Event Schedule

BSP Parasites Online 2021

21-Jun-2021 to 25-Jun-2021
Web Event, , Web Event

BSP PARASITES ONLINE 2021
For 2021, in place of our usual Spring Meeting, our main annual meeting will be held online over five days during the Summer (21st-25th June). We have an exciting programme of scientific content, which will be delivered through a virtual conference interface designed to maximise opportunities for interaction, through live Q&A sessions, breakout discussion rooms and virtual trade stands for our exhibitors and sponsors.

All oral presentations will need to be pre-recorded and uploaded to the site, and then broadcast during the assigned slot. Presenters will be asked to be available for a live Q&A session at the end of their assigned slot. This approach should minimise any issues associated with poor internet connections, while maintaining an element of live face to face interaction. Presenters will have the option of making their content available on the conference website for a period of 1 year, but can opt out of this without issue. Full instructions and details on all of this will be provided after you submit an abstract.

The meeting will run across two streams. Our main science stream will incorporate our usual mix of varied high quality themed scientific sessions, keynote speakers and presentations by postgraduate and postdoctoral researchers. Our second, specialist stream, will include: (1) A series of talks from the Infectious Diseases Data Observatory (IDDO; www.iddo.org); (2) Sessions focused on schistosomiasis, curated by Prof Mike Doenhoff and Prof Tony Walker; (3) A session on gender and racial equality in science, focusing on what we as parasitologists can do to address those issues.

There will also be interactive poster sessions, where delegates will have the opportunity for discussion with poster presenters (although this year we're sorry to say that you will have to bring your own refreshments).

Click on the links above to register and/or submit an abstract!

Registration charges for the full 5 day meeting:
> Members: £90
> Students: £30
> Member in low-income countries: FREE; note also that researchers in LMIC and Least Developed Countries can join BSP FOR FREE.
> Non-members: £180

We are very pleased to announce the following confirmed invited speakers:

MAIN SCIENCE STREAM
Prof Maria-Gloria Basanez (Imperial College London)
Dr Emma Briggs (University of Glasgow)
Dr Krystyna Cwiklinski (University of Ireland Galway)
Dr Carmen Faso (University of Bern)
Prof Phillipe Guerin (Infectious Disease Data Observatory)
Prof Neil Hall (Earlham Institute)
Prof Matt Higgins (Oxford University)
Prof Achim Hoerauf (University Hospital Bonn)
Dr Rhys Jones (Aberystwyth University)
Dr Ben Makepeace (Liverpool School)

Prof Eric Morgan (Queen's University Belfast)
Dr Russ Morphew (Aberystwyth University)
Prof Sarah Reece (University of Edinburgh)
Prof Koert Ritmijer (Médecins Sans Frontières)
Dr Claire Rogers (London School of Hygiene and Tropical Medicine)
Prof Bernd Sures (Universität Duisburg-Essen)

PARALLEL STREAM: INFECTIOUS DISEASES DATA OBSERVATORY
Prof Mitali Chatterjee (Infectious Diseases Data Observatory)
Dr Prabin Dahal (Infectious Diseases Data Observatory)
Dr Martin Walker (Royal Veterinary College)
Dr Nathalie Strub-Wourgraft (Drugs for Neglected Tropical Diseases Initiative)
Prof Sir Nicholas White (University of Oxford)

PARALLEL STREAM: TOWARDS GENDER AND RACIAL EQUALITY IN SCIENCE
Dr Regina Cordy (Wake Forest University)
Dr Elisabeth English (University of Pennsylvania)
Prof Elena Gomez-Diaz (Institute of Parasitology and Biomedicine Lopez-Neyra)
Prof Debbie Smith (University of York)
Prof Santuza Teixeira (Federal University of Minas Gerais)

PARALLEL STREAM: SCHISTOSOMIASIS
Prof Coen Adema (University of New Mexico)
Prof Matt Berriman (Wellcome Sanger Institute)
Dr Conor Caffrey (University of California San Diego)
Prof Dan Colley (University of Georgia)
Dr Jim Collins (University of Texas Southwestern Medical Centre)
Prof Christoph Grevelding (Justus Liebig Universitat Giessen)
Prof Peter Hotez (Baylor College of Medicine)
Prof Andrew McDonald (University of Manchester)
Prof Joanne Webster (Imperial College London)

Organiser Contact: **Julian Fuller**
Organiser Phone: **01234 211015**
Organiser Email: **Info@bsp.uk.net**

The Full Programme

Cell and Molecular Biology and Biochemistry

Day 1 - Cell and Molecular Biology and Biochemistry I - (Conference room 1)

21-June-2021, at 11:00 to 12:15

Chair - Dr Russell Morphew

11:00 (30 mins)

A23367 - Big things start small: what we've learnt and have yet to learn from Giardia on endocytosis and secretion (Carmen Faso)

11:30 (15 mins)

A23337 - Trends in temporal gene expression in adult Parasitic and Free-living Strongyloides ratti (Abbie Williams)
11:45 (15 mins)
A23466 - Chemical genetic approaches to study the role of protein kinases in Leishmania cell cycle regulation. (Juliana Brambilla Carnielli Trindade)
12:00 (15 mins)
A23410 - Deciphering the heme homeostasis puzzle: A transcriptomic analysis of Trypanosoma cruzi epimastigotes. (Cecilia Beatriz Di Capua)

Day 1 - Session 1:Live Q & A - (Conference room 1)
21-June-2021, at 12:15 to 12:45

Day 1 - Cell and Molecular Biology and Biochemistry II - (Conference room 1)
21-June-2021, at 13:00 to 14:15
Chair - Dr Benjamin Makepeace
13:00 (30 mins)
A23157 - Helminth Extracellular Vesicles: Drugs and Bugs (Russell Morphew)
13:30 (15 mins)
A23295 - Biochemical and inhibition studies on Leishmania donovani tyrosine aminotransferase (Santanu Sasidharan)
13:45 (15 mins)
A23153 - Deciphering mitochondrial quality control in Trypanosoma brucei (Caroline Dewar)
14:00 (15 mins)
A23510 - Regulation of transposable elements in the absence of piRNAs in a clade IV nematode during a parasitic infection (Mona Suleiman)

Day 1 - Session 2:Live Q & A - (Conference room 1)
21-June-2021, at 14:15 to 14:45

Day 1 - Cell and Molecular Biology and Biochemistry III - (Conference room 1)
21-June-2021, at 15:00 to 16:15
Chair - Prof Carmen Faso
15:00 (30 mins)
A23145 - Wolbachia symbiont genomes and their transcriptional regulation in filariae and ectoparasites (Benjamin Makepeace)
15:30 (15 mins)
A23386 - The role of VEX complex proteins in the insect to mammalian host transition of Trypanosoma brucei (Karinna Rubio-Peña)
15:45 (15 mins)
A23445 - Investigating mitochondrial glycosylation in the African Trypanosome (Samuel Duncan)
16:00 (15 mins)
A23158 - p197 as the missing link between the outer mitochondrial membrane and the basal body in T.brucei (Salome Aeschlimann)

Day 1 - Session 3:Live Q & A - (Conference room 1)
21-June-2021, at 16:15 to 16:45

Day 1 - IDDO I - (Conference room 2)
21-June-2021, at 11:00 to 11:40
Chair - Prof Simon Croft
11:00 (40 mins)
A23440 - Methodological challenges in measuring drug efficacy for the treatment of visceral leishmaniasis (Prabin Dahal)
11:00 (40 mins)
A23440 - Methodological challenges in measuring drug efficacy for the treatment of visceral leishmaniasis (Mitali Chatterjee)

Day 1 - IDDO II - (Conference room 2)
21-June-2021, at 11:45 to 12:25
Chair - Prof Russell Stothard

11:45 (40 mins)
A23119 - Developing a research agenda for the sharing and reuse of clinical data on schistosomiasis & soil-transmitted helminthiases (Martin Walker)

Day 1 - IDDO III - (Conference room 2)
21-June-2021, at 12:45 to 13:25
Chair - Prof John Kelly
12:45 (40 mins)
A23362 - The value of a data platform for drug development and for regulatory agencies: the case of Chagas disease (Nathalie Strub-Wourgraft)

Day 1 - IDDO IV - (Conference room 2)
21-June-2021, at 13:30 to 14:10
Chair - Dr Colin Sutherland
13:30 (40 mins)
A23174 - Reflections on the achievements of 10 years of the WWARN global malaria clinical platform (Nicholas White)

Day 1 - Plenary 1 - (Conference room 1)
21-June-2021, at 10:00 to 10:45
Chair - Prof Maria-Gloria Basanez
10:00 (45 mins)
A23156 - Exploring the re-use of existing data for poverty-related diseases – a scientific or an ethical imperative or both? (Philippe Guérin)

Day 2 - Drugs, Vaccines and Disease Control I - (Conference room 1)
22-June-2021, at 11:00 to 12:15
Chair - Prof Eric Morgan
11:00 (30 mins)
A23070 - An integrated omics approach for Fasciola hepatica vaccine target identification (Krystyna Cwiklinski)
11:30 (15 mins)
A23455 - Disparities in drug sensitivity of T. congolense and brucei group trypanosomes is related to differences in adenosine transporters and aquagyceroporins (Marzuq Ungogo)
11:45 (15 mins)
A23452 - Deazapurine nucleoside analogues for the treatment of Trichomonas vaginalis (Harry De Koning)
12:00 (15 mins)
A23381 - In vitro analysis of the effects of acetaminophen, ibuprofen and aspirin on motility of female adult Onchocerca volvulus worms (Rhoda Antwi)

Day 2 - Session 4:Live Q & A - (Conference room 1)
22-June-2021, at 12:15 to 12:45

Day 2 - Drugs, Vaccines and Disease Control II - (Conference room 1)
22-June-2021, at 13:00 to 14:15
Chair - Dr Krystyna Cwiklinski
13:00 (30 mins)
A23209 - Challenges in combining drugs, vaccines and other helminth control tools in livestock under climate change (Eric Morgan)
13:30 (15 mins)
A23516 - Understanding the structure and function of Fatty Acid Pathway proteins of Leishmania major to identify potent anti-leishmanials (Chetna Dhembla)
13:45 (15 mins)
A23306 - Pan-Phylum Characterisation of Helminth Endocannabinoid Signalling Systems (Bethany Crooks)
14:00 (15 mins)
A23536 - Repurposing trypanocidal drugs to tackle amoebic gill disease in Atlantic Salmon (Bachar Cheaib)

Day 2 - Session 5:Live Q & A - (Conference room 1)
22-June-2021, at 14:15 to 14:45

