensitive to melarsoprol, and 40-fold more sensitive to pentamidine. Therefore, an understanding of the mechanisms of AQP2-mediated drug uptake in African trypanosomes will facilitate the advancement of diagnostic tools in melarsoprol resistance, and perhaps at the same time the development of improved treatments. We report here the construction of several genetic mutations (single or multiple amino acid substitutions) at three positions that were rationally selected from the structure in AQP2 to investigate their effects on the ability of the gene for drug sensitivity and drug transport. As part of this strategy, leucine residues at the cytoplasmic end of the aquaporin channel were replaced by tryptophan and methionine, potentially allowing us to distinguish between models of pentamidine uptake by receptor-mediated endocytosis (binding only to AQP2) and transport through the aquaporin channel. The introduction of tryptophan residues in positions L84 and L118 of TbAQP2 caused some loss of pentamidine susceptibility compared to the wild-type cells, whereas L218W showed equal sensitivity to pentamidine compared to the wild-type cells. A double mutant of L84W/L118W displayed an even greater loss of pentamidine susceptibility. Replacement of leucine with methionine instead of tryptophan had less impact on pentamidine susc

Poster 50 : Provision of *B. glabrata* infected with *S. mansoni* to the scientific community within the UK

Presenter: **Dr Josephine Forde-Thomas**, *Research Assistant, Aberystwyth University*

J Forde-Thomas[1]; K F Hoffmann[1];
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Schistosoma mansoni is a parasitic trematode that contributes to the infectious human disease schistosomiasis, which affects in excess of 240 million people worldwide. According to the WHO more than 700 million people live in endemic areas. The disease is generally found in Africa, Asia and South America in areas where there is poor sanitation and limited access to clean drinking water.
Currently a single chemotherapeutic agent, praziquantel (PZQ), has been identified to combat this disease. However, PZQ is ineffective against juvenile worms, often necessitating repeated treatment. With no anti-Schistosoma vaccine on the horizon, mass drug administration programs form the only line of defence in controlling this disease. Clearly, further research efforts are essential for reducing the impact of this helminth on human populations. Many of these research efforts rely on the continuous supply of parasite material, a service previously fulfilled by the US NIH-funded Biodefense and Emerging Infectious (BEI) research resources repository. However, recent changes in circumstances have meant that provision of this material to the UK is unlikely to be sustainable.
Here in Aberystwyth, we maintain the full *S. mansoni* life-cycle. In response to the increasing demand for parasite material within the UK, we propose to scale-up our production of parasite material in order to meet these demands as a payable service.
Our method of batch-infection results in >85% of snails becoming infected with *S. mansoni* following miricidia exposure.
The number of cercariae that can be recovered is dependent on a number of factors, but on average, our snails produce ~1500 cercs/snail when shed for 1 hour twice weekly. Furthermore, in our experience, once they reach patency and begin shedding cercariae, our snail stocks have an excellent survival rate with more than 60% of our population still alive and shedding 8 weeks post-miracidia exposure.

We are confident that our methods will make it possible to supply UK research groups with good quality, consistent material that will continue to provide parasites for extended periods of time.
If you are interested in accessing our service, please do get in touch!

Poster 51 : Exploring the Nedd8 pathway of *Plasmodium falciparum*

Presenter: **Dr Maryia Karpiyevich**, *Postdoctoral Research Associate, University of Cambridge*

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Nedd8 is a conserved ubiquitin-like protein that is conjugated to protein substrates, resulting in a post-translational modification referred to as neddylation. As a regulator of numerous cellular processes, protein neddylation is essential in a wide range of organisms including mammals, plants, and fission yeast. Nedd8 is a dynamic modification that is attached to substrates via a three-step enzymatic cascade mediated by the E1, E2, and E3 enzymes and can be removed by deneddylases. Orthologs of Nedd8, Nedd8 E1, E2, and E3 enzymes, as well as two cullin substrates with conserved neddylation sites, were identified in *Plasmodium* using bioinformatics approaches. However, key deneddylating enzymes NeddP1, CSN5/COP9 signalosome, UCHL1, and USP21 were not found, indicating that the Nedd8 pathway may be regulated differently in *Plasmodium* and its human host. We have identified a panel of potential *P. falciparum* deneddylases through the use of activity based probes and proteomic analysis and assessed their enzymatic activity. We further characterised the molecular determinants underlying the Nedd8 specificity of *P. falciparum* UCH37 and elucidated its contribution to parasite viability.

Poster 52* :Functional expression of *Aspergillus nidulans* uracil transporter gene in *T. b. brucei* and *L. mexicana* 5FU-resistant cell lines

Presenter: **Mr Ibrahim Alfayez**, *PhD student, University of Glasgow*

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Kinetoplastid parasites are a widespread group of flagellated protozoan pathogens and the defining feature of these parasites is the presence of a large mitochondrial DNA structure known as the kinetoplast. The most common human diseases caused by kinetoplastid parasites are: 1) African trypanosomes (African sleeping sickness), 2) *Leishmania* species (leishmaniasis) and 3) *Trypanosoma cruzi* (Chagas' disease). Kinetoplastid protozoa express many membrane transport proteins which enable them to take up nutrients, efflux metabolites, regulate physiological concentrations, translocate various molecules, and import or export drugs. Kinetoplastid parasites are capable of salvage as well as synthesis of pyrimidine nucleotides. The gene family encoding pyrimidine nucleobase transporters in kinetoplastid parasites has not yet been identified. In this study, the pyrimidine analogue 5-fluorouracil is used as a tool to try to identify uracil transporter in *Trypanosoma* and *Leishmania* species. Resistance to 5-fluorouracil (5-FU) was generated in *T. b. brucei* s427 bloodstream forms and *Leishmania mexicana* M379 promastigotes, yielding clonal lines *Tbb-5FURes* and *Lmex-5FURes*, respectively. Uracil/5-FU transport rates in these cell lines are strongly reduced, particularly in the *L. Mexicana* line.Uracil transporter mutants have been identified to be resistant to 5-FU in several instance. For instance, previous studies have identified that the deletion of the uracil transporter *FurD* from *Aspergillus nidulans* has contributed to full

resistance to 5-FU, and reduced the uptake of [^{3}H]-uracil. However, protozoan genomes do not contain any *FurD* homologues and the uracil uptake must be mediated by a transporter from a different gene family. For that reason, it is of interest to clone and functionally express *FurD* in the 5-FU resistant cell lines (*Tbb-5FURes* and *Lmex-5FURes*) in order to investigate whether the sensitivity to 5-FU in vitro resistant strains could be restored by the introduction of a confirmed uracil/5-FU transporter. This would allow a functional screening of potential transporter genes. The effect of expressing *FurD* in 5-FU-resistant lines *Tbb-5FURes* and *Lmex-5FURes* on sensitivities to 5-FU and 6-AU were analysed using the alamar blue viability assay. However, results showed no significant differences in the EC_{50} values of 5-FU and 6-AU between the expressing cell lines and the 5-FU resistant cell lines, although the effect of expression of *FurD* in *Lmex-5FURes* revealed a very high level of [^{3}H]-uracil/5FU uptake, even much above the wild type activity. Therefore a metabolic adaptation appears to have rendered these cells insensitive to intracellular 5-FU. Similarly, the introduction of *FurD* into *Tbb-5FURes* did not significantly increase the rate of transport of [$^{3<}$

Poster 53* :An *in vitro* study of the modulation of astrocytes in the blood brain barrier during cerebral malaria

Presenter: **Mr Atieme Joseph Ogbolosingha**, *PhD Student, Keele University*

A J Ogbolosingha[2]; N E Andoh[2]; M F Stins[1]; S J Chakravorty[2];
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Cerebral malaria (CM) is the most life-threatening complication of *Plasmodium falciparum* infection. *P. falciparum*-infected red blood cells (PRBC) sequester within microvasculature adhering to endothelial cells (EC) of the blood brain barrier (BBB) resulting in the activation and disruption of the endothelium. Consequently, there is entry of blood borne toxins, inflammatory molecules, parasite products and water into the brain parenchyma leading to cerebral perivascular oedema and long term neurological sequelae. The current study aims to investigate the activation of astrocytes following sequestration of PRBC in the endothelium of the BBB. We coculture EC and PRBC that mimics *P. falciparum* sequestration in the brain. Previous findings from our laboratory has shown that supernatants harvested from EC and PRBC cocultures mediates the activation of the BBB endothelium marked by increased expression of ICAM-1. The current study, an advanced *in vitro* model of the BBB consisting of EC and astrocytes grown in tandem on a transwell filter shows that the underlying astrocytes ensheathing the endothelium with their end feet are also activated by the EC and PRBC coculture supernatant as seen in the upregulation of astrocyte ICAM-1 and the astrocyte marker, GFAP. Interestingly, the water mobilising membrane protein, aquaporin 4 (AQP4), expressed predominantly in the end feet of astrocytes was concomitantly upregulated by the supernatant, suggesting an increased mobilisation of water into the brain, thus causing cerebral oedema. Collectively, the data shows the activation of the endothelium following PRBC sequestration leads to downstream consequences such as activation of the astrocytes. The increased expression of AQP4, demonstrated in these studies, is indicative of a possible mechanism for the development of the cerebral oedema prevalent in paediatric CM patients.

Poster 54 : *In silico* analysis of putative cell surface proteins of *Tritrichomonas foetus*, the causative agent of bovine trichomoniasis.

Presenter: **Miss Eleanor Senior**, *PhD Student, Eleanor Senior* **r**

E M Senior[1]; A P Jackson[2];
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Tritrichomonas foetus is an anaerobic flagellated protist and the causative agent of the venereal disease bovine trichomoniasis. This disease causes spontaneous abortions and, in some cases, infertility in cows and is responsible for decreased calving rates and milk production; infected animals are usually culled. Bovine trichomoniasis is therefore responsible for significant economic losses to farmers in several countries where the disease is endemic, including Australia, Brazil and the USA. Currently there is no vaccine available that can prevent reinfection.
To identify potential vaccine candidates for this parasite a reverse vaccinology approach was implemented. The *Tritrichomonas foetus* genome was sequenced on the PacBio platform (147Mb, N50 ≤ 84,706), and annotated using automated gene calling, improved with transcriptomic data from multiple cell types. Genes encoding putative cell surface proteins were identified based on in silico prediction of signal peptides (SP), transmembrane domains (TMD) and glycosylphosphatidylinositol (GPI) anchors.
We have identified 84,706 *T. foetus* genes. Among these, there are 1093 single copy encoding proteins with a predicted transmembrane domain,740 multispanning, 35 with GPI anchors and 5,205 proteins with predicted signal peptides. 1,607 predicted proteins are predicted to include both SP and TMD, indicating that they are integral to the plasma membrane, while 11 include both SP and GPI, indicating that they are tethered to the outer face of the cell. To further understand the diversity of these genes, we used sequence clustering to sort them into gene families. We present a sequence network based on PSI-BLAST scores that describes the size and number of predicted cell surface gene families in T. foetus, as well single-copy cell surface genes, and in comparison with a related parasite, *T. vaginalis*. We have found 29 *Tritrichomonas foetus* specific families that fulfil the mentioned criteria.
We have produced the first fully-annotated *T. foetus* genome as the first step in a reverse vaccinology approach to this important livestock disease. This analysis represents a predicted cell surface proteome from which we can begin to refine possible vaccine candidates. Our future work will use transcriptomic analysis of in vitro infection models, cell surface proteomics, protein localisation and *in silico* and *ex vivo* epitope mapping to identify the most plausible targets.