Day 2 - Diagnosis and Biomarkers I - (Conference room 1)
22-June-2021, at 15:00 to 16:15
Chair - Dr Rhys Jones

15:00 (30 mins)
A23534 - Metabarcoding and amplicon sequencing in helminth diagnostics and surveillance (John Gilleard)
15:30 (15 mins)
A23421 - A novel immunoassay to measure human blackfly exposure in onchocerciasis endemic areas (Laura Willen)
15:45 (15 mins)
A23293 - Glycomic analysis of the filarial nematode Brugia malayi and characterization of anti-glycan antibody responses during infection. (Laudine Petralia)
16:00 (15 mins)
A23495 - Developmental and secretory regulation of microRNAs in an expanded Fasciola hepatica dataset (Caoimhe Herron)

Day 2 - Session 6:Live Q & A - (Conference room 1)

22-June-2021, at 16:15 to 16:45

Day 2 - Schistosome Biology I - (Conference room 2)

22-June-2021, at 15:00 to 16:15

Chair - Prof Anthony Walker
15:00 (30 mins)
A23167 - A non-ribosomal peptide pheromone controls male-induced female sexual development in schistosomes (Jim Collins)
15:30 (15 mins)
A23331 - Excretion patterns of Schistosoma mansoni circulating antigens CAA and CCA by adult male and female worms, using a mouse model and ex vivo parasite culture (Miriam Casacuberta Partal)
15:45 (15 mins)
A23332 - In vitro-matured schistosomes, a valuable tool for drug discovery and studying schistosome development (Helmut Haas)
16:00 (15 mins)
A23198 - Cell signalling during Schistosoma mansoni male-female interactions (Eman Shakir)

Day 2 - S1 :Live Q & A - (Conference room 2)

22-June-2021, at 16:15 to 16:45

Day 2 - Towards Gender and Racial Equality in Science I - (Conference room 2)

22-June-2021, at 11:00 to 12:10

Chair - Prof Derrick Robinson
11:00 (25 mins)
A23064 - Picture a Parasitologist (Debbie Smith)
11:25 (25 mins)
A23202 - Building gender equity from the bottom up: the rise and essence of parasitology communities (Elena Gomez-Diaz)
11:50 (20 mins)
A23061 - Creating resources to increase gender equity in Parasitology (Elizabeth English)

Day 2 - Towards Gender and Racial Equality in Science II - (Conference room 2)

22-June-2021, at 13:00 to 13:45

Chair - Dr James LaCourse
Chair - Dr Pegine Walrad
13:00 (25 mins)
A23060 - Centering Diverse Voices and Grappling with Racial Inequities in Parasitology (Regina Cordy)
13:25 (20 mins)
A23063 - WOMEN IN SCIENCE: THE PATH I FOLLOWED AND WHY WE STILL NEED TO DISCUSS GENDER EQUALITY IN BRAZIL (SANTUZA MARIA Teixeira)

Day 2 - 2021 Wright Medal Lecture - (Conference room 1)

22-June-2021, at 10:00 to 10:45

Chair - Dr Colin Sutherland
10:00 (45 mins)
A23068 - Understanding the survival tricks of parasite surfaces (Matthew Higgins)

Day 3 - Interactions with Hosts and Vectors - (Conference room 1)
23-June-2021, at 11:00 to 12:15
Chair - Dr Julius Hafalla
11:00 (30 mins)
A23437 - Secreting and communicating: lessons from a parasite and vaginal bacterial commensals (Augusto Barbosa)
11:30 (15 mins)
A23541 - The intimate and evolutionarily conserved relationship between Trichomonas and Mycoplasma (Nick Bailey)
11:45 (15 mins)
A23515 - What insect resistance against fungal biopesticides can teach us about G x E in host-pathogen interactions (Matthew Tinsley)
12:00 (15 mins)
A23517 - Heligmosomoides polygyrus produces homologues of HpARI and HpBARI which have increased activity against human immune targets (Adefunke Ogunkanbi)
Day 3 - Session 7:Live Q & A - (Conference room 1)
23-June-2021, at 12:15 to 12:45
Day 3 - Interactions with Hosts and Vectors - (Conference room 1)
23-June-2021, at 13:00 to 14:15
Chair - Dr Rod Dillon
13:00 (30 mins)
A23438 - Disparate immunogenic properties of malaria pre-erythrocytic stage antigens and their susceptibility to vaccine-induced CD8+ T cells (Julius Hafalla)
13:30 (15 mins)
A23417 - Turning trypanosomes into a vaccine: The design and application of a brucei-based carrier platform for the targeting of a wide variety of "difficult" antigens (Joseph Verdi)
13:45 (15 mins)
A23383 - Combining a Novel Immunoassay to Quantify Antibodies to Salivary Antigens with Antibody Acquisition Models to Estimate Exposure to Simulium damnosum s.l. Bites (Philip Milton)
14:00 (15 mins)
A23128 - Identification and RNA profiling of ovine tuft cells in response to gastro-intestinal nematode infections (Katie Hildersley)
Day 3 - Session 8:Live Q & A - (Conference room 1)
23-June-2021, at 14:15 to 14:45
Day 3 - Interactions with Hosts and Vectors - (Conference room 1)
23-June-2021, at 15:00 to 16:15
Chair - Prof Robert Hirt
15:00 (30 mins)
A23439 - Scientist at play; artful science to explore Leishmania, sand flies and their gut microbiota. (Rod Dillon)
15:30 (15 mins)
A23351 - High throughput single-cell genome sequencing gives insights into the generation and evolution of mosaic aneuploidy in Leishmania donovani (Gabriel Negreira)
15:45 (15 mins)
A23341 - Functionally mapping the diversification of African trypanosomes using spatial proteomics (Nicola Moloney)
16:00 (15 mins)
A23086 - Rapid egress of Trypanosoma cruzi follows actin cytoskeleton rearrangement and membrane rupture (Eden Ferreira)
Day 3 - Session 9:Live Q & A - (Conference room 1)
23-June-2021, at 16:15 to 16:45
Day 3 - Schistosome ‘omics’ - (Conference room 2)
23-June-2021, at 11:00 to 12:15
Chair - Prof Christoph G. Grevelding
11:00 (30 mins)
A23208 - Towards a chromosomal view of schistosome genome evolution (Matthew Berriman)

11:30 (15 mins)
A23357 - Life stage-specific glycosylation of schistosome-derived extracellular vesicles (EV) directs interactions of EV with lectin receptors on host cells (Cornelis Hokke)
11:45 (15 mins)
A23407 - Genomic landscape of introgression between blood flukes infecting livestock (Schistosoma bovis) and humans (S. haematobium) across Africa (Roy Platt)
12:00 (15 mins)
A23258 - Simultaneous genotyping of snails and infecting trematode parasites using high-throughput amplicon sequencing. (Cyril Hammoud)

Day 3 - S2 :Live Q & A - (Conference room 2)
23-June-2021, at 12:15 to 12:45

Day 3 - Schistosomiasis - Immunology & host-parasite interactions - (Conference room 2)
23-June-2021, at 13:00 to 14:15
Chair - Prof Cornelis Hokke
13:00 (30 mins)
A23175 - Pulmonary and intestinal immune responses during Schistosoma mansoni infection (Andrew MacDonald)
13:30 (15 mins)
A23294 - Nitric oxide harms the neuropathogenic schistosome Trichobilharzia regenti in mice, partly by inhibiting its vital peptidases (Barbora Šmídová)
13:45 (15 mins)
A23291 - In-depth exploration of Trichobilharzia regenti neuroinvasion in mice: host immune response and helminth-induced neuropathogenicity (Tomas Machacek)
14:00 (15 mins)
A23345 - Harnessing the diagnostic potential of highly specific anti-glycan antibodies in schistosomiasis (Anna Kildemoes)

Day 3 - S3 :Live Q & A - (Conference room 2)
23-June-2021, at 14:15 to 14:45

Day 3 - Schistosomiasis - Chemotherapy/new drugs/drug screening - (Conference room 2)
23-June-2021, at 15:00 to 16:15
Chair - Prof Andrew MacDonald
15:00 (30 mins)
A23168 - Schisto drug discovery in Sunny San Diego – tools and technologies (Conor Caffrey)
15:30 (15 mins)
A23509 - Docking-based virtual screening identification of multi kinase-targeting inhibitors with in vitro phenotypic activity against Schistosoma mansoni (Bernardo Moreira)
15:45 (15 mins)
A23344 - From bugs to drugs: discovery of novel antischistosomal compounds from insects (Simone Haeberlein)
16:00 (15 mins)
A23392 - Anti-schistosomal activities of quinoxaline-containing compounds: from hit identification to lead optimisation (Gilda Padalino)

Day 3 - S4 :Live Q & A - (Conference room 2)
23-June-2021, at 16:15 to 16:45

Day 3 - 2020 Wright Medal Lecture - (Conference room 1)
23-June-2021, at 10:00 to 10:45
Chair - Prof Maria-Gloria Basanez
10:00 (45 mins)
A23115 - The private life of malaria parasites: Strategies for survival & reproduction (Sarah Reece)

Day 4 - BES: Ecology and Evolution I - (Conference room 1)
24-June-2021, at 11:00 to 12:15
Chair - Prof Bernd Sures
11:00 (30 mins)

A23066 - Sequencing Protists directly from the environment for the Darwin Tree of Life Project (Neil Hall)
11:30 (15 mins)
A23425 - Who's to blame? Host-vector-parasite interactions in timing transmission. (Petra Schneider)
11:45 (15 mins)
A23379 - A new Plasmodium species in African apes reveals the origin of human Plasmodium malariae (Lindsey Plenderleith)
12:00 (15 mins)
A23113 - Diversity of Strongylid Nematode Communities in Wild Western Lowland Gorillas (Bethan Mason)

Day 4 - Session 10:Live Q & A - (Conference room 1)
24-June-2021, at 12:15 to 12:45

Day 4 - BES: Ecology and Evolution II - (Conference room 1)
24-June-2021, at 13:00 to 14:15
Chair - Prof Neil Hall
13:00 (30 mins)
A23065 - Environmental Parasitology: relevance of parasites in ecotoxicological studies (Bernd Sures)
13:30 (15 mins)
A23330 - Using high throughput sequencing to detect the presence of multiple parasite strains in the rapidly declining European turtle dove (Streptopelia turtur) (Rebecca Young)
13:45 (15 mins)
A22951 - On snail-borne hippo parasites: do artificial lakes and biological invasions pose a burden on Hippopotamus amphibius? (Ruben Schols)
14:00 (15 mins)
A23429 - Zoonotic Implications of parasite helminths among domestic animals in selected communities of Caraga Region, Philippines (Sheina Macy Manalo)

Day 4 - Session 11:Live Q & A - (Conference room 1)
24-June-2021, at 14:15 to 14:45

Day 4 - Diagnosis and Biomarkers II - (Conference room 1)
24-June-2021, at 15:00 to 16:45
Chair - Prof John Gilleard
15:00 (30 mins)
A23520 - Application of environmental DNA analysis for Fasciola hepatica control in livestock (Rhys Jones)
15:30 (15 mins)
A23195 - SHERLOCK4HAT: a new CRISPR-based tool for Human African Trypanosomiasis diagnosis (Nuria Sima Teruel)
15:45 (15 mins)
A23143 - Evaluating the diagnostic test accuracy of molecular xenomonitoring methods for the surveillance of lymphatic filariasis and onchocerciasis (Joseph Pryce)
16:00 (15 mins)
A23416 - Diagnosis of sheep fasciolosis caused by Fasciola hepatica using Cathepsin L ELISA and lateral flow technologies (Amber Dorey)
16:15 (30 mins)
A23176 - Microscopy – relevant or redundant in diagnostic parasitology? (Claire Rogers)

Day 4 - Schistosome Biology II - (Conference room 2)
24-June-2021, at 11:00 to 12:15
Chair - Dr Geoffrey Gobert
11:00 (30 mins)
A23207 - The WEome of Schistosoma mansoni – a non-coding DNA resource shaping schistosome biology, variability, and evolution? (Christoph G. Grevelding)
11:30 (15 mins)
A23075 - Diversity and Evolution of Antigens in the Tetraspanin Protein Family of Schistosoma japonicum (Daniel Parsons)
11:45 (15 mins)
A23418 - Establishing a Female-only Controlled Human Schistosoma mansoni Infection Model: a safety and dose finding study (Jan Pieter Koopman)
12:00 (15 mins)
A23450 - Schistosoma mansoni lacks the homologue of the human telomerase reverse transcriptase (hTERT), and relies on the snail enzyme for its survival. (Matty Knight)

Day 4 - S5 :Live Q & A - (Conference room 2)
24-June-2021, at 12:15 to 12:45
Day 4 - Schistosomiasis - Control, epidemiology and One Health I - (Conference room 2)
24-June-2021, at 13:00 to 14:15
Chair - Dr Poppy Lamberton
13:00 (30 mins)
A23171 - How does one go from schistosome granulomas to schistosomiasis control programs? (Dan Colley)
13:30 (15 mins)
A23523 - The potential of citizen science to tackle the wicked problem of snail-borne diseases (Tine Huyse)
13:45 (15 mins)
A23448 - Citizen scientists versus malacologists: comparing schistosome snail collections in Lake Albert, Uganda (Julius Tumusiime)
14:00 (15 mins)
A23178 - The current and future predicted status of schistosomiasis in South Africa under climate change (Lizaan de Necker)
Day 4 - S5 :Live Q & A - (Conference room 2)
24-June-2021, at 14:15 to 14:45
Day 4 - Schistosomiasis - Molluscan biology & 'omics' - (Conference room 2)
24-June-2021, at 15:00 to 16:15
Chair - Prof Coen Adema
Chair - Prof Anthony Walker
15:00 (30 mins)
A23169 - Snail vector biology, perspectives from genome mining (Coen Adema)
15:30 (15 mins)
A23519 - Bulk segregant analysis of host specificity in schistosome parasites (Frédéric Chevalier)
15:45 (15 mins)
A23415 - Lack of functional chromatin dynamics through nuclear motor proteins in aged Biomphalaria glabrata snails reveals a mechanism of interest with respect to controlling schistosomiasis. (Daniel Horton)
16:00 (15 mins)
A23328 - First molecular identification of Bulinus africanus in Lake Malawi with discussions on its transmission potential for human schistosomes (Mohammad Alharbi)
Day 4 - S7 :Live Q & A - (Conference room 2)
24-June-2021, at 16:15 to 16:45
Day 4 - 2020 President's Medal Lecture - (Conference room 1)
24-June-2021, at 10:00 to 10:45
Chair - Prof Maria-Gloria Basanez
10:00 (30 mins)
A23161 - R-loops of the Trypanosoma brucei genome and single cell transcriptomic reconstruction of bloodstream form differentiation (Emma Briggs)
Day 5 - Drugs, Vaccines and Disease Control III - (Conference room 1)
25-June-2021, at 11:00 to 12:15
Chair - Dr Elmarie Myburgh
11:00 (30 mins)
A23535 - Development of macrofilaricidal drugs for onchocerciasis and lymphatic filariasis (Achim Hoerauf)
11:30 (15 mins)
A23216 - Towards the Structure Based Design of Broad Spectrum Anti-Apicomplexan Drugs (Ashwani Sharma)
11:45 (15 mins)
A23154 - ACT treatment failure and resistance gene variants in African Plasmodium falciparum (Colin Sutherland)
12:00 (15 mins)
A23311 - Disentangling the role of Ascaris β-tubulin isotypes in the emergence of anthelmintic resistance. (Ben Jones)

Day 5 - Session 13:Live Q & A - (Conference room 1)
25-June-2021, at 12:15 to 12:45

Day 5 - Surveillance, Epidemiology, Stigma and Public Health I - (Conference room 1)
25-June-2021, at 13:00 to 14:15

Chair - Dr Martin Walker

13:00 (30 mins)
A23116 - Mathematical modelling and the WHO 2021-2030 roadmap on neglected tropical diseases: Insights and challenges (Maria-Gloria Basanez)

13:30 (15 mins)
A23376 - Force of infection and age-profiles of Taenia solium human taeniasis and cysticercosis: global trends and subnational analysis for Colombia (Matthew Dixon)

13:45 (15 mins)
A23380 - ZooTRIP: Zoonotic transmission of intestinal parasites: implications for control and elimination. (Kezia Whatley)

14:00 (15 mins)
A23487 - Parasite-vaccine interactions through the lenses of meta-analysis and field research (Liana Wait)

Day 5 - Session 14:Live Q & A - (Conference room 1)
25-June-2021, at 14:15 to 14:45

Day 5 - Surveillance, Epidemiology, Stigma and Public Health II - (Conference room 1)
25-June-2021, at 15:00 to 16:15

Chair - Dr Helen Price

15:00 (30 mins)
A23160 - Leishmaniasis and Conflict (Margriet den Boer)

15:30 (15 mins)
A23289 - Are Parasitic Diseases still a Continuing Health Problem in Gaza Strip, Palestine? (Adnan Alhindi)

15:45 (15 mins)
A23422 - Community practices and Environmental Reservoir as risk factor of Soil-Transmitted Helminths in Selected Rural Communities in the Philippines (Kim Louisse Patagnan)

16:00 (15 mins)
A23388 - Unusual localization of blood-borne Loa loa microfilariae in the skin depends on microfilarial density in the blood: Implications for onchocerciasis diagnosis in co-endemic areas (Yannick NIAMSI EMALIO)

Day 5 - Session 15:Live Q & A - (Conference room 1)
25-June-2021, at 16:15 to 16:45

Day 5 - Schistosomiasis - Control, epidemiology and One Health II - (Conference room 2)
25-June-2021, at 11:00 to 12:30

Chair - Dr Tine Huyse

11:00 (30 mins)
A23170 - Reaching the WHO elimination targets for schistosomiasis: the importance of a One Health perspective (Joanne Webster)

11:30 (15 mins)
A23372 - Remaining pockets of moderate to high endemicity of schistosomiasis and soil-transmitted helminthiasis in selected communities in Caraga region, the Philippines (Allen Jethro Alonte)

11:45 (15 mins)
A23528 - How much variation in drug response is found in schistosome populations? (Winka Le Clec'h)

12:00 (15 mins)
A23527 - Standardising the interpretation of point-of-care circulating cathodic antigen diagnostics for Schistosoma mansoni: A Bayesian latent class analysis study (Jessica Clark)

12:15 (15 mins)
A23482 - Spatial analysis of Schistosomiasis in Endemic Communities in Southern Mindanao, Philippines (Vachel Gay Paller)

Day 5 - S8 :Live Q & A - (Conference room 2)
25-June-2021, at 12:30 to 13:00

Day 5 - Schistosomiasis - Control, epidemiology and One Health III - (Conference room 2)

25-June-2021, at 14:00 to 15:15

Chair - Prof Joanne Webster

14:00 (30 mins)

A23172 - Schistosomiasis vaccines: their role in disease prevention and elimination (Peter Hotez)

14:30 (15 mins)

A23529 - Using choice modelling to identify popular and affordable alternative interventions for schistosomiasis in Uganda (Poppy Lamberton)

14:45 (15 mins)

A23267 - The Enemy of My Enemy is Perhaps My Friend: Intestinal schistosomiasis is associated with reduced malaria intensity in preschool children in Uganda. (Daniel McDowell)

15:00 (15 mins)

A22981 - New dynamics of schistosomiasis in Lake Malawi (Russell Stothard)

Day 5 - S9 :Live Q & A - (Conference room 2)

25-June-2021, at 15:15 to 15:45

Day 5 - Plenary II - (Conference room 1)

25-June-2021, at 09:00 to 09:45

Chair - Prof Maria-Gloria Basanez

09:00 (45 mins)

A23537 - Fascioliasis control in human endemic areas: one health action to complement preventive chemotherapy (Santiago Mas-Coma)

Index by Authors

A

B

C

D

d

D

d

D

d

D

d

D

E

F

G

H

I

J

K

L

M

N

O

P

Q

R

S

Š

S

Ś

S

T

U

V

W

Y

y

Y

- Yoshida, A, *A23510*
- Young, R, *A23330*
- Younger, J, *P124*

Z

- Zaheer, T, *P34*
- Zanatta, J M, *P71, P12, P13*
- Zhang, N, *P91*
- ZhenZhen, W, *A23337*
- Zoltner, M, *P91*

Oral Abstracts

Plenary 1 - (Conference room 1)

21-June-2021, at 10:00 (45 mins)

Exploring the re-use of existing data for poverty-related diseases – a scientific or an ethical imperative or both?*A23156*

Presenter: **Prof Philippe Guérin**, *Director, IDDO*

Over the last two decades, renewed attention has been given to neglected tropical diseases (NTDs), a subset of poverty-related illness. While irrefutably it was acknowledged that the “classical” market approach could not respond to the challenges of NTDs, a series of initiatives have now been established and are already supporting new research and development for drugs, vaccines and diagnostic tools and this effort should be applauded. Up until now, one thing that all poverty-related infectious diseases shared in common is the overall limited volume of research conducted to understand and test new approaches or guide control programmes. More specifically, the number of clinical trials conducted in the last few decades to support current therapeutic or prophylaxis recommendations are limited in numbers all together: in number of patients recruited, in geographical representation of endemic settings and they often lack representation of the affected population. The root of the problem lies in the limited funding to support larger clinical trials, but also in the challenges in recruiting patients in remote areas and this is sometimes overcomplicated by security concerns and the limited number of research teams working together in each of these diseases. If, by pooling ALL existing individual patient data for each of those diseases generated over the last few decades, we could generate new evidence which could not have been generated by single trials, would it be worth doing? We will discuss the case study of the WorldWide Antimalarial Resistance Network (WWARN), a global data platform for malaria and the subsequent development of the Infectious Diseases Data Observatory (IDDO) as an attempt to establish global data platforms for NTDs and to optimise the re-use of data to maximise the scientific impact of existing knowledge and guide future research.