Poster 55 : Dysregulated gene expression in oocysts of *Plasmodium berghei* LAP mutants

Presenter: **Dr Annie Tremp**, *Research Fellow, London School of Hygiene and Tropical Medicine*

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Malaria parasite oocysts generate sporozoites by a process termed sporogony. Essential for successful sporogony of *Plasmodium berghei* in *Anopheles stephensi* mosquitoes is a complex of six LCCL lectin domain adhesive-like proteins (LAPs). LAP null mutant oocysts undergo growth and mitosis but fail to form sporozoites. At a cytological level, LAP null mutant oocyst development is indistinguishable from its wildtype counterparts for the first week, supporting the hypothesis that LAP null mutant oocysts develop normally before cytokinesis. We show here that LAP1 null mutant oocysts display highly reduced expression of sporozoite proteins and their transcription factors. Our findings indicate that events leading up to the cytokinesis defect in LAP null mutants occur early in oocyst development.

Poster 56 : Diagnostic challenges in male genital schistosomiasis (MGS): Preliminary real-time PCR results of a longitudinal cohort study in Malawi.

Presenter: **Dr Sekeleghe Kayuni**, *, Liverpool School of Tropical Medicine / UoL*

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Introduction: Male genital schistosomiasis (MGS), is an under-reported manifestation of urogenital schistosomiasis (UGS), defined by schistosome eggs in seminal fluids, genitalia and their associated pathologies. At present, semen microscopy is considered as a standard technique for diagnosing active MGS infection and urine filtration with microscopy in presence of MGS symptoms serves as a convenient but error-prone diagnostic proxy of MGS. Unlike the advances made in defining a gold standard technique for diagnosis of female genital schistosomiasis (FGS), MGS remains inadequately defined. Longitudinal cohort study among fishermen along southern shoreline of Lake Malawi was conducted to investigate the current prevalence of MGS using parasitological and molecular diagnostic techniques including real-time polymerase chain reaction (PCR).
Methods: Participants (fishermen) recruited in the cohort MGS study at baseline, were interviewed with individual knowledge, attitudes and practices questionnaires, and requested to submit mid-morning urine and semen. The urine was assessed visually, with reagent (Siemens multistrix 10G)
and point-of-care circulating cathodic antigen (POC-CCA) strips before filtration through a polycarbonate membrane before microscopy to detect schistosome ova. Direct microscopy of semen submitted in a clean, transparent plastic bag was conducted to diagnose MGS before centrifugation and repeat microscopy of the sedminent. The sediment was preserved in ethanol and shipped frozen to a molecular laboratory for real-time Polymerase chain reaction analyses. Transabdominal and scrotal ultrasonography were conducted on the participants to investigate for genital pathologies. Praziquantel treatment at 40 mg / kg was offered at the end and were invited to follow-up studies after 1-, 3-, 6- and 12-months.
Results: A total of 376 participants, aged 18 to 70 years (mean = 30.6 years), were recruited into the study and had questionnaire interviews. Preliminary results at baseline indicate 17.1% prevalence of UGS (n = 210, mean egg count = 15 per 10mL and range = 0 - 137.8). 3.8% participants tested positive for POC-CCA indicating the presence of (most probably) hepato-intestinal S. mansoni infection. For MGS (S. haematobium eggs in semen), was observed in 10.7% of participants (n = 112, mean = 6 eggs per mL, range = 0 - 30 eggs). On semen real-time PCR analyses with positive control Ct-value of 27.7, the prevalence of MGS went up to 26.6% and 75% of participants who were positive on PCR had undetectable eggs in the semen.
At 1-month follow-up study, prevalence of UGS reduced to 11.1% (n = 56, mean = 13.5 eggs per 10 mL). While no participant had schistomome eggs seen in semen (n = 40), the prevalence of MGS on PCR was 24.2%. At 3-months follow-up, UGS prevalence rose to 11.7% (n = 56, mean = 15.6 eggs per 10 mL) and MGS prevalence was 8.9% and 26.1% on microscpy and PCR respectively (n = 60, mean = 3.6 eggs per mL).
Follow-up at 6-months, revealed UGS prevalence was reduced further to 3.7% (n = 54, mean = 0.4 eggs per 10 mL and MGS prevalence was 4.1% on microscpy and 9.5% on PCR (n = 49, mean = 0.9 eggs per mL). At 12-months follow-up, UGS prevalence was 8.9% (n = 45) while MGS prevalence on microscopy was 2.4% (n = 41); PCR analyses still in progress .
Conclusion: MGS is prevalent among fishermen along Lake Malawi, known to be endemic for UGS, with increase in prevalence rates when using real-time PCR. On interest, the current treatment of choice, praziquantel, can clear the infection highlighting the importance of wider availability and accessibility in endemic areas. Since, the current low-cost standard technique (semen microscopy) misses a substantial number of infected individuals and the lower sensitivity of urine filtration as a proxy for MGS diagnosis, there is need to improve the diagnostic platform by developing higher sensitive and specific POC tests to diagnose and readily manage MGS.

Poster 57 : Adrenal hormones mediate disease tolerance in malaria

Presenter: **Prof Philippe Van den Steen**, *Professor in Immunoparasitology, KU Leuven - University of Leuven*

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Malaria reduces host fitness and survival by pathogen-mediated damage and inflammation. Disease tolerance mechanisms counter these negative effects without decreasing pathogen load. Here, we demonstrate that in four different mouse models of malaria, adrenal hormones confer disease tolerance and protect against early death, independently of parasitemia. Surprisingly, adrenalectomy differentially affects malaria-induced inflammation by increasing circulating cytokines and inflammation in the brain but not in the liver or lung. Furthermore, without affecting the transcription of hepatic gluconeogenic enzymes, adrenalectomy causes exhaustion of hepatic glycogen and insulin-independent lethal hypoglycemia upon infection. This hypoglycemia is not prevented by glucose administration or TNF-α neutralization. In contrast, treatment with a synthetic glucocorticoid (dexamethasone) prevents the hypoglycemia, lowers cerebral cytokine expression and increases survival rates. Overall, we conclude that in malaria, adrenal hormones do not protect against lung and liver inflammation. Instead, they prevent excessive systemic and brain inflammation and severe hypoglycemia, thereby contributing to tolerance.
Ref.: Vandermosten et al., Nat Commun. 2018 Oct 30;9(1):4525. doi: 10.1038/s41467-018-06986-5.

Poster 58* :Population genetics as a tool for the detection of vertical transmission of *Toxoplasma gondii* in a wild population of *Apodemus sylvaticus* (long-tailed woodmouse) from Malham Tarn, UK.

Presenter: **Dr Sameena Haq**, *Researcher, University of Salford*

S Haq[1]; G Hide[1];
[1] University of Salford, UK

Toxoplasma gondii is an intracellular protozoan parasite, with the cat as a definitive host that causes significant human and animal disease. Different strains of the parasite have been identified – classically defined as Type I, II or III although, recently, other genotypes have been discovered. The relationship between parasite genotype and infection is unknown. The routes of transmission of the parasite are also unclear and recent studies have highlighted the involvement of vertical transmission. This study involved looking at the use of alternative molecular techniques such as population genetics thus developing novel approaches to investigate the presence and epidemiology of *T. gondii* in a wild population of *Apodemus sylvaticus* (Haq *et al*., In Press).
Found in Western Europe and considered a pest, few studies have been conducted on the prevalence of *Toxoplasma* in the long-tailed woodmouse *Apodemus sylvaticus* and none reported in the UK. Furthermore, to date, there were no studies which have attempted to investigate infection in *A. sylvaticus* in relation to cats. Also, previous studies showed high levels of congenital transmission of *Toxoplasma* in murine hosts experimentally infected (Beverley, 1959; Owen and Trees, 1998). Additionally in a naturally infected population of the urban house mouse (*Mus domesticus*) it was found that there was a 59% prevalence for *T. gondii* within that species (Marshall *et al*., 2004) and thus a high level of transmission in natural urban populations was occurring (Murphy *et al*., 2008).

This hypothesis further casts doubts as to the involvement of mice in the prevalence of *T. gondii* in cats and requires further studies to clarify the issue (Marshall *et al*., 2004). However, conversely to this some studies have reported very low prevalence's of *T. gondii* of less than 1% suggesting that mice may not be an important reservoir (Smith and Frenkel, 1995) until further alternative scientific evidence is available. Earlier studies must be analysed and questioned in great depth, in order to steer any new research towards a robust answer and thus a more definite conclusion.
With regards to the study by Murphy *et al*. (2008) *Mus domesticus* mice were collected from a predominantly cat ridden area of Greater Manchester. This presented opportunity of comparison to *A. sylvaticus* where there were no known cats in the area surrounding. Further studies with different species of mice and controlled habitats are necessary as this could prove a vital piece in the jigsaw taking us even closer to the roles of rodents as intermediate hosts. Furthermore, the use of the same techniques i.e. DNA extraction, PCR protocol etc in both rodent populations enabled a direct comparison in terms of technical aspects (Gerwash, 2007).

Poster 59 : Reduced *Eimeria* and pinworms loads in hybrid mice of the European house mouse hybrid zone

Presenter: **Mrs Alice Balard**, *PhD student, Humboldt University Berlin*

A Balard[1]; V H Jarquín-Díaz[1]; J Jost[1]; I Martincová[4; 5]; L Ďureje[4; 5]; J Piálek[4; 5]; M Macholán[2; 3]; J Goüy de Bellocq[4; 5]; S J Baird[4; 5]; E Heitlinger[1];
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Differential parasite loads in hybrid hosts compared to parental species have been observed in various hybrid systems. Compared to host-parasite interactions within parental host, parasites encountering admixed, recombinant hosts for the first time in the centre of a host hybrid zone have been shown to reproduce less within the host for several nematodes. We hypothesize that this mechanism of hybrid vigour is general and can be found for parasites of various pathogenicity. We therefore assessed intracellular infections by *Eimeria*, a parasite of high pathogenicity, and infections by pinworms, assumed less pathogenic, and compared their intensity in two house mouse subspecies and their natural hybrids from a novel transect of the European hybrid zone. We found both lower parasite intensities in hybrid hosts than in parental mice and no evidence of a lower parasite prevalence in the centre of the hybrid zone, the latter disproving ecological epidemiological factors as responsible of the observed pattern. Using the same approach, we also corroborated hybrid vigour against pinworm infections reported in previous studies. We further questioned whether differences in body condition during infection would indicate different impacts on hybrid vs. parental hosts health, but couldn't show such an effect. We argue that studying parasites in hosts hybrid zones provides a unique opportunity to study host-parasite interactions in two types of interactive states, namely long term and short term evolutive interactions.