Cell and Molecular Biology and Biochemistry I - (Conference room 1)

21-June-2021, at 11:00 (30 mins)

Big things start small: what we've learnt and have yet to learn from Giardia on endocytosis and secretion*A23367*

Presenter: **Prof Carmen Faso**, *Assistant Professor, Institute of Cell Biology-University of Bern*

C Faso[1];
[1] Institute of Cell Biology-University of Bern, Switzerland

Eukaryotic subcellular diversity is awe-inspiring and, as parasitologists, we have the rare privilege of experiencing this diversity in our daily work. Work on so-called model organisms tends to dismiss discoveries in cell and molecular parasite biology as exclusive adaptations with low relevance to the rest of the cell

biology community. However, in my presentation I'd like to share with the audience what we learned from genera such as Giardia that has actually chipped away at the feet of dogma in endocytic and secretory trafficking. I will also present our ongoing work on trying to understand unconventional protein secretion at the interface of two species, in terms of its components and phylogenetic history, using both *Giardia lamblia* and *Entamoeba histolytica* as simplified models for protein trafficking.

IDDO I - (Conference room 2)

11:00 (40 mins)

Methodological challenges in measuring drug efficacy for the treatment of visceral leishmaniasis*A23440*

Presenter: **Prof Mitali Chatterjee**, *Institute of Postgraduate Medical Education & Research, Kolkata*

Synopsis: In this presentation, we summarise the spectrum of methodological variations adopted in VL studies using the Infectious Diseases Data Observatory (IDDO) living systematic review of clinical studies. Results are presented for variations in case definition adopted for patient screening, diagnosis method for confirmed parasitological presence for patient enrolment, quality control of VL microscopy, duration of post-treatment follow-up and outcome definitions adopted. Detailed abstract: Background: In Visceral Leishmaniasis (VL), heterogeneity in study design(s), conduct and reporting methodologies adopted has been relatively under-researched. A systematic review (SR) of all published treatment efficacy trials in VL was carried out to characterise analytical variations in design and conduct. Methods: All studies (158 trials; 1980–2019) indexed in Infectious Diseases Data Observatory (IDDO) VL clinical study library were eligible for inclusion. The IDDO VL library is a living SR updated bi-annually and searches the following databases: PubMed, Embase, Scopus, Web of Science, Cochrane, clinicaltrials.gov, WHO ICTRP, Global Index Medicus, IMEMR, IMSEAR, and LILACS. Results: Case definition for patient screening was defined solely based on compatible clinical diagnosis in 27 (17.1%) trials, parasitological/serological confirmation in 38 (24.1%) or a combination of compatible clinical diagnosis and/or parasitological/serological method in 76 (48.1%), and was poorly defined in 17 (10.8%).Patient enrolment required confirmation of VL based on demonstration of parasites in spleen in 54 (34.2%) trials, bone marrow in 22 (13.9%), bone marrow and/or spleen in 49 (31.0%), lymph node in 1 (0.6%), a combination of one or more of the above in 19 (12.0%), blood in 4 (2.5%), and was not specified in 9 (5.7%). The time-point for test of cure assessment ranged from <15 days of post-treatment in 7 (4.4%) studies, 16–70 days in 131 (82.9%), and was not specified in 20 (12.7%). Similarly, post-treatment follow-up ranged from <6months in 7 (4.4%) studies, 6 months in 110 (69.6%), >6months in 35 (22.2%), and not specified in 6 (3.8%). Relapse was vaguely defined solely based on clinical suspicion in 3 (1.9%) trials, presence of parasites in 22 (13.9%), a combination of clinical suspicion and/or parasitological/serological approach in 33 (20.9%) and was not specified in 100 (63.3%). Conclusions: This study highlights the substantial methodological variations in definitions adopted for patient screening, disease diagnosis and therapeutic outcomes emphasising the need for a harmonised protocol/algorithm for enrolment in VL clinical studies.

Cell and Molecular Biology and Biochemistry I - (Conference room 1)

11:30 (15 mins)

Trends in temporal gene expression in adult Parasitic and Free-living Strongyloides ratti *A23337*

Presenter: **Miss Abbie Williams**, *Post graduate researcher (PhD), University of Bristol*

A WilliamsA Hino[3]; W ZhenZhen[3]; L Peachey[1]; T Kikuchi[3]; V Hunt[2];
[1] University of Bristol, UK; [2] University of Bath, UK; [3] University of Miyazaki, UK

Amongst the neglected tropical diseases, soil transmitted helminths remain a substantial one-health challenge. In particular, the parasitic nematode, *Strongyloides stercoralis*, is estimated to infect around 600 million people globally, constraining physical and socio-economic development. The distinct lifecycle of *Strongyloides* which produces genetically identical parasitic and free-living adult female populations offers a unique opportunity to explore the genetic basis of parasitism through comparative analyses. Previous work comparing the transcriptome at single time points has identified several gene families that are highly upregulated in the parasitic female and are expanded amongst parasitic *Strongyloididae*, suggesting that they have an active role in parasitism. However, the temporal expression of genes throughout the course of infection, and thereby relative activity in parasitism, remains unknown. Here, we present novel insight into temporal regulation of the *S. ratti* transcriptome through time-course RNAseq analysis, focusing on co-expressed genes both between and within the parasitic and free-living adult female populations. Differentially expressed clusters of co-expressed

genes between generations largely captured reproductive and developmental differences. Gene families believed to be active in parasitism were largely upregulated and co-expressed in the parasitic female, with evidence of physical clustering within the genome into “parasitism hotspots”. In the free-living female, co-expressed gene clusters similarly isolate reproductive and developmental activity, but also offer insight into potential mechanisms of aging with decreasing regulation of the response to oxidative stress. Understanding both the activity and wider context of parasitism associated gene families allows us to refine the scope of interest for future work that holds potential for developing novel therapeutic interventions.

11:45 (15 mins)

Chemical genetic approaches to study the role of protein kinases in Leishmania cell cycle regulation.*A23466*

Presenter: **Dr Juliana Brambilla Carnielli Trindade**, *Postdoctoral Research Associate, University of York*

J Brambilla Carnielli Trindade[1]; J Brannigan[1]; M Saldivia[2]; T Wilkinson[1]; J C Mottram[1];
[1] University of York, UK; [2] Novartis Institute for Tropical Diseases, United States

Cell division is a core biological process during the development of both multicellular and unicellular organisms. It is a conserved process throughout eukaryotes, which has diverse evolutionary roots, resulting in a unique repertoire of protein component in Trypanosomatids, including *Leishmania*. Some of these components has been identified in *Leishmania*, but the extension of its repertoire and their role in the coordination of the cell cycle remains unclear. Here, we used genetic and chemical approaches to explore the role of some essential protein kinases in cell cycle progression. We used CRISPR-Cas9 to perform precision editing of the *L. mexicana* genome to generate analogue sensitive mutants suitable for chemical genetic inhibition. For the kinetochore protein kinase KKT2, CRK9 and CMGCa replacement of the bulky gatekeeper methionine residue with a glycine in the ATP-binding site makes the enzymes sensitive to the bulky inhibitor 1NM-PP1. For the kinetochore protein kinases CLK1 and CLK2 (also known as KKT10 and KKT19, respectively) replacement of a cysteine near to the ATP-binding domain prevents binding of the covalent Michael-acceptor in the inhibitor AB1, validating the specificity of this compound against CLK1/CLK2. The specific inhibition of CLK1, CLK2, KKT2 caused a cell cycle arrest in G2/M stage of the promastigote. A further investigation, by fluorescence microscopy labelling the mitotic spindle, revealed that KKT2 inhibition is followed by a significant accumulation of cells in early mitosis, where mitotic spindle coordination in the nucleus failed. Furthermore, it was observed that CMGCa inhibition also impaired chromosome segregation, but the cell body development reaches a more advanced stage, suggesting CMGCa activity is required later in mitosis than KKT2. In addition, CLK1/CLK2 inhibition doesn’t affect the coordination of the mitotic spindle, but it blocks cell cycle progression in cytokinesis. These studies bring new insights into the essential biological process of cell division in *Leishmania* and provide a source of new potential therapeutic targets.