Poster 60 : Malaria co-infection with typhoid fever, Hepatitis B Virus (HBV) and Human Immunodeficiency Virus (HIV) infections among pregnant women in Ikere-Ekiti, local government area of Ekiti State, Southwestern, Nigeria

Presenter: **Dr Charles Ologunde**, *Lecturer/Researcher, The Federal Polytechnic Adoekiti*

C A Ologunde[1];
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This study is carried out to investigate the prevalence of co-infection of malaria, typhoid fever, hepatitis B virus and HIV infections among 400 pregnant women between the age range of 15-48 years stratified in age groups (15-19, 20-24, 25-29, 30-34, >≤35) from Ikere Local Government Area of Ekiti state. The incidences of the four diseased agents as derived by the examination of blood samples for malaria fever, typhoid fever, hepatitis B virus and HIV were 59(14.8%), 27(6.8%), 29(7.3%) and 17(4.3%) respectively. The number and prevalence of double and triple co-infection was 22(5.5%) and 3(0.8%) respectively. The highest number of double infection occurred in malaria and typhoid fever with a percentage of 2.8%. The prevalence of those that are not infected with any of these diseases was 268(67%) and the prevalence of infected ones was 132(33%). The rate at which the pregnant women are positive to the test carried out on their blood sample could be as a result of poor hygiene, lack of potable water, poverty, consumption of contaminated food and lack of public health education. Further studies are required to understanding the complex immune interactions involved in the co-infection and its effect on the outcome of disease presentation with the aim of designing control intervention.

Poster 61 : Identification and functional characterization of *Acanthamoeba* secretory M28 peptidase for using as a potential diagnostic marker

Presenter: **Mr Jian-Ming Huang**, *Ph. D. student, National Cheng Kung University*

Withdrawn

Poster 62 : An enhanced toolkit for the generation of knockout and marker-free, fluorescent *Plasmodium chabaudi*

Presenter: **Dr Joanne Thompson**, *Senior Lecturer, University of Edinburgh*

J Thompson[1];
[1] University of Edinburgh, UK

The rodent parasite *Plasmodium chabaudi* chabaudi is an important in vivo model. The ability to produce chronic infections makes it particularly useful for investigating the development of anti-Plasmodium immunity, as well as features associated with parasite virulence during both the acute and chronic phases of malaria infection. *P. chabaudi* also undergoes asexual maturation (schizogony) and erythrocyte invasion in culture, so offers an experimentally-amenable in vivo to *in vitro* model for studying gene function and drug activity during parasite replication and proliferation. To extend the usefulness of this parasite model we have further optimised transfection protocols and plasmids for *P. chabaudi* and generated stable, fluorescent lines that lack drug-selectable marker genes. These lines are viable throughout the lifecycle in mice and mosquitoes and show the same infection kinetics and attenuation of growth and virulence after mosquito transmission as wild-type parasites. We have also adapted the large-insert PlasmoGEM vectors that have revolutionised the scale of experimental genetics in another rodent model, and used them to generate, *P. chabaudi* gene-targeting and –tagging vectors, for transfection with our fluorescent *P. chabaudi* mother lines. This produces a tool-kit of *P. chabaudi* strains, vectors and transfection approaches that will be of broad utility to the research community.

Poster 64* :Prevalence of parasitic infections in surgically removed appendices: parasitological and histopathological studies

Presenter: **Dr Alaa Amer**, *Assistant lecturer of Parasitology, Faculty of Medicine Tanta University*

A Amer[1];
[1] Faculty of Medicine Tanta University, Egypt

Intestinal parasites may cause symptoms similar to acute appendicitis. Moreover, the diagnosis of parasitic infections is only done by post-operative histopathological examination of the appendices. Therefore, our aims are to assess the prevalence of intestinal parasitic infections among patients who were be appendectomized at Tanta Hospitals, Egypt and to investigate the possible association between these parasitic infections and appendicitis. To achieve these objectives, we performed a cross-sectional study including 65 patients chosen randomly who had undergone appendectomy over a period of one year from Oct 2015 to Oct 2016. Demographic data were retrieved. Complete blood picture was done. Moreover, appendiceal faecolithwere examined macroscopically then by direct smear examination, formol-ether concentration technique, modified Ziehl-Nelseen stain and rapid immunochromatographic test. Histopathological examination of resected appendices was done. We found that parasitic infections were detected in 24.6 % of examined cases. Most of parasitic infections were prevalent in patients belonging to the school age group. Different parasitic infections were detected in the faecolith specimens. Moreover, *Enterobious vermicularis* adult female and *Schistosoma mansoni* granuloma were detected in histopathological sections. Also, a spectrum of pathological changes in the appendices was found ranging from lymphoid hyperplasia to acute inflammation with peritonitis. In conclusion, intestinal parasites may cause clinical picture similar to that of acute appendicitis. Therefore, careful attention to clinical history, stool examination and high eosinophilia may aid diagnosis and avoid unnecessary appendectomy. Moreover, the presence of different parasitic stages in the narrow lumen of the appendix may have a role in the development of appendicitis and this needs further studies. Keywords: appendicitis; immunochromatographic test; intestinal parasites; *Hymenolepis nana*; *Enterobious vermicularis*; appendiceal faecolith

Poster 64 – Withdrawn

Poster 65 : Detection of parasitic protozoa using peptide and antibody phage display technologies.

Presenter: **Mrs Khawlah Salman**, *PhD researcher, Sunderland University*

K Salman[2];
[1] Sunderland university, Iraq; [2] Sunderland University, UK

Acanthamoeba is an opportunistic parasitic protozoa that causes a variety of disease in humans. These include a severe keratitis, a disseminating skin infection and granulomatous amoebic encephalitis. Although *Acanthamoeba* infections are rare Acanthamoeba keratitis (AK) is the most commonly observed infection with an approximate annual incidence of 1–2 cases per million people. Acanthamoeba keratitis is a serious eye infection that often result in permanent loss of visual acuity or blindness if not diagnosed quickly and managed effectively. Treatment of this infection is difficult as there are currently few drugs available for use. Early symptoms of AK are similar to those seen with fungal or viral infections thus accurate identification of this organism is vital. Clinical diagnostic options currently available include PCR/sequencing, culture and confocal microscopy. PCR is the most useful approach but this is only performed in specialist laboratories (4 centres in the UK). It has been suggested that corneal confocal microscopy would be the most clinically useful diagnostic tool as this would allow treatment to occur in a timely fashion. However, distinguishing host cells (particularly lymphocytes) from *Acanthamoeba* can be difficult thus limiting its value as a stand-alone tool for diagnosing AK. This can be overcome by using *Acanthamoeba* specific fluorescently labelled peptides for detection using confocal microscopy.With this in mind, the aim of this project was focused on generating novel fluorescent peptides that can be used for identification of *Acanthamoeba* in the clinical environment. For this work bacteriophage antibody (peptide) display technology was used as a source of peptides. This library expresses human antibody viable heavy domains as a construct with minor phage coat protein (pIII) on the surface of bacteriophage. Using a modified panning method, bacteriophage clones from a library bacteriophage clones that bound to *Acanthamoeba* via the heavy chain peptides were identified using enzyme-linked immunosorbent assays (ELISA). From this screen, 23 bacteriophage clones were identified that showed binding. Further analysis of these clones was performed including binding to the two life cycles forms seen during infection (cysts and trophozoites); from the 23 clones, nine were selected for further study.

The nine selected phage clones were induced to produce soluble antibody fragments (peptides) constructed with a myc Tag for detection. Soluble fragment production by the clones was assayed using ELISA and all nine clones produced peptides. To purify theses antibody fragments for further analysis (size and amino-acid sequence) anti-c-myc Tag (9E10) Affinity Gel Chromatography and sodium dodecyl sulphate-polyacrylamide gel electrophoresis (SDS-PAGE) was performed. This was not successful thus an alternative approach for accessing the peptides was used. The DNA sequences of of the peptide expression regions were determined for the clones and from the DNA, peptide sequences from each clone were inferred. One of these peptides was then synthesized and binding to 15 clinical Acanthamoeba isolates (cyst and trophozoite) was assessed using ELISA, confocal microscope, and flow cytometry. Interestingly, this one peptide chosen recognized all 15 Acanthamoeba isolates and both morphological forms (cyst and trophozoite).

This approach has successfully generated a fluorescently labelled synthetic peptide that bound Acanthamoeba (cyst and trophozoite). To our knowledge this is the first time this has been achieved for any pathogen and shows that this approach may generate useful diagnostic tools for the in situ detection of Acanthamoeba in the eye using confocal microscopy. We also suggest that with the right fluorophore (using fluorescent molecules that have the potential for light activated cell killing), this/ these reagent(s) have theranostic potential.

Poster 66 : Polyomics analyses reveal a role for nucleobase transporter in gentamicin-attenuated *Leishmania mexicana*

Presenter: **Mr Abdulbaset Kabli**, *PhD student, University of Glasgow*

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Leishmania have the ability to subvert the host immune system and adopt sophisticated strategies to develop and survive within the mammalian host. *Leishmania* parasites survive within macrophages, inside a parasitophorous vacuole. The molecular communication between host and parasite decides the outcome of infection, but is incompletely understood. We have compared genotype and phenotype of an attenuated *Leishmania mexicana* line with a virulent, isogenic wild type precursor. We aim to identify key virulence factors and to explore the potential of the attenuated line as a vaccine candidate.
This study was conducted on promastigotes of *Leishmania mexicana* and involved comparative polyomics approaches to identify the molecules that contribute to Leishmania virulence. Log phase promastigotes of wild type and gentamicin-attenuated (H-line) were grown in parallel in media containing 10% FBS, and they were harvested for polyomics analyses. For comparative proteomic analysis, protein extracts were labelled using 6-plex TMT and analyzed with LC-MS/MS. For metabolomics, metabolites were extracted with Chloroform/ Methanol/ Water (1:3:1) and analyzed with LC-MS. For transcriptomics, RNA was isolated and converted into a library of cDNA molecules for cluster generation and DNA sequencing. We found 18 proteins differentially expressed in attenuated *Leishmania* (FC ≥1.5 and FDR ≤0.05) and 26 identified metabolites (FC ≥1.5 and FDR≤0.05), whereas transcriptomics data found 481 transcripts were differentially expressed (FC ≥1.5 and FDR ≤0.05). Most of the differentially expressed proteins and transcripts are metabolic enzymes, and the majority of the differentially expressed metabolites are substrates that involved in nucleotide, carbohydrate and amino acid metabolisms. Correlation of polyomics datasets reveals that nucleotide metabolism (pyrimidine and purine) is significantly altered in gentamicin-attenuated *Leishmania*. Furthermore, nucleobase and nucleoside transporters were significantly down regulated in proteomics analysis. Modulation of gene expression, observed through polyomics analyses, may relate to gentamicin selection. ΔNT3 cells become more sensitive to allopurinol at lower concentrations (EC_{50}), suggesting that this may contributes to *Leishmania* avirulence.