12:00 (15 mins)

Deciphering the heme homeostasis puzzle: A transcriptomic analysis of Trypanosoma cruzi epimastigotes.*A23410*

Presenter: **Dr Cecilia Beatriz Di Capua**, *Posdoc, Universidad Nacional de Rosario*

C B Di Capua[1]; L Berná[2]; E Tevere[1]; C Robello[2]; J A Cricco[1];
[1] IBR-CONICET, Facultad de Ciencias Bioquímicas y Farmacéuticas, Universidad Nacional de Rosario, Argentina; [2] Institut Pasteur Montevideo; Facultad de Medicina, Universidad de la República, Uruguay

Chagas disease (also called American trypanosomiasis) is caused by the protozoan parasite *Trypanosoma cruz*i. The infection is mostly spread by triatomine insects but congenital and transfusional transmission is also common. Similarly to *T. brucei* and *Leishmania spp*., *T. cruzi* lacks for a heme synthesis route but present several heme-proteins involved in the respiratory chain complexes and other essential metabolic pathways (Tripodi, 2011). For this reason, trypanosomatids must scavenge this molecule from the host or vector. Being heme an essential cofactor for *T. cruzi*, the heme homeostasis represents a promising target to inhibit *T. cruzi* proliferation and infectivity. *T. cruzi* is able to import heme from the hosts during the replicative stages and a protein we named *Tc*HRG is essential for heme transport activity (Merli, 2016). We observed that the expression of *Tc*HRG is modulated by heme availability. Heme is also a highly toxic molecule, then this parasite must present a strict control on heme homeostasis (import, trafficking, and detoxification) where *Tc*HRG and other unknown proteins are directly involved. Therefore, it was postulated that *T. cruzi* may sense intracellular heme and adjust *Tc*HRG expression and accumulation to promote or reduce heme transport activity (Pagura, 2020). In order to assess the puzzle pieces of heme homeostasis we designed a transcriptome experiment where

we evaluated the effect of hemin and hemoglobin supplementation as heme source in previously heme-starved epimastigotes of *T. cruzi* during a time course of 24hs. The parasites were cultures for 48 h in LIT-10% BFS medium without heme supplementation. Cultures were then washed and resuspended in fresh medium with 5 uM heme as hemin or hemoglobin and in medium without heme as control. Samples from 3 biological replicas were taken at 0, 4 and 24 h after treatment. Total RNA samples were sent to the NGS service and raw data were analysed to obtain the differentially expressed genes (DEG). Reads were mapped to the *T. cruzi* DM28c 2018 genome from TriTrypDB platform where 17197 genes are annotated (Berna, 2018). We detected a total of 303 DEG in both hemin and hemoglobin supplemented cultures 4 hours post-treatment and 171 DEG after 24 hours of heme supplementation. Among the down-regulated genes in treated epimastigotes we pointed these cellular functions: flagellum structure, protein modification, transporters, and signal transduction. We also observed a down regulation of several genes encoded for respiratory complex and electron transfer. The processes up regulated in supplemented epimastigotes were gene expression regulation, translation and protein synthesis, protein transport, protein-protein interaction, protein folding and modification, transporters, cystathionine synthesis and NAD(P)+/NAD(P)H metabolism. These results denote that changes in heme availability in epimastigotes have a general effect on the metabolic state of the parasite. We observed modifications in gene expression with specific down-regulated and up-regulated metabolic pathways. Biochemical assays should be performed in order to validate the data obtained from this transcriptome analysis. Our results reinforce the statement that heme homeostasis is essential for the parasite. Puzzling over the heme transport and utilization will contribute to find an Aquiles' heel of the parasite as well as discover new target molecules to control *T. cruzi*

IDDO II - (Conference room 2)

11:45 (40 mins)

Developing a research agenda for the sharing and reuse of clinical data on schistosomiasis & soil-transmitted helminthiases*A23119*

Presenter: **Dr Martin Walker**, *Royal Veterinary College*

M Walker[1];
[1] Royal Veterinary College, UK

The Infectious Diseases Data Observatory (IDDO) is building a data sharing and reuse platform for clinical data on the treatment of schistosomiasis and soil-transmitted helminthiases (STHs). The platform is designed as a resource to facilitate research that will enhance the treatment of schistosomiasis and STHs and will thus ultimately enhance prospects for controlling and eliminating these neglected tropical diseases. The IDDO principles of collaboration, inclusivity and transparency to achieve equitable data sharing and reuse are embodied in our process for developing a research agenda. Our broad consultative approach aims to ensure that we reach a set of pertinent research questions and themes that reflect the prevailing—but not immutable—consensus of the scientific community. The approach also serves to promote early engagement and participation, fostering the platform as a shared scientific resource. This talk will outline our process for developing a schistosomiasis and STHs research agenda and highlight some disease-specific research questions that are best addressed—or can only be addressed—by actively embracing data sharing and reuse.

IDDO III - (Conference room 2)

21-June-2021, at 12:45 (40 mins)

The value of a data platform for drug development and for regulatory agencies: the case of Chagas disease*A23362*

Presenter: **Dr Nathalie Strub-Wourgraft**, *Director, Dndi*

NTDs can also be called diseases of poverty … affecting poor populations often living in remote aeras in LMICs. Typically, NTDs have been neglected by research and even if several initiatives, such as DNDi, have emerged in the past 20 years, they are characterised by many gaps including tremendous knowledge ones. But NTDs affect over a billion of individuals, result in increased poverty, and significant morbi-mortality: most still require affordable and field-adapted tools to control eliminate or eradicate them by 2030. Indeed, twenty of them have been prioritised by WHO and a detailed roadmap, highlighting the gaps & needs per disease do show that many are still missing proper test and treat strategies. Any treatment will need to be developed according to a plan that will secure its approval by endemic regulatory authorities and acceptance by policy makers for recommendation as a public health measure. As of now, in contrast with other diseases, they are only a very limited amount of guidance from regulators to support developers in building solid R&D strategic plans. Chagas

disease, identified over 100 years ago, is a complex NTDs, caused by a parasite transmitted by a triatome. It starts by an acute, often poorly symptomatic disease, and continues by a chronic phase, silent that will – or not, evolve in a final cardiac or digestive symptomatic one, the cardiac complication being until now fatal. For now, most therapeutic approaches tackle the chronic indeterminate phase of the disease, hoping that the effect on the circulating parasite observed after one or 2 years is predictive of cure. But still very little is known and today, we do not have tools to either prevent or definitely cure the chronic phase of Chagas preventing disease progression. There has been a wealth of clinical research conducted in the past decade, aiming at identifying treatments for this indeterminate phase of CD. Sometimes in adults, children, for prevention … A recent study (Maguire B et al. Submitted PlosNTD) shows the diversity and heterogeneity of studies, populations, definition of endpoints, outcomes but also the often-insufficient sample size … so that signal detection from each study remains low. Pooling all individual data in a systematic and consistent way would allow to increase the ability to better analyse the data and respond to critical questions, such as "are there predictors of worse outcome, what is the best predictor of response, are there sub-types (lineages of T. cruzi) related progression and/or treatment effects, among others " … We will discuss the opportunity of setting up this data-sharing platform for Chagas disease.

Cell and Molecular Biology and Biochemistry II - (Conference room 1)

21-June-2021, at 13:00 (30 mins)

Helminth Extracellular Vesicles: Drugs and Bugs*A23157*

Presenter: **Dr Russell Morphew**, *Senior Lecturer in Biochemistry, Aberystwyth University*

Research into helminth derived extracellular vesicles (EVs) has exploded since their first discovery. Initial forays aimed at characterising the constituent components of these EVs, often using a range of omic technologies, has revealed proteins and microRNAs as some of the key biomolecules. Helminth EV research has now progressed into more functional studies aimed at uncovering their role in the host-parasite interaction including host cell incorporation of helminth EVs and the potential impacts of EVs on the host immune response. Our research has focused on alternative aspects of helminth EV biology. Our starting position was to evaluate EV purification and we have progressed utilising size exclusion chromatography as our technology of choice for future functional EV studies. We have since explored EVs in a variety of flatworms including *Fasciola hepatica*, *Calicophoron daubneyi* and *Anoplocephala perfoliata* incorporating GeLC based proteomics supported by electron microscopy and nano-particle tracking. Functional analysis has then focused on the role EVs may play in anthelmintic exposure with evidence supporting a role for EVs in sequestering anthelmintics. Further evidence likely supports a detoxification capacity within helminth EVs. Further functional experimentation has driven research into the role EVs likely play with the host microbiome. We have demonstrated the first direct evidence of helminth EV microbiome manipulation. Using an *in vitro* model of rumen fermentation we demonstrate that EVs produced from *C. daubneyi* directly influence rumen bacteria. There are likely several proposed mechanisms as to how the microbiome will be influenced through EV interaction but one proposed mechanism is through a direct exertion of antimicrobial activity. Here we also demonstrate early data of antimicrobial activity exhibited in helminth EVs. These avenues represent novel areas to explore in further depth to uncover new insights of helminth EV host interactions.

13:30 (15 mins)

Biochemical and inhibition studies on Leishmania donovani tyrosine aminotransferase*A23295*

Presenter: **Mr Santanu Sasidharan**, *Research Scholar, National Institute of Technology-Warangal*

Santanu Sasidharan[1]; Prakash Saudagar[1];
[1] National Institute of Technology-Warangal, India

Leishmaniasis is a neglected tropical disease affecting millions worldwide every year. The treatment regimen currently includes miltefosine and liposomal amphotericin B. However, these drugs are toxic and non-economical. Considering these drawbacks and the dearth of drugs against *Leishmania*, Tyrosine aminotransferase (TAT), an enzyme that catalyzes the transamination of amino acids in *Leishmania*, was studied. The full-length TAT from *Leishmania donovani* LDP18 was cloned, expressed, and purified by affinity chromatography. Biochemical studies revealed the K_m and V_{max} values as 3.5 ± 0.9 mM and 11.7 ± 1.5 $\mu M.min.\mu g^{-1}$ with a three-state folding mechanism. The recombinant TAT was catalytically active over a wide range of pH (3.5-10.5) and temperature (20-75 °C). Spectroscopic and computational studies found that the pH tolerance was due to the concerted action of the charges between active site and co-factor and structural folding. Moreover, the non-conserved N-terminal (NTAT) and conserved C-terminal domains (CTAT) of TAT were

truncated, cloned, and purified to determine their roles in regulating the enzyme activity. NTAT, like TAT, was stable at extreme temperatures and pH conditions, whereas CTAT was relatively susceptible to these variations. The unfolding studies indicated that the full-length TAT and NTAT unfolded via a three-state mechanism, while the CTAT exhibited two-state folding. From this, N-terminal was determined to be responsible for the stabilization of the co-factor (PLP) in the active site while C-terminal conferred active site protection to extreme conditions. Further, a curated ZINC15 database containing 1,83,659 natural compounds was screened against the full-length TAT, and the top five compounds (TI1-TI5) were chosen based on their binding scores. Molecular dynamic simulations revealed the high-affinity interactions of TI1, TI3, TI4, and TI5 towards the active site residues. *In vitro* inhibition studies indicated K_i values of 0.9 ± 0.2 µM and 0.3 ± 0.1 µM for TI3 and TI4, respectively. Notably, TI3 and TI4 exhibited anti-leishmanial activity with IC50 values of 5.6 ± 1.72 µM and 9.6 ± 3.11 µM, respectively. We conclude that the lead inhibitors TI3 and TI4 offer huge potential as anti-leishmanial candidates and require further characterization in cell and animal systems to validate their potential as an anti-leishmanial drug.

13:45 (15 mins)

Deciphering mitochondrial quality control in Trypanosoma brucei *A23153*

Presenter: **Dr Caroline Dewar**, *Postdoc, University of Bern*

C E Dewar[1]; S Oeljeklaus[2]; B Warscheid[2]; A Schneider[1];
[1] University of Bern, Switzerland; [2] University of Freiburg, Germany

Mitochondrial quality control (MQC) is the network of pathways by which eukaryotic cells monitor and maintain the function of their mitochondria. *Trypanosoma brucei* has a large single mitochondrion, which prevents the elimination of dysfunctional mitochondria as in some other organisms. When this essential mitochondrion is not functioning correctly, for example when mitochondrial protein import is defective, cell viability suffers. The processes by which this parasite regulates its mitochondrial function are of great interest, particularly in relation to its life cycle, where the mitochondrion undergoes massive programmed morphological and functional alterations.

MQC pathways in yeast and metazoa are regulated on the transcriptional level. However, in *T. brucei*, due to polycistronic transcription, MQC regulation in this way is not possible. Additionally, other than ubiquitin and the proteasome, orthologues of most common MQC factors found in yeast and metazoa are absent in *T. brucei.* Mitochondrial biogenesis in general in *T. brucei* has been shown to be greatly impacted by convergent evolution, and we expect the same to be the case for mechanisms governing MQC.

95% of mitochondrial proteins in *T. brucei* are encoded in the nuclear DNA. The multisubunit ATOM complex is the mediator of protein import through the mitochondrial outer membrane in trypanosomes (Pusnik et al., 2011, Mani et al., 2015). We previously defined the *T. brucei* mitochondrial importome as being the proteins which decreased in level when ATOM40, the central import pore, was knocked down (Peikert et al., 2017). We will show data demonstrating the existence of a MQC pathway in *T. brucei* triggered when mitochondrial protein import is blocked, where the endpoint is the proteasomal degradation of specifically mislocalised mitochondrial proteins. Using a variety of proteomic and biochemical approaches, we show that the proteasome and putative components of a ubiquitin-driven pathway are recruited to the mitochondrion upon the induction of an import defect. Trypanosomatid-specific candidates are being investigated as to their roles within this MQC pathway. Of particular interest is a nuclearly-localised protein with a ubiquitin-like domain which is released into the cytoplasm upon the induction of a mitochondrial import defect. Nuclear release of this protein is required for this MQC mechanism to function.

14:00 (15 mins)

Regulation of transposable elements in the absence of piRNAs in a clade IV nematode during a parasitic infection *A23510*

Presenter: **Miss Mona Suleiman**, *Student, University of Bath*

M Suleiman[1]; A Kounosu[2]; M Dayi[2]; A Yoshida[2]; B Murcott[1]; T Kikuchi[2]; V Hunt[1];
[1] University of Bath, UK; [2] University of Miyazaki, UK

Small RNAs (sRNAs) are short non-coding RNAs that regulate more than 30% of gene expression associated with chromatin structure, mRNA translation and transposable element activity via post-transcriptional gene silencing. Although sRNAs were first discovered in the free-living nematode *Caenorhabditis elegans*, little is known about their role in parasitic nematodes. The gastrointestinal parasitic nematode *Strongyloides*, like most other nematode species outside of clade V, have lost the PIWI pathway involved in piRNA production and

suppression of transposable element activity. Here, we investigated the role of endogenous sRNAs in the gastrointestinal parasitic nematode *Strongyloides ratti* and compared sRNAs expressed in genetically identical adult parasitic and free-living life cycle stages. We identified two different classes of small-interfering RNAs (siRNAs); a class of 21-22 nucleotide-long siRNAs with a 5' uracil (21-22Us) and a 5' monophosphate modification, as well as a class of 27 nucleotide-long siRNAs with either guanine or adenine at the 5' end (27GAs), and a polyphosphate 5' modification. We found that unlike the 27GAs that were associated with both the parasitic and free-living stages, 21-22Us were specifically expressed in the parasitic stage. Both 21-22Us and 27GAs were largely targeting a diverse set of transposable element sequences within the X-chromosome. Our results suggest that distinct classes of sRNAs are associated with parasitism or features associated with the parasitic life cycle and that these sRNAs are involved in regulating the activity of transposable elements.

IDDO IV - (Conference room 2)

13:30 (40 mins)

Reflections on the achievements of 10 years of the WWARN global malaria clinical platform*A23174*

Presenter: **Sir Prof. Nicholas White**, *Oxford University*

The Worldwide Antimalarial Resistance Network grew out of a collective wish by malaria researchers to share data, exchange information, standardize methods and pool resources. WWARN was launched ten years ago with four modules; clinical studies, in-vitro susceptibility, molecular genotyping, and pharmacology. WWARN was supported initially by funding from the Bill and Melinda Gates foundation. Early efforts were directed towards gaining the confidence of the malaria community to share data and methods so that individual patient data meta-analyses could be conducted. This grew gradually and today WWARN now has data from over two thirds of all post-registration randomised trials of antimalarial drugs. This has enabled large and definitive assessments of the determinants of antimalarial therapeutic efficacy and characterization of tolerability and safety at an unprecedented scale. These analyses have changed recommended antimalarial drug dose regimens. The evolution and geographic spread of antimalarial drug resistance have been mapped in a living and constantly updated dynamic website. WWARN has also generated methods and approaches for the malaria community. The platform and the methodologies developed in WWARN enabled formation of a broader organization addressing other neglected diseases; the infectious diseases data observatory (IDDO).

Cell and Molecular Biology and Biochemistry III - (Conference room 1)

21-June-2021, at 15:00 (30 mins)

Wolbachia symbiont genomes and their transcriptional regulation in filariae and ectoparasites*A23145*

Presenter: **Dr Benjamin Makepeace**, *Reader, University of Liverpool*

B Makepeace[1];
[1] University of Liverpool, UK

Wolbachia, an intracellular alpha-proteobacterium, is the most prevalent symbiont of animals on the planet, infecting more than half of terrestrial arthropods and a small proportion of parasitic nematodes. Notably, it is very common in arthropods of medical and veterinary importance, including biting Diptera, lice, bedbugs, fleas and mites, as well as approximately half of filarial nematode species. *Wolbachia* can induce detrimental reproductive phenotypes, such as cytoplasmic incompatibility and male killing, whereas in a minority of hosts it appears to be mutualistic. Its remarkable ability to block pathogen transmission in transinfected insect vectors has stimulated an explosion of basic and applied research on *Wolbachia*, especially the parasitic strains of the A and B clades, but the wider diversity of this highly plastic symbiont remains neglected. Here, I explore the genomic features of some newly characterised clades from filarial nematodes, fleas and bedbugs and reveal how they threaten to raise more questions than answers. I also consider how technical advances are allowing transcriptional regulation in *Wolbachia* to be explored in unprecedented detail and depth, and present new findings on the dynamic transcriptome of two *Wolbachia* strains in use for vector-borne disease control as they are exposed to stressors *in vitro*. Finally, our culture and genome sequencing of a putatively mutualistic *Wolbachia* from cat fleas provides exciting opportunities to dissect the regulation of vitamin biosynthesis under a variety of conditions.

15:30 (15 mins)

The role of VEX complex proteins in the insect to mammalian host transition of Trypanosoma brucei*A23386*

Presenter: **Dr Karinna Rubio-Peña**, *Post-doctoral researcher, Institut Pasteur*

K Rubio-Peña[1]; E Thion[1]; A Dujeancourt-Henry[1]; A Crouzols[1]; B Rotureau[1]; L Glover[1];
[1] Institut Pasteur, France

The Trypanosoma (T) brucei life cyclealternates between the tsetse fly vector and the mammalian host. In the insect, *T. brucei* undergoes several developmental stages until it reaches the salivary gland and differentiates into the metacyclic form (MCF), which is capable of infecting mammals. Mammalian infectivity is dependent on expression of the metacyclic variant surface glycoprotein (m*VSG*) genes in the mature metacyclic. Recently, VEX complex proteins had been identified as essential for monoallelic *VSG* expression in *T. brucei* bloodstream form, however, monoallelic expression during metacyclic differentiation is poorly understood. To better understand the transition to mature metacyclics and the control of *mVSG* expression we are studying the role of the VEX complex in this process. We show that modulating VEX1 expression leads to a dysregulation of monoallelic mVSG expression during MCF differentiation. Additionally, following both *in vivo* and *in vitro* metacyclic differentiation, we observed a relocation of VEX1, suggesting a role for VEX1 in *mVSG* expression. Additionally, preliminary results show that constitutive over-expression of VEX1 in the pleomorphic Antat1.1 cell line, promotes colonization of the tsetse fly salivary gland. This suggest a role for the VEX complex in the metacyclic differentiation process and their capacity to become infectious to the mammalian host.

15:45 (15 mins)

Investigating mitochondrial glycosylation in the African Trypanosome*A23445*

Presenter: **Dr Samuel Duncan**, *Postdoctoral Researcher, University of Dundee*

S M Duncan[3]; S Damerow[4]; G Bandini[5]; S Vaughan[1]; M A Ferguson[2];
[1] Department of Biological and Medical Sciences, Oxford Brookes University, Oxford, UK; [2] Wellcome Trust Centre for Anti-Infectives Research, School of Life Sciences, University of Dundee, UK; [3] The University of Dundee, UK; [4] Richter-Helm BioLogics GmbH, Germany; [5] York Biomedical Research Institute, UK

Trypansoma brucei is a protozoan parasite that infects humans and cattle via a tsetse fly vector. Key to parasite survival during progression through this complex life cycle is the expression of cell surface and endocytic pathway glycoproteins, modified with glycosylphosphatidylinositol (GPI) membrane anchors and/or N-linked oligosaccharides. The biosynthesis of guanosine 5′-diphospho-β-L-fucose (GDP-Fuc), the activated donor for fucose, has been shown to be essential in *Trypanosoma brucei*. Fucose is a common constituent of eukaryotic glycan structures, but it has been rarely found in trypanosomatid glycoconjugates. A single putative *T. brucei* fucosyltransferase (TbFUT1) gene was identified in the genome. Unexpectedly, TbFUT1 was localized in the mitochondrion of *T. brucei*, suggesting that this kinetoplastid parasite possesses unprecedented mitochondrial fucosyltransferase activity. Loss of TbFUT1 by conditional knockout (cKO) in bloodstream form (BSF) mutants results in growth arrest and the accumulation of dyskinetoplastid cells lacking mitochondrial kinetoplast DNA (kDNA) yet has no pronounced effect on mitochondrial volume or structure as assessed by electron microscopy. Loss of TbFUT1 results in loss of mitochondrial membrane potential ($\Psi\Delta m$) and collapse of the monomeric and dimeric forms of the F_OF_1-ATP synthase complex, as assessed by Native PAGE and Western blot analysis. However, loss of both kDNA and TbFUT1 expression is tolerated in BSF TbFUT1 cKO parasites upon mutation of the F1-γ subunit to enable $\Psi\Delta m$ maintenance by F_1 activity independent of F_O. Interestingly, *in vitro* assays indicate that a TbFUT1 preferred substrate is the Galβ1-3GlcNAc disaccharide, indicating that further glycosyltransferases (GTs) may be active in the mitochondria of *T. brucei*. Indeed, the mitochondrial localisation of two putative TbGTs was confirmed by C-terminal epitope tagging, and RNAi of their respective transcripts caused growth arrest, suggesting their functions may lie upstream of TbFUT1. We aim to further investigate the function of mitochondrial glycosylation by identifying the substrate(s) of TbFUT1 and characterising the activity of the remaining, putative mitochondrial TbGTs.