Poster 67 : Schistosomiasis in Ogbese-Ekiti, re-infection after successful treatment with praziquantel

Presenter: **A Ogunlade**, *Department of Science Technology, The Federal Polytechnic*

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Urinary Schizostosomiasis infection is one of the major public health problem facing developing countries with school age children at great risk. Previous studies showed that Ogbese Ekiti is endemic for Urinary schistosomiasis. The impact of chemotherapy was evaluated using praziquantel (40mg/kg body weight) on *S. haematobium* among school pupils in Ogbese Ekiti, Ekiti state Nigeria. Urine samples were collected between the hours of 7.00am and 10.00 am. The number of eggs in 10ml of each urine sample was calculated from the means of two counts. At baseline one hundred and seventy two (172) pipils were screened for eggs of the *S. haematobium* out of which 75.6% were positive with high egg intensity ranging between 440-780 eggs/10ml of urine. Out of the one hundred and seventy two screened, thirty subjects with high egg intensity (440-780 eggs/10ml of urine) were treated with praziquantel in January 2009. After 10 days post treatment, the urine sample of the thirty subjects were negative for *S. haematobium*. The subjects were monitored monthly for re-infection for

seven consecutive months (February-August). Re-infection was first noticed in May. Keywords: Schistosomiasis, praziquantel, *S. heamatobium*, endemicity, Macrohaematuria *Bulinus (B) globossus*, cercariae

Poster 68 – Withdrawn

Poster 69* :Vivaxin: a novel cell-surface gene family in *Trypanosoma vivax* with potential applications in an animal trypanosomiasis vaccine

Presenter: **Miss Alessandra Romero Ramirez**, *PhD student, University of Liverpool*

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Trypanosoma vivax causes African Animal Trypanosomiasis (AAT), a vector-borne, infectious livestock disease in Africa and South America. While vaccination is the ideal strategy to protect animals from infection, no vaccine is available, principally because antigenic variation of the Variant Surface Glycoprotein (VSGs) by *T. vivax*, and other African trypanosomes, is thought to prevent any lasting humoral protection against heterologous challenge. Previously, we identified diverse *T. vivax*-specific genes with predicted cell-surface location and preferential expression during the bloodstream stage of the parasite, which offered invariant antigens for development of a potential vaccine. Here, we further examine one of these *T. vivax*-specific gene families, which we call *Vivaxin*, consisting of44 paralogs divided in 14 clades. Analysis of in vivo gene expression indicates that specific paralogs are expressed constitutively, while fluorescent microscopy of ex vivo parasites confirms that vivaxin localizes to the cell surface. We used peptide microarrays to show that vivaxin encodes the most immunogenic non-VSG antigen in natural *T. vivax* infections across Africa and South America. We then expressed multiple vivaxin proteins and investigated the murine immune response after immunization, observing a predominantly Th2 immune response with high IgG1 antibody titres. Vivaxin is an abundant gene family unique to *T. vivax*, and a prominent feature on the bloodstream-stage cell surface. This work indicates that there is structural diversity within the *T. vivax* surface glycocalyx, that is recognized strongly by the immune system in natural settings, and so offers some opportunity for vaccination against AAT.

Poster 70 : Impaired development of miltefosine-resistant *Leishmania infantum* in the sand fly vectors *Phlebotomus perniciosus* and *Lutzomyia longipalpis*

Presenter: **Miss Lieselotte Van Bockstal**, *PhD student, University Antwerp*

L Van Bockstal[3]; J Sadlova[1]; H Aslan[3]; S Hendrickx[3]; C Meneses[2]; S Kamhawi[2]; P Volf[1]; L Maes[3]; G Caljon[3];
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Introduction: Visceral leishmaniasis (VL) is a lethal neglected tropical disease caused by *Leishmania donovani* and *Leishmania infantum*. It is a vector-borne disease transmitted by the bites of infected female phlebotomine sand flies. Oral miltefosine (MIL) is used to treat VL, but is increasingly failing. To gain insight into the propagation

of miltefosine resistance in VL, this study explored development of resistant parasites with a defective miltefosine transporter (MT) in sand flies.
Methodology: Infectivity, colonization of stomodeal valve and metacyclogenesis of a MIL-resistant (MIL-R) *Leishmania infantum* LEM3323 line with a defective MT were assessed in the natural sand fly vectors *Phlebotomus perniciosus* and *Lutzomyia longipalpis*. Given our recent description of partial drug dependency of the MT-deficient line, the impact of MIL pre-exposure on sand fly infectivity was explored as well.
Results: A significant reduction in sand fly infection (3-fold), stomodeal valve colonization (7-fold) and differentiation into metacyclics (2-fold) was observed for MIL-R as compared to the isogenic parent MIL-susceptible line in both vectors. Re-introduction of the wildtype MT gene into MIL-R partially restored these parameters. Pre-exposure to MIL did not significantly alter the infectivity of the MIL-R line.
Conclusions: A defect in the inward translocation machinery through inactivation of the MT protein does not only cause MIL resistance but also negatively impacts *L. infantum*development and transmissibility potential in its natural sand fly vector.

Poster 71 : Hand washing as an effective method for intestinal parasites control among school children in Gaza city: Public Health point of view

Presenter: **Prof Adnan Al-Hindi**, *Dean, Faculty of Health Sciences, Islamic University-Gaza, Faculty of Health Science*

A Al-Hindi[2]; A Radwan[2]; S Abu Ouda[2]; Y Erqyq[2]; M Al-Kariri[3]; [4]; S Al-Hindi[1];
[1] Faculty of Medicine, Islamic University of Gaza, Palestinian Territory; [2] Islamic University of Gaza, Palestinian Territory; [3] Ministry of Health, Palestinian Territory; [4]Ministry of Health, Uganda;

Background. Hand washing is one of the most effective ways to prevent the spread of many types of infection and illness especially those spread through oral-faecal route. The present study aimed to examine the effect of hand washing technique on the control of intestinal parasites among school children in Gaza. Methods. A total 508 children from primary school children were examined for the presence of intestinal parasites and then the infected children were divided into case and control groups based on match criteria. Hand washing and health education were applied on case group and then the second stool sample was examined from both case and control groups. . Results and analysis. It was found that 118 child (23.2 %) was infected with intestinal parasitic infection in the base line sample. *Entamoeba histolytica/dispar* was the highest protozoa detected among school children in this study (73.3%), the prevalence of intestinal parasites became 15.5% for case group after application of hand washing technique, abdominal pain was the highest symptom that children suffering from it. The prevalence of intestinal parasites among children was reduced after the application of hand washing from 23.2% to 15.5%, the prevalence of intestinal parasites in male higher than female due to variant behaviour of both sexes. Conclusions and implications for policy, practice or additional research. The prevalence of intestinal parasites among children was reduced after the application of hand washing from 23.2% to 15.5%, the prevalence of intestinal parasites in male higher than female due to variant behaviour of both sexes. It is recommended to apply hand washing in Gaza Strip schools and engage both health authorities and community in this task. .Key words:.Hand washing technique, Intestinal parasites, Primary school children, Gaza city.

Poster 72 – Withdrawn

Poster 73 : Withdrawn

Poster 74 : Miltefosine restores the infectivity of miltefosine resistant *Leishmania* parasites by attenuating the innate immune response

Presenter: **Mr Dimitri Bulté**, *PhD Student, Laboratory of Microbiology, Parasitology and Hygiene (LMPH), University of Antwerp, Belgium*

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Introduction: Miltefosine (MIL) is an oral drug that is used to treat Visceral Leishmaniasis (VL) but is failing to permanently clear parasites in an increasing number of patients. Especially immunocompromised patients are prone to relapse. Parasites isolated from these relapse cases do not seem to display an increased resistance, but are hypothesized to interact differently with the immune system in favour of survival inside macrophages even under drug pressure. Only four MIL resistant (MIL-R) parasites have been isolated so far, although mutations in a single gene can render parasites MIL resistant. In this study, the infection characteristics of parasites with acquired resistance were explored under conditions with and without drug pressure.
Methodology: In order to study the impact of drug treatment on survival of MIL sensitive (MIL-S) and MIL-R parasites, double reporter lines were generated expressing both the *PpyRE9* (*in vivo/ex vivo*bioluminescent imaging) and the *DsRed* gene (flow cytometry, fluorescence microscopy). *In vivo*bioluminescent infection studies were complemented with the analysis of cellular immunological responses in the liver and spleen. Major inflammatory cytokine responses were monitored in plasma and correlated with the host infection dynamics. The role of selected immune cell types [natural killer(NK) cells, NKT cells and neutrophils] during the early stage of the infection was assessed by specific depletion protocols and by flow cytometry. The impact of MIL was evaluated by *in vitro* pretreatment of parasites prior to inoculation of C57Bl/6 and BALB/c mice.
Results: The MIL-R parasite line showed a reduced infectivity when compared to the isogenic MIL-S line. This reduced infectivity was accompanied by an increased monocyte and neutrophil influx in the spleen and liver during the early stage of the infection. This was associated with elevated IFN-γ, TNF-α and IL-6 levels in the blood. This early cytokine storm, either directly or indirectly, lead to the rapid clearance of MIL-R parasites from the liver and abrogated further dissemination to spleen and bone marrow. Experiments where NK and/or NKT cells were depleted in C57Bl/6 and BALB/c mice, identified these cells as the main source of IFN-γ during infection onset and moreover, in the absence of these cells, infectivity of the MIL-R line was partially restored. Finally, infections with MIL-S and MIL-R parasites under drug pressure have revealed that both *in vivo* MIL-treatment and *in vitro* MIL pre-exposure significantly rescues the *in vivo* infectivity of the MIL-R parasite. During these infections under MIL-treatment, the early induction of IFN-γ was less prominent, indicating a reduced activation of NK and NKT cells and a reduced clearance of the MIL-R parasite. These observations emphasize the risk of MIL treatment in sustaining infections with MIL-R parasites that are attenuated under drug-free conditions.

Poster 75 : Profiling the best-performing community medicine distributors for mass drug administration: a comprehensive, data-driven analysis of treatment for schistosomiasis, lymphatic filariasis, and soil-transmitted helminths in Uganda

Presenter: **Dr Goylette Chami**, *Research Fellow, University of Cambridge*

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Background: The most prevalent neglected tropical diseases are treated through blanket drug distribution reliant on lay community medicine distributors (CMDs). Yet, treatment rates achieved by CMDs vary widely and it is not known which CMDs treat the most people
Methods: In Mayuge District, Uganda, we tracked 6,779 individuals (aged 1+ years) in 1,238 households across 31 villages. Routine, community-based mass drug administration (MDA) was implemented for schistosomiasis, lymphatic filariasis, and soil-transmitted helminths. For each CMD, the percentage of eligible individuals treated (offered and ingested medicines) with at least one drug of praziquantel, albendazole, or ivermectin was examined. CMD attributes (>25) were measured, ranging from altruistic tendencies to socioeconomic characteristics to MDA-specific variables. The predictors of treatment rates achieved by CMDs were selected with least absolute shrinkage and selection operators and then analyzed in ordinary least squares regression with standard errors clustered by village. The influences of participant compliance and the ordering of drugs offered also were examined for the treatment rates achieved by CMDs
Results: Overall, only 44.89% (3043/6779) of eligible individuals were treated with at least one drug. Treatment rates varied amongst CMDs from 0-84.25%. Treatment rate increases were associated (p-value<0.05) with CMDs who displayed altruistic biases towards their friends (13.88%), had friends who helped with MDA (8.43%), were male (11.96%), worked as fishermen/fishmongers (14.93%), and used protective drinking water sources (13.43%). Only 0.24% (16/6779) of all eligible individuals were noncompliant by refusing to ingest all offered drugs. Distributing praziquantel first was strongly, positively correlated (p-value<0.0001) with treatment rates for albendazole and ivermectin.
Conclusions: These findings profile CMDs who treat the most people during routine MDA. Criteria currently used to select CMDs—community-wide meetings, educational attainment, age, years as a CMD, etc.—were uninformative. Participant noncompliance and the provision of praziquantel before albendazole and ivermectin did not negatively impact treatment rates achieved by CMDs. Engaging CMD friend groups with MDA, selecting CMDs who practice good preventative health behaviours, and including CMDs with high-risk occupations for endemic infections may improve MDA treatment rates. Evidence-based guidelines are needed to improve the monitoring, selection, and replacement of CMDs during MDA.