16:00 (15 mins)

p197 as the missing link between the outer mitochondrial membrane and the basal body in T.brucei*A23158*

Presenter: **Ms Salome Aeschlimann**, *PhD, University of Bern*

S Aeschlimann[2]; A Kalichava[1]; B Schimanski[2]; T Ochsenreiter[1]; A Schneider[2];
[1] Institute of Cell Biology, University of Bern, Switzerland; [2] Department of Chemistry, Biochemistry and Pharmaceutical Sciences, Bern, Switzerland

Basal bodies (BB) are highly conserved essential structures throughout the eukaryotic tree of life. In trypanosomes the basal body not only serves as the microtubule organization center but also as the base of the flagellum and the anchoring point of the tripartite attachment complex (TAC). The TAC is a unique structure essential for the correct segregation of the replicated kinetoplast DNA (kDNA). It reaches via the exclusion zone filaments (EZFs) from the BB to the mitochondrial outer membrane (OM), spans both mitochondrial membranes and finally connects to the kDNA in the mitochondrial matrix.

How this complex attaches itself to the BB, how its assembly is orchestrated as well as its precise architecture are not fully understood yet. In order to investigate these questions, we focused on the TAC component p197, which is the subunit most proximally localized to the BB known so far. We generated a cell line which exclusively expresses a p197 variant that is both C-terminally tagged with an HA-epitope and N-terminally with a c-Myc epitope. The cell line was viable indicating that the double tagged p197 is functional. Using super resolution expansion microscopy this allows us to precisely localize both the N- and the C-termini of the p197 molecules within the TAC structure. The result shows that p197 binds to both the mature BB and the pro BB with its C-terminus. More precisely it localizes adjacent to SAS6, the cartwheel protein of the mature and the pro BB. Interestingly however the N-terminus of p197 does not localize to the BB but to an area close to the mitochondrial OM. p197 is predicted to have an alpha helical structure. Should this be case the protein could theoretically span a distance of more than 250nm, which is much more than would be required to connect the basal body to the OM in trypanosomes. To further investigate whether p197 indeed forms this connection several deletion mutants of p197 were generated. Both C- and N-terminal truncations are nonfunctional, yet able to correctly localize. Moreover, the N-terminal truncation of p197 binds to both the mBB and the pBB, as expected, whereas the C-terminal truncation of the protein behaves like a mitochondrial protein in biochemical assays, and therefore most probably binds to one of the OM components of the TAC. Altogether, our results demonstrate that surprisingly the exclusion zone filaments of the TAC are made up of a single large molecule, p197.

2021 Wright Medal Lecture - (Conference room 1)

22-June-2021, at 10:00 (45 mins)

Understanding the survival tricks of parasite surfaces*A23068*

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

The surface of a parasite lies at the front line of its interaction with its mammalian host. Here are located proteins which help parasites to take up nutrients, or to interact with invariant receptors, during processes such as invasion of erythrocytes by malaria parasites. But these parasite molecules are also under attack from components of the mammalian immune system. They therefore diversify into large families and/or evolve the ability to bind to human immune receptors and modulators to avoid causing detection and immune clearance of the parasite. In this talk, Matt will discuss how molecular insights reveal some of the tricks which these parasite surface proteins use to help their parasite to survive.

Drugs, Vaccines and Disease Control I - (Conference room 1)

22-June-2021, at 11:00 (30 mins)

An integrated omics approach for Fasciola hepatica vaccine target identification*A23070*

Presenter: **Dr Krystyna Cwiklinski**, *Research Fellow, National University of Ireland, Galway*

K Cwiklinski[1];
[1] National University of Ireland, Galway (NUI Galway), Ireland

Fasciolosis caused by the liver fluke *Fasciola hepatica* is an economically important disease of people and their livestock worldwide, affecting between 2.4 to 17 million people and more than 300 million animals (cattle, sheep and goats). Control is currently reliant on the use of drugs, with triclabendazole being the current drug of choice as it kills all developmental stages. However, the emergence of drug resistant parasites is now a global concern. Novel approaches need to be developed for the control of fasciolosis and amongst these vaccines would be considered a high priority.

The ongoing effort to develop a liver fluke vaccine has been greatly enhanced by the major step-change advances in our knowledge of liver fluke biology facilitated by the availability of large sequencing datasets from genomic, transcriptomic and proteomic analyses. In-depth molecular analyses of the juvenile stages responsible for early, acute infection that have been previously difficult to study can now be performed. These studies have identified several molecules, including proteases, protease inhibitors and anti-oxidants, critical for this stage of the parasite life cycle, as potential targets for liver fluke control strategies. These molecules are the current focus of our *F. hepatica* vaccine development strategy, where we are exploring combination subunit vaccines, using various recombinant proteins known to be important for parasite invasion and survival. The efficacy of these vaccine cocktails has been assessed in several sheep vaccine trials in UK, Ireland and Spain. These studies have highlighted the need for reproducible studies using large numbers of animals due to the inherent variability in sheep vaccine trials.

Towards Gender and Racial Equality in Science I - (Conference room 2)

11:00 (25 mins)

Picture a Parasitologist *A23064*

Presenter: **Prof Debbie Smith**,

tba

11:25 (25 mins)

Building gender equity from the bottom up: the rise and essence of parasitology communities*A23202*

Presenter: **Dr Elena Gomez-Diaz**, *CSIC*

E Gómez-Díaz[1];
[1] CSIC, Spain

Women scientists struggle and face many barriers, biases and stereotyping throughout their careers that undermine their career progression and success. These also apply to women in parasitology and global health-related fields including malaria, and are more severe in low and middle income countries. The lack of women leadership in malaria-related research, implementation and policy, threatens progress towards disease elimination. This talk focuses on how building communities of women represents an effective and efficient bottom-up approach to fight gender inequalities. The women in malaria community was created in 2018 to visibilize, empower, connect, and support (through training and mentoring) women scientists in the field. As a culmination of the rise and essence of WiM, the community came together for its first virtual conference this year with an all-women line up of organizers, presenters, and chairs. I will end up outlining what that conference achieved, and which are the future challenges of the WiM community.

Drugs, Vaccines and Disease Control I - (Conference room 1)

11:30 (15 mins)

Disparities in drug sensitivity of T. congolense and brucei group trypanosomes is related to differences in adenosine transporters and aquagyceroporins *A23455*

Presenter: **Mr Marzuq Ungogo**, *PhD student, University of Glasgow*

M A Ungogo[3]; M J Natto[1]; G D Campagnaro[4]; A H Alghamdi[2]; H P de Koning[1];
[1] Institute of Infection, Immunity and Inflammation, University of Glasgow, UK; [2] Institute of Infection, Immunity and Inflammation, University of Glasgow, United Kingdom, UK; [3] Institute of Infection, Immunity and Inflammation, UK; [4] Institute of Infection, Immunity & Inflammation, University of Glasgow, UK

Control ofAfrican Animal Trypanosomiasis (AAT) is seriously undermined by the challenge of drug resistance. *Trypanosoma brucei*, one of the three species that cause AAT, has been extensively studied, and the mechanism of drug resistance in this species depend mostly on mutations in transmembrane transporters that import the drugs. However, advances in molecular parasitology have revealed enormous genetic differences between *T. brucei* and other animal trypanosomes especially *T. congolense*. Thus, there is need to understand the genetic and molecular basis of drug resistance in *T. congolense* in order to aid rational drug design and development and verify whether the *brucei* models apply. Drug sensitivity assays showed that the EC_{50s} of diminazene aceturate and melarsominein *T. congolense* were 3 and 20 times higher than in *T. brucei*, respectively. In addition, *T. congolense* was 151 times less sensitive to pentamidine and 296 times

resistant to suramin relative to *T. brucei.* It is hypothesised that lack of authentic orthologues of some *T. brucei* transporters (TbAQP2, TbAT1, and a lysosomal MFST) is responsible for low sensitivity to these drugs in *T. congolense*. Expression of *T. brucei* AQP2 (TbAQP2) in *T. congolense* resulted in an approximately 8-fold increase in sensitivity to pentamidine and 6-fold increase in sensitivity to melarsomine compared to wild type. The *T. congolense* + TbAQP2 also displayed a higher rate of uptake of [^{3}H]-pentamidine, as well as faster lysis when exposed to melarsomine. On the other hand, *T. congolense* clones expressing *T. brucei* P2 adenosine transporter (TbAT1) show a 30-fold increased sensitivity to melarsomine and a 12-fold increase in sensitivity to diminazene, pentamidine and isometamidium. In addition, there is a higher uptake of [^{3}H]-diminazene and [^{3}H]-pentamidine in *T. congolense* clones expressing TbAT1 compared to the wild type. This indicates that differences in transporters between *Trypanosoma* species play important role in differential sensitivity and should be considered in the development of new drugs for AAT.

11:45 (15 mins)

Deazapurine nucleoside analogues for the treatment of Trichomonas vaginalis*A23452*

Presenter: **Prof Harry De Koning**, *Professor of Biochem. Parasitol., University of Glasgow*

M J Natto[3]; F Hulpia[4]; Y Miyamoto[2]; L Eckmann[2]; S Van Calenbergh[4]; **H P De Koning**
[1] University of Glasgow , UK; [2] Department of Chemistry and Biochemistry, University of California San Diego, United States; [3] University of Glasgow, Institute of Infection, Immunity & Inflammation,, UK; [4] University of Ghent, United States

Deazapurine nucleoside analogues for the treatment of *Trichomonas vaginalis*

Natto MJ, Hulpia F, Miyamoto Y, Eckmann S, Van Calenbergh S, De Koning HP

Trichomoniasis is an important sexually transmitted infection, caused by the human-only protozoan parasite *Trichomonas vaginalis*. Treatment of this disease is essentially by metronidazole although in recent years the related nitro-heterocyclic compound tinidazole is also increasingly used. However, resistance to either drug implies cross0resistance to the other, owing to their identical mechanism of action. In an effort to identify new anti-trichomonal treatments, we scaled-up our resorufin based fluorescence assay for medium throughput, using 386-well plates, automated liquid handling and improved micro-aerobic incubation conditions. A number of compound series were screened and a series of 7-deaza-7-substituted adenosine analogues displayed by far the most promising activity ibn vitro. The structure activity relationship was systematically explored through the synthesis of additional nucleoside analogues and the most promising lead, TH1012 displayed an EC_{50} of 0.035 ± 0.007 µM compared to an EC_{50} ~0.3 µM for metronidazole. Fluorescence microscopy with DAPI revealed that TH1012 disrupted proper nuclear division n trophozoites while growth curves showed almost immediate action on cell density in culture. TH1012 was curative in a mouse model of Tritrichomonas foetus, applied topically, despite being much less active against this species *in vitro*. We believe that these adenosine analogues have genuine promise as anti-trichomonal agents and are currently studying *T. vaginalis* adenosine transporters and attempting to create a TH1012-resistant cell line for studies of the mechanism of action.