Poster 76 : Inferring clearance and reinfection dynamics of *Schistosoma mansoni* from Kato-Katz and circulating cathodic antigen-based diagnostics.

Presenter: **Miss Jessica Clark**, *Researcher, University of Surrey*

J Clark[1]; P H Lamberton[2]; J M Prada[3];
[1] Faculty of Health & Medical Sciences, University of Surrey, UK; [2] Institute of Biodiversity, Animal Health and comparative Medicine, and Wellcome Centre for Parasitology, University of Glasgow, UK; [3] University of Surrey, UK

Schistosomiasis is a debilitating disease causing chronically poor health with over 240 million people infected. The World Health Organization has set ambitious control and elimination goals, though key to their success, are suitable diagnostic tools and efficacious treatment programmes. The predominant intervention strategy is mass drug administration (MDA), implemented in response to baseline infection prevalence estimates. However, though treatment may immediately reduce infection prevalence and intensity, prevalence commonly returns to pre-treatment levels within 6 months. This suggests that successful clearance is followed by rapid re-infection, however, as adult *Schistosoma* clearance and reinfection cannot be directly observed these dynamics remain unclear. The clarification of these dynamics is further hindered by reliance on excreted egg counts and antigen

detection as proxy infection measures. The egg-count based Kato-Katz (KK) technique, which is highly *Schistosoma* specific, lacks sensitivity when infection burdens are low, including post-treatment. Alternatively, Circulating Cathodic Antigen (CCA) tests have proven to be more sensitive to low intensity infections, but suffer from inconsistencies in the interpretation of "trace" results, leading to highly divergent epidemiological and drug efficacy estimates. To understand post-treatment dynamics, and to improve upon prevalence estimates, a hidden Markov model was developed drawing on longitudinal KK and CCA diagnostics data, to infer the proportion of children in a cohort that experience clearance and reinfection. In addition to the conventional "trace", +, ++, +++ scale of CCA results, a newer 1-10 scale was used, allowing for increased precision, particularly at low antigen levels. This work provides valuable insight into *Schistosoma* infection dynamics and emphasises the strengths and short-comings of current diagnostic strategies.

Poster 77 : A library of *Schistosoma mansoni* cell surface and secreted proteins for the identification of vaccine candidates and early serological markers of infection

Presenter: **Dr Cecile Crosnier**, *Senior Staff Scientist, Wellcome Sanger Institute*

C Crosnier[4]; M Roestenberg[2]; A Protasio[4]; C Brandt[4]; G Rinaldi[4]; C McCarthy[4]; J J Janse[1]; M C Langenberg[1]; S Clare[4]; C Hokke[2]; S Wilson[3]; M Berriman[4]; G J Wright[4];
[1] Leiden University Medical Center, Netherlands, Netherlands; [2] Leiden University Medical Centre, Netherlands; [3] University of Cambridge, UK; [4] Wellcome Sanger Institute, UK

Schistosomiasis is a major global health problem caused by blood-dwelling parasitic worms. Infection of the human host starts with the penetration through the skin of free-swimming cercariae upon contact with contaminated water. The parasites first develop into schistosomula before maturing into adult worms that can survive for many years within their host's bloodstream. Despite intensive efforts from the research community, only few vaccine candidates have progressed to clinical trials so far and treatment mostly relies on the mass administration of praziquantel in endemic areas. Appropriate drug treatment strategies are informed by diagnostics that establish the prevalence and parasite burden, which, in regions of low transmission should be highly sensitive. With the aim to identifying new vaccine candidates and serological markers of infection, we have used proteomics and transcriptional data to compile a library of 115 *S. mansoni* cell surface and secreted proteins that we expressed recombinantly in mammalian cells. Overall, expression of 90% of the selected proteins could be detected by Western blot and the vast majority of them were shown to be immunoreactive and to contain heat-labile conformational epitopes when tested against pooled hyperimmune sera. Ninety-six of these proteins were used to immunise BALB/C mice in a systematic screen for the identification of new vaccine candidates. While most proteins triggered antibody titres with half-maximal reactivity > 1:10,000, none of them were associated with strong repeatable protection against reinfection. Using human and mouse sera from experimental infections, we were able to monitor the host humoral reactivity to 103 of these proteins and showed that members of the saposin-domain containing family were particularly antigenic, showing reactivity as early as five weeks post-infection. We envisage that this protein library will be useful to the wider scientific community to further understand *Schistosoma* biology.

Poster 78 : *T. b. gambiense*; evidence of absence in NW Uganda

Presenter: **Dr Lucas Cunningham**, *PDRA, LSTM*

L J Cunningham, J K Lingley, M J Lehane, S J Torr
[1] Liverpool School of Tropical Medicine , UK

Background: Around the turn of the century the last major epidemic of Gambian sleeping sickness was being brought to an end thanks to a concerted effort to control the disease. The prevalence of disease has since gradually decreased with the number of new cases being reported, per year, now numbering 1,420. This success indicates that there is a good chance that the disease could be eliminated, as a public health problem, by 2020. Although close to achieving this goal there may still be obstacles blocking the road to success, chief amongst these is the still unanswered question of cryptic reservoirs. Previous studies have found *T. b. gambiense* in both wild and domestic animals, however, transmission of disease from animals to humans, via the tsetse vector has not been proven. Finding positive zoonotic hosts for *T. b. gambiense* in an area of control would indicate that the current strategy of surveillance of the human population may not be enough. Our work was carried out in the NW of Uganda, a historic sleeping sickness focus, that had seen a reduction of the disease from >100 prior to 2010 to current levels of <5 new cases reported annually, making it an ideal example of a setting approaching elimination.
Objective: To carry out a large-scale surveillance campaign on local cattle, pigs and tsetse in the historic sleeping sickness foci of Arua, Maracha and Koboko in NW Uganda, using molecular methods to screen for *T. b. gambiense*.
Methods: From the districts of Arua, Maracha and Koboko a total of 2088 cattle, 400 pigs and 2,184 flies were sampled and screened for *T. b. gambiense* using species and sub-species specific PCR assays. A sub-sample of positives underwent sequencing to better characterise the trypanosomes detected. The Cattle were enrolled as part of a larger, vector control study, while the pigs were sampled from communities with a history of sleeping sickness that were located outside of tsetse control areas. The tsetse were caught from four traps deployed in Koboko along the Kochi river.
Results: Initial screening of samples with the TBR-primer found that 1.9% (95% CI≤1.9-2.5) of cattle, 6.2% (95% CI≤4.1-9.1) of pigs and 1.8% (95% CI≤1.3-2.5) of tsetse were positive for *T. brucei* s.l.. Further analysis revealed that not all the *T. brucei* s.l. positive samples contained enough DNA for the detection of the single copy TgsGP gene used to characterise the *T. b. gambiense,* with ~40% of positive samples lacking sufficient DNA. Of the cattle and pig samples with a sufficient amount of DNA all failed to produce a PCR product indicative of *T. b. gambiense*, but of the tsetse positive samples 16 produced a faint band of 281 bp in size. When a sub-sample were sequenced all returned the same sequence, however this sequence failed to match the reference sequence of *T. b. gambiense* in both length and composition.
Conclusion: Despite a large-scale screening operation in which over a two thousand cattle, flies and several hundred pigs from a historic sleeping sickness focus were sampled, no animals were positive for Gambian sleeping sickness. Interestingly 16 tsetse samples produced a product that differed in size and sequence to that of *T. b. gambiense* when screened with the sub-species specific TgsGP primers. The low sensitivity of the TgsGP primers mean that a significant (~40%) number of *T. brucei* s.l. samples are unsuitable to undergo sub-species specific analysis. Of equal iinterest is the apparent amplification of non-target DNA by the TgsGP primers.

Poster 79 : Unraveling the effects of cl-CD95L on macrophage - Toxoplasma gondii interactions

Presenter: **Miss Ellen Alana Tiffney**, *Postgraduate Researcher , University of Liverpool*

E Tiffney[1];
[1] University of Liverpool, UK

Approximately 1-2 billion people are infected with T. gondii globally, making it one of the most successful protozoan parasites. With this in mind, we believe it is critical to better understand immunogenic ligands that may increase the pathogenicity of T. gondii during mammalian infections. Previous research on Systemic Lupus Erythematosus (SLE) demonstrated that cl-CD95L aggravates inflammation. Therefore, this study will delve into

the role of cl-CD95L as an aggravating factor in the development of pathogenic T. gondii responses. To carry out this investigation VERO cells were used to deliver preliminary results on the impact cl-CD95L has on cell viability and cytotoxicity. Following on from this, bone-marrow derived macrophages (BMDM) were stimulated with cl-CD95L and infected with T. gondii. BMDM cultures were analysed to uncover through which pathways cl-CD95L may lead to an increase in parasitemia during infection. Finally, a Phospho-Kinase Array was utilized and determined that cl-CD95L amplifies protein expression in non-infected BMDM. Interestingly, the proteins expressed are similar to those of a myeloid-derived suppressor cell (MDSC). From the data collected we believe that cl-CD95L causes an MDSC like phenotype in previously un-polarized BMDM. The hallmark of MDSC activity is the increase in Arginase-1 expression which leads to the depletion of L-arginine, this in turn decreases the immune response against T. gondii, leading to an increase in parasite replication.

Poster 80 : Gastrointestinal parasites on cattle in Kulon Progo district of D.I. Yogyakarta, Indonesia

Presenter: **Mrs Fitrine Ekawasti**, *researcher, Indonesia Research Center for Veterinary Science*

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[1] Indonesia Research Center for Veterinary Science, Indonesia

Gastrointestinal parasites are the main cause of losses the weight, disrupting growth and even death of heavily infected animals in cattle farms, especially in calves. To evaluate the presence of gastrointestinal parasites on calves in Kulon Progo district of D.I. Yogyakarta, Indonesia because the prevalence of parasites varies between countries depending on the terrain surrounding livestock farms. Fecal samples from calves, ongole and local cattle (PO) cross breed has examined using whitlock-universal technique, glucose saturated floatation technique (sentrifuse modification) and sedimentation technique to identify the parasitic present in the coprological samples. The test results showed that approximately 81.8 % of the calf population was infected by parasitic, such as *Nematode* (22.7%), *Eimeria* sp. (50%), *Giardia* sp. (6.8%), *Trematode* (9.1%). Although this evaluate is preliminary, the results showed that the infection of parasitic was high, these infected could be as a potential source leading to economic losses in livestock production. We need to find adequate control measures against infection of pathogen parasitic in order to reduce the impact of parasitic infection of cattle in Indonesia.

Poster 81 : Test-and-treat with doxycycline as an alternative strategy for the acceleration of onchocerciasis elimination in a loiasis co-endemic region of South-West Cameroon

Presenter: **Dr Armelle Forrer**, *postdoctoral research associate, Liverpool School of Tropical Medicine*

S Wanji[2]; A Forrer[1]; K Ozano[1]; S Theobald[1]; L Hamill[1]; P W Chounna Ndongmo[2]; T Nji[2]; A J Njouendou[2]; H Piotrowski[1]; P Enyong[2]; J D Turner[1]; M Taylor[1];
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Annual Community Directed Treatment with ivermectin (CDTi), the cornerstone of onchocerciasis control, has reached elimination targets in some areas but high infection levels persist despite long-term ivermectin distribution in other foci, including in South-West Cameroon. Challenges include program coverage, adherence to and acceptability of ivermectin in an area of *Loa loa* co-endemicity. Loaisis patients harbouring heavy infections are at risk of potentially fatal serious adverse events (SAEs) following CDTi. Alternative strategies are therefore needed to achieve onchocerciasis elimination where CDTi effectiveness is suboptimal.

The CouNTDown consortium has implemented two WHO-endorsed alternative strategies for the elimination of onchocerciasis in the Meme River basin, South-West Cameroon, where 15 rounds of CDTi MDA has not delivered expected impact on skin infection prevalence. Alternative strategies consist of testing and treating *O. volvulus* cases with doxycycline (DOX T&T), an anti-*Wolbachia* macrofilaricide, either alone or in combination with ground larviciding vector control (temephos).
A community-based before-after treatment cohort study is being conducted among the general population of the Meme River Basin, South-West Cameroon. Participants were diagnosed using skin snipping. *O. volvulus* patients enrolled in the DOX T&T study were treated daily with 100mg of Doxycycline for five weeks. Structured questionnaires were used to collect data on demographics, completion of treatment and onchocerciasis-related clinical signs. Focus-group
s and in-depth interviews were used to investigate the acceptability of CDTi and DOX T&T strategy.
Logistic (prevalence) and negative binomial (infection intensity) mixed regression models will be used to assess the association between adherence to CDTi and infection levels, onchocercal skin disease or severe itching as well as the impact of DOX T&T on *O. volvulus* infection levels.
Here, we present the results of the baseline survey, including infection levels, prevalence of onchocercal skin disease and severe itching as well as their association with reported participation in CDTi, and the perceptions and attitudes towards CDTi.

Poster 83 : Withdrawn

Poster 86 : Withdrawn

Poster 87 : Thrombocytopenia as a clue of *vivax* Malaria in endemic region of Sudan

Presenter: **Professor Bakri Nour**, *Professor, Dean of BNNICD, Blue Nile National Institute for Communicable Diseases, University of Gezira*

B Nour[1]; **A Talha**[2];
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Reduction in circulating platelets is observed relativity frequently in cases of malaria due to *P.vivax*. 61 Patients with confirmed *vivax* malaria were enrolled in this study and the plarelets were counted by hermatological analyzer. Our study revealed that 77.1% had platelet counts less than 1500,00/µl, thrombocytopenia grade 1 represents, % 43 grade 2 represents 19.8%, grade 3 represents 9.8% and grade 4 represents 4.9%. Thrombocytopenia should be a consideration as a clue to the presence of malaria in endemic regions.

Poster 88 : Evaluating the effect of hen age on poultry red mite feeding and mortality

Presenter: **Dr Francesca Nunn**, *Postdoc, Moredun Research Institute*

F Nunn,[2]; K Bartley[2]; J Palarea-Albaladejo[1]; A J Nisbet[2];
[1] Biomathematics & Statistics Scotland, UK; [2] Moredun Research institute, UK

Poultry red mites (PRM) are small and highly mobile blood feeding ectoparasites that live off-host, only seeking a bird to rapidly engorge every few days. PRM are therefore difficult to contain in a controlled experimental environment that allows natural feeding on the host and in vitro feeding techniques have been previously employed to overcome containment issues (e.g. McDevitt et al., 2006). The original in vitro feeding technique was refined by Bartley et al., (2015) but has several drawbacks, including a high background mite mortality and variability in mite feeding rates, requiring increased levels of technical replication and it also requires invasive blood sampling of hens. In addition, previous studies have shown that vaccine efficacy measured using the in vitro feeding device is not always translated into mite population reduction in field trials (Bartley et al., 2017) leading to false indications of the potential of a vaccine. Previously we described the optimisation of an on-hen feeding device for protonymph, deutonymph and adult life stages and optimised mite conditioning in order to reduce background mortality of mites (Nunn et al., 2019). This has been developed as an alternative to the in vitro assays for more accurate pre-screening of potential novel interventions before embarking on field studies and is an important development in reduction and refinement of animals, in keeping with 3R's approaches.Here, we used this on-hen feeding device to assess mite feeding on hens from 18 until 38 weeks of age. Hens wore one device containing adult female and proto- or deutonymph mites for 3 hours, once every 2 weeks. Fed mites were recovered and monitored for mortality and egg production for 144h. Throughout the trial adult mite feeding rates were significantly higher than those of deutonymphs and protonymphs and egg laying by female mites significantly reduced as the hens aged ($p < 0.0001$). No significant differences were demonstrated in mortality or feeding rates for any of the life stages feeding on hens as they aged. This device represents a high hen-welfare method of allowing mites to feed on the live host whilst maintaining PRM containment and the data presented here demonstrate that it has great potential as a tool to allow feeding of nymph and adult life stages to evaluate systemic PRM controls (e.g. vaccines, systemic acaricides) across longitudinal experiments with repeated measures.

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Poster 89 : More than just chips: what are you getting with your fish?

Presenter: **Dr Shokoofeh Shamsi**, *Senior Research Fellow, Charles Sturt University*

S Shamsi[1];
[1] Charles Sturt University, Australia

Global consumption of seafood is steadily increasing, as is the variety of seafood, including dishes with raw or undercooked fish, leading to an increased risk of seafood-borne parasitic diseases. To address today's challenges to understand the biology and ecology of these parasites in an ever-changing environment and to tackle their pathogenicity, multidisciplinary research is needed. In addition the gap between research and stakeholders must be bridged to decrease the risk these parasites pose to public health. A One Health approach to research is necessary to ensure that consumers, aquatic animals, and environmental health questions are assessed in an integrated and holistic manner, resulting in a more comprehensive understanding of the issues associated with seafood-borne parasitic diseases and potential solutions. However, when it comes to seafood-borne parasitic diseases there is limited guidance available for a One Health approach since these diseases can be less well-known. In this article the focus is on parasitic diseases caused by seafood, which have been less studied even in some developed countries where seafood is popular. A brief overview of some of the seafood-borne parasitic diseases is provided followed by the significance of the awareness among various stakeholders in a country. In this

presentation it is argued that researchers and stakeholders are closely connected and a knowledge gap in one can result in a gap in knowledge and awareness in the other, causing an inability to accurately estimate the issues caused by these parasites. It is suggested that raising awareness, supporting research and training of all stakeholders are crucial for the prevention of seafood-borne parasitic diseases and the protection of the health of seafood consumers.

Poster 90 : Speaking with a forked tongue: pentastomid parasites in man's best friend

Presenter: **Dr Shokoofeh Shamsi**, *Senior Research Fellow, Charles Sturt University*

S Shamsi[1];
[1] Charles Sturt University, Australia

Pentastomids are obligate arthropod parasites that are found in the lymph nodes, liver and lungs of various species of livestock. In this presentation pentastomid parasites from four continents are morphologically and genetically characterised and their phylogenetic relationship is investigated. Our results show presence of new species in Australia and Africa and suggest transmission of the parasite from Palearctic region to Europe and other countries may have occurred. The outcome if this project is essential for future biosecurity plans in Australia to prevent entry of parasites.

Poster 91 : Diagnostic screening for *Plasmodium falciparum* by Illumigene.

Presenter: **Dr Foekje F. Stelma**, *Medical Microbiologist, MD-PhD, Radboud University Medical Center*

F Stelma[1]; C Handgraaf[1]; R Sauerwein[1];
[1] Radboudumc, Netherlands

Introduction and methods: Screening for malaria infection in travelers with fever by conventional microscopy requires qualified technicians. As most patients test negative, screening by a point of care method like the Illumigene LAMP Plasmodium assay (Meridian Bioscience, London, UK) will reduce the need for qualified technicians. This study describes the performance of the Illumigene LAMP malaria assay in 1) samples of 12 volunteers participating in a protocol of controlled experimental malaria infections (CHMI) and tested by qPCR, and 2) samples from n≤7 *Plasmodium falciparum* positive travelers, stored at -80^{o}C at the Radboudumc. The latter were tested by conventional microscopy (QBC (Drucker diagnostics, Port Matilda, USA) and thick smear). Results: Of 78 CHMI samples tested, n≤50 (64%) and n≤41 (53%) tested positive by respectively qPCR and Illumigene LAMP malaria assay. Compared to qPCR the sensitivity and specificity of Illumigene was 76% and 89% respectively. The density threshold for 100% positivity in this population was 676 parasites/ml. In travelers the Illumigene tested positive in 7/7 cases. The thresholds were 1-5 *10^{3} parasites/ml for the QBC, 5 *10^{3} parasites/ml for thick smear and 1 *10^{3} parasites/ml for Illumigene respectively. The Illumigene tested positive up to 7 days longer after successful treatment compared to conventional microscopic analysis. Conclusion: Illumigene LAMP malaria assay performed well as first screening for *P. falciparum*, but shows prolonged positivity post-treatment.

Poster 92 – Withdrawn

Poster 93 : Type i interferon enhances sialoadhesin (cd169/siglec-1) expression on macrophages in favour of *Leishmania* multiplication

Presenter: **Miss Lieselotte Van Bockstal**, *PhD student, University Antwerp*

L Van Bockstal[1]; P Delputte[1]; L Maes[1]; G Caljon[1];
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Introduction: Type I interferons (IFNs) induced by an endogenous *Leishmania* RNA virus or exogenous viral infections were shown to exacerbate infections with New World Cutaneous *Leishmania* parasites. The impact of type I IFNs in visceral *Leishmania* infections and implicated mechanisms remain to be unravelled. This study assessed the impact of type I IFN on macrophage infection with visceral *Leishmania* parasites and the implication of sialoadhesin (Siglec-1/CD169, Sn) as a typical IFN-inducible, virus-responsive surface receptor.
Methodology: Bone marrow derived macrophages from wildtype and sialoadhesin knock out ($Sn^{-/-}$) C57BL/6 mice were collected and cultivated *in vitro*. Macrophages were stimulated with type I IFN (IFN-a) prior to infection with *L. infantum* and *L. donovani* laboratory strains and a set of recent clinical isolates. After two days of stimulation, cells were incubated with an anti-sialoadhesin monoclonal antibody (mAb) or a bivalent nanobody (Biv-Nb). One hour after blocking with the mAb or Biv-Nb, cells were infected with metacyclic promastigotes and parasite multiplication was measured at 48 hours post infection.
Results: Stimulation of bone marrow-derived macrophages with type I IFN (IFN-a) significantly enhanced susceptibility to *Leishmania* infection. Stimulation experiments in Sn-deficient macrophages and macrophage pretreatment with monoclonal anti-Sn antibodies or bivalent anti-Sn nanobodies restored normal susceptibility levels. Infections with bioluminescent *L. infantum* promastigotes revealed a moderate role for Sn during visceral infections under the used experimental conditions *in vivo*.
Conclusions: These data indicate that IFN-responsive Sn expression can enhance the susceptibility of macrophages to infection with visceral *Leishmania* promastigotes and that targeting of Sn may have some protective effects during an early infection.

Poster 94* : The vector biology of ectoparasites on rodents from the 'Asir Region of Saudi Arabia

Presenter: **Mrs Samia Alghamdi**, *student, Infection Biology Institute of Infection & Global*

S Alghamdi[2]; A Alagaili[1]; A Darby[3]; A Stekolnikov[4]; J McGarry[3]; B Makepeace[3];
[1] Department of Zoology, King Saud University, Saudi Arabia; [2] Uinversity of Liverpool, UK; [3] University of Liverpool, UK; [4] Zoological Institute RAS, Russian Federation

Background: Rodents have become increasingly recognised as hosts of ectoparasites and reservoirs of numerous human diseases including scrub typhus (*Orientia* spp.), bartonellosis (*Bartonella* spp.), hantaviruses, Lyme disease (*Borrelia burgdorferi* complex), and plague (*Yersinia pestis*). Vector-borne bacterial zoonoses associated with rodents are a particularly large group of diseases that are emerging/re-emerging worldwide.
Objectives: This study aimed to define the taxonomic diversity and bacterial microbiome of ectoparasites collected from wild rodents in the 'Asir Region of southwestern Saudi Arabia, with a main focus on chigger mites (family Trombiculidae), the vectors of scrub typhus.
Methods: Wild rodents were trapped in scrubland across one site on the slopes of the Asir Mountains in 2016 (Al Ous') and four sites in 2017 (Al Ous', Al Jarf, Alogl and Wosanib). Rodents were euthanized prior to examination and all ectoparasites were collected and stored in absolute ethanol. A 10% subsample of ectoparasites was selected from each rodent for mounting in Berlese fluid and morphometric examination. Following DNA extraction, the v4 region of bacterial 16S rRNA was amplified by PCR, and amplicons were sequenced on an Illumina MiSeq. Specific PCRs were used to confirm the presence and strain of selected bacterial pathogens and symbionts.

Results: A total of 7,802 ectoparasites were obtained from 74 rodent specimens, comprising 6,135 chigger mites, 119 fleas in one species (*Parapulex chephrenis*), 770 ticks of at least two species (*Haemaphysalis erinacei* and *Rhipicephalus* spp.), 589 lice in two species (*Polyplax brachyrrhyncha* and *Polyplax oxyrrhyncha*), and 189 gamasid mites in two species (*Laelaps lamborni*, *Ornithonyssus bacoti*). The rodents belonged to three main species: *Acomys dimidiatus*, *Myomys yemeni* and *Meriones rex*. Based on the morphology of the scutum (or dorsal shield), chiggers were assigned to subgenera and provisionally into 17 species, including four putative new species: *Neotrombicula* sp. n., *Microtrombicula* aff. *machadoi*, *Schoutedenichia*. aff. *thracica* and *Schoutedenichia* sp. n. The most abundant chigger species were *Ericotrombidium kazeruni*, *Schoutedenichia* aff. *geckobia* and *Ascoschoengastia browni*. The site with the highest mean chigger infestation (139) was Al Ous', and the host species with the greatest mean infestation rate (114) was the Eastern spiny mouse (*A. dimidiatus*).Ectoparasite-associated bacteria were investigated using a 16S rRNA amplicon sequencing approach. Potentially pathogenic bacteria included *Borrelia* spp. in chiggers, *Bartonella* spp. in fleas, and *Coxiella* spp., *Francisella* spp. and *Anaplasma bovis* in ticks. Symbiotic bacteria with putative mutualistic or parasitic phenotypes were present in fleas (*Wolbachia* and *Spiroplasma* spp.) and lice (*Candidatus Legionella polyplacis*).
Conclusion: This is the first survey of rodent ectoparasite diversity and zoonotic bacterial pathogens performed in the 'Asir Region of Saudi Arabia. The chigger diversity in the region is especially high, and the presence of Borrelia spp. in these mites should be investigated further to determine if they might be vectors of Lyme borreliosis or relapsing fever.

Poster 95 : Activity of Imidocloprid against *Hyalomma marginatum* in Nili Ravi Buffalo (*Bubalus bubalus indicus*)

Presenter: **Dr Muhammad Mazhar Ayaz**, *Assistant Professor, Faculty of Veterinary Sciences*

M Mazhar Ayaz[1];
[1] Bahauddin Zakariya University, Multan, Pakistan

Activity of imidocloprid (18.20% w/v) commercially available was assessed against *Hyalomma marginatum* in Nili Ravi buffalo (*Bubalus bubalus indicus*) at Multan, Pakistan. Various concentrations i.e. 0.01% and 0.02% of imidocloprid (18.20% w/v) were prepared. The live ticks were obtained from buffalo(s) with no history of any acaricidal drug prior 60 days and beyond. The tick(s) male and females were identified as *Hyalomma marginatum* on the basis of pictorial key and morphology and their photograph were preserved and saved for further study. The live tick(s) were immersed in preparation(s) 0.01% and 0.02% in petri-dish(s). Anti-tick activity of imidocloprid against ticks *Hyalomma marginatum* was observed in 3-5 minutes after application and immersion. There was no any significant difference of anti-tick activity of various concentrations of imidocloprid on *Hyalomma marginatum*. The treatment was highly effective against the ticks in buffalo.

Poster 96* :Diagnosis of intestinal schistosomiasis by POC-CCA. A new field applicable approach to quantify score intensities

Presenter: **Miss Miriam Casacuberta Partal**, *PhD student, LUMC*

M Casacuberta Partal[1]; P T Hoekstra[1]; D Kornelis[1]; L van Lieshout[1]; G J van Dam[1];
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The point-of-care strip assay for the detection of the schistosome Circulating Cathodic Antigen (POC-CCA) in urine has shown to be a user-friendly and accurate alternative to stool microscopy for the diagnosis of *Schistosoma mansoni* infections. However, visual scoring of the test is by definition observer dependent which may lead to

s about the qualitative interpretation, in particular in low infection intensities when test lines tend to be less strong. The current proof-of-concept study evaluates an innovative approach for semi-quantification of the POC-CCA readings which is applicable to field settings. Scoring of the cassettes was done by visual comparing of the test line against a series of artificial cassettes (inkjet-printed strips with different test line intensities). These artificial cassettes are designed to grade the POC-CCA test line intensity on a scale of 1 to 10, named G1 to G10, or G scores. This approach will allow to standardize the scoring procedure and to minimize observer dependency and different quantitative interpretations.
Here we selected a representative series of urines (n≤110) from an *S. mansoni* endemic area and tested them with the POC-CCA using the G scores method. Results showed a significant correlation between the line intensity based on the G scores and the visual scoring system as well as with the intensity of the infection determined by Kato-Kats microscopy stool examination, expressed as eggs per gram of faeces. This study demonstrates the usefulness and applicability of the G score scale for standardized scoring and interpretation of the POC-CCA urine strip assay.

Poster 97* :Bioavailability improvement of Artemisinin through cocrystal approach: *in vivo* and *in vitro* studies

Presenter: **Miss Manreet Kaur**, *PhD candidate, De Montfort University*

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Bioavailability improvement of Artemisinin through cocrystal approach: *in vivo* and *in vitro* studies Malaria, caused by the protozoal parasites of the genus *Plasmodium*, is a potentially life-threatening disease which causes more than 200 million clinical cases and 450,000 deaths annually. Artemisinin is the preferred treatment for malaria, which is both effective and well tolerated in patients, but has the problem of low bioavailability after oral administration due to its low solubility. This leads to inadequate treatment. Additionally the complicated chemical structure structural of artemisinin requires costly modification. Although many potent derivatives of artemisinin with better bioavailability have been found, they are all associated with toxicity, metabolic instability and short half-life. A substantial amount of research is ongoing in order to develop methods that can overcome issues related to the solubility and dissolution rates of drugs. In recent years, pharmaceutical cocrystals have attracted remarkable interest for enhancing solubility and dissolution rates of poorly water soluble drugs. A pharmaceutical cocrystal is formed by combining an active pharmaceutical ingredient (API) with an inactive coformer through a specific stoichiometric composition. The aim of this work was to improve the bioavailability of Artemisinin through a cocrystal approach. The API, Artemisinin, was formulated with orcinol and resorcinol coformers to obtain two artemisinin cocrystals. The performance of the artemisinin drug and its two cocrystal based formulations have been investigated through *in vitro* studies such as dissolution and permeability tests. The anti-malarial activity of drug alone and two cocrystals was tested against *Plasmodium berghei* infection in female BALB/c mice in a 4-day Peter's test. The *in vivo* study results have shown a significant improved parasite clearance with cocrystal formulations as compared to the artemisinin drug alone. The artemisinin concentrations in serum samples were tested using LC-MS/MS and the results showed higher artemisinin concentration in serum for both cocrystal formulations, as compared to the artemisinin drug alone. Through the study artemisinin cocrystal formulations would open new opportunities for development of novel anti-malarial medicines.
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Poster 98* :Novel cystatin of *Trichinella spiralis* inhibits inflammation mediated by bone marrow-derived macrophages

Presenter: **Miss Porntida Kobpornchai**, *Ph. D student, Mahidol University*

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To survive in their host, *Trichinella spiralis* exerts molecular machineries to regulate host environments and immune responses. Releasing of immunomodulatory molecules is one of an important strategy that can suppress host inflammation and may be used for treatment of unrelated inflammatory diseases in patients. In this study, we identified and characterized a novel immunonomodulatory protein derived from excretory-secretory (ES) product of muscle stage *T. spiralis.* ES products cultured from the larvae were fractionated by the anion exchange chromatography and evaluated an effect on cytokine responses by treatment with LPS-induced mouse bone marrow-derived macrophages (mBMDMs). Three fractions showing high immunomodulatory property by decreasing pro-inflammatory cytokines or increasing anti-inflammatory cytokines, were subjected to protein identification using nano-LC/MS/MS. In this regard, the conserved hypothetical protein (Tsp_04814) was presented the significant highest MS score and the structural homology comparison suggested that Tsp_04814 is closely similar to cysteine protease inhibitor (renamed as TsCstN). In silico 3D structure of TsCstN contains N-terminal region, four β-sheet and two α-helix, which the conformation among N-terminal region, loop1 and loop2 is a key inhibition of cathepsin L. The recombinant TsCstN (rTsCstN) was expressed in *E. coli* and used for production of mouse polyclonal antibody (pAb) and functional analysis. The pAb could detect native TsCstN in crude parasite and ES of muscle stage and predominantly localized in the stichosome. rTsCstN could inhibit cysteine proteases, especially cathepsin L. Incubation of rTsCstN with LPS-induced mBMDMs exhibited a downregulaton of MHC class II and CD40 expression. Moreover, the protein could suppress an inflammation by reduction of pro-inflammatory cytokines in both mRNA and protein level. In conclusion, TsCstN is a novel cysteine proteases inhibitor eliciting an anti-inflammatory property, which may be used as an alternative treatment for inflammatory diseases in the future

Keywords: *Trichinella spiralis*; immunomodulation; cystatin; macrophages; inflammation

Poster 99* :Novel water treatments for the zoonotic waterborne pathogen *Cryptosporidium*

Presenter: **Mr Bozo Lugonja**, *PhD Student, Cardiff University*

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Cryptosporidium, cause of the gastrointestinal illness cryptosporidiosis, is a waterborne, apicomplexan parasite of global importance. Claiming hundreds of thousands of lives annually, it is the second most important pathogen responsible for deaths due to diarrhoea. It is a particularly devastating disease for children under 5 years old and those with impaired immune systems. With anti-rotavirus vaccinations implemented recently, *Cryptosporidium* is predicted to become the leading cause of death due to diarrhoea globally. As a waterborne parasite, *Cryptosporidium* can cause mass outbreaks, is a danger to not only human but also animal health and may significantly impact the economies of affected communities. The *Cryptosporidium* oocyst is highly infectious, with just one oocyst capable of causing disease. Due to the robust nature of the oocyst wall ultrastructure, chlorine

treatment is largely ineffective and currently UV is the gold standard for water treatment. However, due to expense it is not present in all water treatment plants; particularly in developing countries. This, coupled with a lack of therapeutics, puts transmission prevention at the centre of *Cryptosporidium* research, however the challenge remains as to how to prevent transmission by efficiently removing the parasite from our water systems. Novel microwave technology may provide an effective solution. Our interdisciplinary project, in collaboration with Cardiff University's Centre for High Frequency Engineering and Water Research Institute, is assessing the effect of cutting edge patented microwave technologies on the viability and infectivity of *Cryptosporidium* parasites present in water. In addition, we are investigating whether exposure of *Cryptosporidium* to microwave frequencies in conjunction with UV may improve current treatment systems. The ultimate aim of our work is to enable the development of a novel water treatment system that can be adaptable for use in industrial, commercial and domestic settings to prevent *Cryptosporidium* transmission.

Poster 100* :Revising the transmission biology of schistosomiasis in Zanzibar

Presenter: **Mr Tom Pennance**, *PhD Student, Natural History Museum*

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The causative agent of urogenital schistosomiasis*, Schistosoma haematobium,* has historically been considered to be the only schistosome species transmitted specifically through *Bulinus globosus* on Unguja and Pemba Islands (Zanzibar, United Republic of Tanzania). For insights into the environmental risk of *S. haematobium* transmission on Pemba, malacological surveys for *Bulinus globosus* and *B. nasutus*, closely related and morphologically similar freshwater snail species acting as potential intermediate hosts of *S. haematobium* were conducted across the island from November 2016 to November 2018.
Of the 10,871 snails collected during malacological surveys over this time, 19 (0.17%) *B. globosus* from 5 sites had patent schistosome infections, initially assumed to be *S. haematobium*. However, when these cercariae were identified by sequencing a region of the *cox*1 and the nuclear internal transcribed spacer (ITS1+2), schistosomes from seven *B. globosus* (five in November 2016 and two in November 2018), from a single locality in Kinyasini, were in fact *S. bovis*, a closely related schistosome species that infects ungulates. In February 2019, a single cow from this site was later diagnosed, through screening faeces, with a *S. bovis* infection.Moreover, one wild-caught *B. nasutus* (a species typically considered refractory to infection on Zanzibar) from Kangagani was found to be infected with *S. haematobium*.
These new molecular data implicating *B. globosus* in the transmission of *S. bovis* in East Africa and *B. nasutus* in the transmission of *S. haematobium* on Pemba, add to earlier observations and complicate on-going transmission monitoring of *S. haematobium* on the islands.

Poster 101 : Host specificity of bat flies in South-Eastern Europe

Presenter: **Mr Áron Péter**, *PhD. student, Department of Parasitology and Parasitic Diseases,*

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Bat flies are the most abundant ectoparasites of bats, they have a quiet interesting biology, their morphology shows a remarkable adaptation to the parasite life style and the relationships with their hosts is characterized by high level of host specificity. After recent studies indicated their ability to transmit diverse pathogens (*Bartonella* spp. or trypanosomes) we intended to evaluate the seasonality and host specificity of the bat fly species in the South-Eastern region of Europe and to discuss the factors regulating the level of host specificity. Samples were collected at 18 different location (caves and human made roost too) in Romania and Bulgaria in the period of 2015-217. In this study we collected more than 2200 bat flies belonging to 9 species, by capturing and sampling 2801 bats. From the 28 bat species, 13 were infested with bat flies and the overall prevalence of the individuals was 36%. Our primary results indicate that the prevalence and the intensity of infestation is higher in the fall season and the truly specific bat fly species are *Basilia nana, Nycteribia pedicularia, N. vexata* and *Penicillidia conspicua.* Our results somewhat differed from previous findings, mostly in the case of primary host composition of the *Phthiridium biarticulatum,* since the Blasius's horseshoe bat (*Rhinolophus blasii)* and Mehely's horseshoe bat (*R. mehelyi*) dominated as host not the conventional greater horseshoe bat (*R. ferrumequinum*) and lesser horseshoe bat (*R. hipposideros).*We conclude that the composition of host community (present host species in the roost), the season and the intensity of infestation all have an effect on the level of host specificity of bat flies.

Poster 102* :The role played by B cells in supporting protective immunity against *Trichuris muris* infection is dependent on host genetic background and is independent of antibody

Presenter: **Mr Rinal Sahputra**, *PhD student, The University of Manchester*

R Sahputra[1]; D Ruckerl[1]; K Couper[1]; W Muller[1]; K J Else[1];
[1] The University of Manchester, UK

This study investigates the role of B cells in immunity to *Trichuris muris* (*T. muris*) infection in two genetically distinct strains of mouse, using anti-CD20 monoclonal antibody (mAb) (Genentech-clone 5D2) to deplete B cells. Data is presented for the mouse strains: C57BL/6 and BALB/c, which mount mixed Th1/Th2, and highly polarised Th2 immune responses to *T. muris*, respectively. C57BL/6 mice receiving anti-CD20 treatment prior to and during, or anti-CD20 treatment that commenced two weeks post infection (p.i.), were susceptible to *T. muris*. Parasite-specific IgG1 antibodies were absent and Th2 type cytokines produced by mesenteric lymph nodes cells from mice receiving α-CD20 mAb treatment were significantly lower than produced by cells from isotype control treated mice. T follicular helper cells were also significantly reduced. Importantly, and in complete contrast, BALB/c mice were still able to expel *T. muris* in the absence of B cells, revealing that the essential role played by B cells in protective immunity was dependent on genetic background. To explore whether the important role played by the B cell in the protective immune response of C57BL/6 mice was in enabling strong Th2 responses in the presence of IFN-γ, IFN-γ was blocked using anti-IFN-γ mAb post B cell depletion. Depleting IFN-γ, in the absence of B cells restored worm expulsion in the absence of parasite-specific IgG1/IgG2c and partially rescued the *T. muris* specific IL-13 response. Thus, our data suggest an important, antibody independent role for B cells in supporting Th2 type immune responses in mixed IFN-γ-rich Th1/Th2 immune response settings.

Poster 103* :Diagnostic performance of the Alere™ Ultra-sensitive rapid diagnostic test for *Plasmodium falciparum* malaria infections in asymptomatic pregnant women in Timika, Indonesia

Presenter: **Miss Vera Unwin**, *PhD Student, LSTM*

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Introduction: The diagnostic performance of existing malaria RDTs is inadequate for detecting low-density infections. Although "sub-microscopic" infections are commonly asymptomatic, they contribute to the overall infectious reservoir, particularly in low-transmission areas. Detecting malaria infections during pregnancy poses a further challenge to diagnosis. During pregnancy *P. falciparum* can sequester in the placenta, reducing the number of circulating parasites, remaining undetected and untreated with potential adverse consequences for the pregnancy. There is an urgent need for sensitive diagnostics in these populations.
The new Alere™ Ultra-sensitive Malaria Ag *P. falciparum* RDT (uRDT) was developed to address the need for more sensitive, field-ready diagnostics.
Aim: To compare the performance of the uRDT with the currently used CareStart™ Malaria HRP2/pLDH VOM Combo RDT (csRDT) in asymptomatic pregnant women in a low-transmission setting in Indonesia.
Methods: As part of a larger malaria in pregnancy trial in Timika, West Papua (ISRCTN34010937), a subset of 270 stored red blood cell pellets and plasma samples were used in this study. These included 158 *P. falciparum* positive samples and 112 *P. falciparum* negative samples. Using a composite molecular reference standard comprising LAMP, qPCR and nPCR, we compared the diagnostic performance of both RDTs.
Results: The uRDT had a sensitivity of 19.6% (95% CI 13.9-26.8) and specificity of 95.5 % (89.4-98.3%), whilst these were 22.8% (16.7- 30.3%) and 98.2% (93.1- 99.7%) respectively with the conventional CareStart combo-RDT. Overall, the performance of the RDTs was not significantly different.
Conclusion: In these settings and populations of asymptomatic pregnant women, the uRDT offers no significant improvement in detecting low-density infections. Alternative diagnostic tests are urgently needed.

Poster 104* :Knowledge, attitudes and practices (KAP) of owners, veterinarians and policy makers in relation to animal schistosomiasis risk and control in Senegal: a One-Health approach.

Presenter: **Dr Louise Vince**, *Doctoral Scholar, Royal Veterinary College,*

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Molecular genetic studies of schistosomes isolated from children and adults in West Africa have identified viable hybrids between human *Schistosoma haematobium* with livestock *S. bovis* and/or *S. curassoni,* demonstrating a zoonotic component. The knowledge of farmers and local veterinarians towards the disease pathology, clinical diagnosis, impact of the disease, anthelmintic usage and health seeking behaviours relating to animals has, however, had little attention. The potential emergence and establishment of drug resistance is a concern for current mass drug administration of human populations, as there is only available drug, praziquantel, for both humans and, potentially, livestock.
The aim of this work is to ascertain the knowledge, attitudes and practices of both villagers and farmers to schistosomiasis risk and control in both animal and humans in Senegal.
Focus groups ($n \leq 30$) were carried out with farmers in four areas of Senegal (Barkadji, Richard Toll, Dakar and Koungheul). In-depth interviews ($n \leq 32$) were conducted with veterinarians, human health workers and policy makers to ascertain knowledge, attitudes and practices in relation to schistosomiasis. Interviews were recorded,

transcribed, and transcripts were anonymised and translated. NVivo qualitative data analysis software, QSR International Pty. (Version 11, 2016), was used for thematic analysis.
Knowledge of the disease in both humans and animals varied by region, participants had most knowledge of human disease in Richard Toll, and animal disease in Linguere. Knowledge of severe disease in people or longer term squeal was not well known by villagers in any region. Farmers and veterinarians familiar with the disease in livestock had reliable knowledge of the prognosis, pathogenesis and zoonotic component; a local name for the disease was verified. Clinical signs in animals included ocular musculature changes, which have not previously been described in detail. Owners and veterinarians consider this diagnostic for clinical schistosomiasis and an indicator of high infection intensity and poor prognosis without treatment. The perceived impact of the disease in livestock is variable by regions, due to seasonality, access to water and grazing for the animals. Avoidance of contaminated water was not attempted for livestock, due to the need to obtain grazing at the water's edge and the cost of well / tap water.
The villagers had good knowledge of recent preventative chemotherapy (PC) in the Richard toll region, but not in rural villages in Linguere or Kougheul, reasons stated for this were lack of funds for petrol. Families attend the clinic for their children when they suspect the disease, although they were prevented from doing so by the distance travelled, money for travel, lack of discomfort in the children, normative nature of the disease and lack of perceived squeal.
Praziquantel was used to treat schistosomiasis in livestock.

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