Towards Gender and Racial Equality in Science I - (Conference room 2)

11:50 (20 mins)

Creating resources to increase gender equity in Parasitology*A23061*

Presenter: **Dr Elizabeth English**, *University of Pennsylvania*

E D English[1];
[1] University of Pennsylvania, United States

Despite efforts to address gender equality and barriers to career progression of women in science, women remain underrepresented in positions of power and decision-making across science, technology, engineering, and mathematics (STEM) fields. Even with their contributions to groundbreaking research, women in STEM remain underrepresented among citations, editorial staff, and invited speakers. While closing the gender gap will require solutions across institutional and global levels, personal efforts towards addressing inequity can be advantageous. To address the underrepresentation of women in the role of invited speakers at parasitology conferences, seminars, and panels, I created and maintained a database of women who study a variety of topics within the field of parasitology. This “Women in Parasitology” database includes searchable keywords to identify areas of expertise, location, and contact information to facilitate connecting with potential invited speakers. To date, this database contains over 600 women from over 40 countries, including graduate students,

research technicians, postdocs, staff scientists, and group leaders. To increase visibility of this resource, I used social media, specifically twitter, to reach members of the parasitology community. The “Women in Parasitology” twitter account (@WiParasitology) has more than 3,500 followers and highlights new and exciting parasitology research conducted by women around the world. Additionally, this account spreads the news of job openings and funding opportunities for women and historically excluded racial and ethnic groups. Most recently I have also implemented a “Tuesday Takeover” program to allow women to increase the visibility of their own research by “taking over” the “Women in Parasitology” twitter account for a day. It is my hope that the efforts of the “Women in Parasitology” community will help increase the representation of women at conferences and seminars within the field of parasitology as we strive towards gender equity in STEM.

Drugs, Vaccines and Disease Control I - (Conference room 1)

12:00 (15 mins)

In vitro analysis of the effects of acetaminophen, ibuprofen and aspirin on motility of female adult Onchocerca volvulus worms *A23381*

Presenter: **Miss Rhoda Antwi**, *Researcher, University of Energy and Natural Resources*

K B Otabil[1]; R Antwi[1]; P Nyarko[1]; R Kyei[1]; J Ameyaw[2]; J G Bamfo[3]; H D Schallig[4];
[1] University of Energy and Natural Resources, Ghana; [2] Happy Family Hospital, Ghana; [3] Tain District Hospital, Ghana; [4] University of Amsterdam, Ghana

In view of the very ambitious global timelines for elimination of onchocerciasis in 2030, the search for alternative antifilarials cannot depend on drug development from scratch, and repurposed drugs offer cheaper and faster alternatives. Previous studies had demonstrated the presence and potential expression of amidase, an enzyme that can be targeted by repurposed analgesics, in Onchocerca volvulus worms. The aim of this study was to determine the effects of acetaminophen, ibuprofen and aspirin on the motility of adult O. volvulus worms. In total, thirty (30) female O. volvulus worms were exposed to acetaminophen, ibuprofen and aspirin in concentrations of either 5mg/ml, 2.5mg/ml, 1.25mg/ml, 0.63mg/ml and control in duplicates. Worm motility was observed and recorded using the WormAssay software and a darkfield imaging apparatus starting on day 2 of incubation and ending on day 8. Acetaminophen, ibuprofen and aspirin inhibited O. volvulus motility by 2-fold compared to control in the first 24 hours of drug exposure. However, an extended exposure of the worms to these test drugs rather improved the motility of the worms. The study has demonstrated that a 24-hour exposure of O. volvulus worms to the analgesic drugs studied, results in significant inhibition in worm motility when compared with the control group, but extended duration of exposure led to an enhancement in motility of the previously immobile worms. This finding supports the idea that aspirin and ibuprofen may have some longevity enhancing properties. Further research on the utility of these analgesics as possible antifilarial drugs is thus warranted

Drugs, Vaccines and Disease Control II - (Conference room 1)

22-June-2021, at 13:00 (30 mins)

Challenges in combining drugs, vaccines and other helminth control tools in livestock under climate change*A23209*

Presenter: **Prof Eric Morgan**, *Queen's University Belfast*

Anthelmintic resistance is now taking a serious hold on livestock farms, especially in grazing ruminants. This parlous situation has accelerated research into alternative control tools, including vaccines, selective breeding, bioactive plants (as mixed species swards and feed supplements), biological control (mainly nematophagous fungi), and more. While results are promising in some cases, performance is variable and unlikely to provide like-for-like replacements for anthelmintics, rather requiring strategic and complementary use. The bewildering array of options poses a challenge for advisors, and for researchers who are developing new control tools and seeking to contextualise their likely impact; all the more so given changing epidemiological patterns under climate warming. This presentation explores how novel control tools, and interactions between them, could affect the future of helminth management on farms, and how increasingly accessible computer models might help researchers, farm advisors and farmers to navigate the complex new world of worm control.

Towards Gender and Racial Equality in Science II - (Conference room 2)

13:00 (25 mins)

Centering Diverse Voices and Grappling with Racial Inequities in Parasitology*A23060*

Presenter: **Prof Regina Cordy**, *Assistant Professor, Wake Forest University*

R J Cordy[1];
[1] Wake Forest University, United States

During the fall of 2020, several panel discussions were held on online platforms to highlight the perspectives of Black parasitologists. In this session, I will summarize some of the themes raised during three of these such discussions, and will illustrate several examples of strategies that can be used to enhance the equality and diversity within the academic field of parasitology.

13:25 (20 mins)
WOMEN IN SCIENCE: THE PATH I FOLLOWED AND WHY WE STILL NEED TO DISCUSS GENDER EQUALITY IN BRAZIL *A23063*

Presenter: **Prof SANTUZA MARIA Teixeira**, *FEDERAL UNIVERSITY OF MINAS GERAIS*

In my presentation I will discuss the changes that have occurred (and that have not!) in Brazil regarding the participation of women in science. Although some progress towards gender equality has occurred, two main limitations are still in place. Firstly, even though the proportion of women researchers in Brazil is higher than the global average, gender equality has not improved in the fields of Engineering, Math and Physics. Secondly, gender equality has not changed significantly in the past 20 years when the upper levels of the academic/ scientific careers are considered. Based on my own experience, I listed seven main attitudes that have helped me and that need to be reinforced if we want to support young women scientists: (1) having early/deep exposition to Science, starting in high school; (2) finding women role models early on in your career and carefully select the type of mentors you should listen to; (3) planning family life together with your career plan: finding the right time to have kids is essential for a woman scientist to be able to experience the best of both worlds; (4) finding good advices that can help you become a group leader as soon as you create your own lab; (5) exercising good mentorship abilities with your students, both males and females; (6) finding different strategies for networking/collaborations so you can interact with top level scientists and, (7) finding a good balance between research, teaching and administration duties while moving up the academic ladder.

Drugs, Vaccines and Disease Control II - (Conference room 1)

13:30 (15 mins)
Understanding the structure and function of Fatty Acid Pathway proteins of Leishmania major to identify potent anti-leishmanials*A23516*

Presenter: **Ms Chetna Dhembla**, *PhD Scholar, University of Delhi, South Campus*

C Dhembla[1]; M Sundd[2]; S Kundu[1];
[1] University of Delhi, South Campus, India; [2] National Institute of immunology, India

Leishmaniases imposes devastating impacts on world's population. The increasing prevalence of drug resistance, necessity for long-term treatment regime, unavailability of functional drugs, the related expenditure, and the growing number of immuno-compromised individuals, due to coinfection of HIV underscores the need for new drugs as well as drug targets. Proteins of the fatty acid biosynthetic pathway (FAS) are validated drug targets in pathogenic bacteria and certain viruses. Likewise, this pathway has been speculated as a suitable target against parasite infections. The FAS pathway is highly active in blood stream stage (virulent stage) of the parasite and also found to be altered in the drug resistant strains, directly associating it with virulence and pathogenesis of the disease. Moreover, being distinct from the counterpart mammalian host makes the fatty acid pathway proteins as viable and attractive drug targets for emerging therapeutics.

Genome sequencing has led to the discovery of Type II Fatty acid synthesis pathway in *Leishmania*. An indispensable enzyme of the pathway is 4' phosphopantetheinyl transferase (PPT) which catalyzes the transfer of 4'-phosphopantetheine arm from Coenzyme A to the conserved serine residue of the Acyl carrier protein. Phosphopantetheinyl transferase from other pathogens viz *M. tuberculosis, P. aeroginosa* have been shown to be important for the survival and pathogenecity of the microorganism. Since, *Leishmania* genome encodes a

single PPT, it can act as a potential drug target and the understanding of the PPT as well ACP proteins may lead to the design of novel therapeutics against the deadly disease leishmaniasis.

Thus, the present study involves biophysical (Fluorescence, Circular Dichroism Spectroscopy) and biochemical characterization (Native PAGE, C18 reverse phase HPLC, Surface Plasmon Resonance) along with structure determination (X-ray crystallography and Nuclear Magnetic Resonance) of 4' phosphopantetheinyl transferase (PPT) and its substrate Acyl carrier protein (ACP) of the type II fatty acid pathway of *Leishmania*. Followed by insights into the interaction interface of both the proteins. To speed up the search of a novel inhibitor the study also focuses on exploring the current state-of-the-art of drug repurposing strategies by screening small molecule chemical libraries as well as synthesized compounds against the *Leishmania donovani* promastigotes, axenic amastigotes and intramacrophagic stages of the parasite followed by calculation of the IC_{50} values and determining the cytotoxic effects of the molecules.

In future the hits obtained from whole cell based screening can be evaluated against the characterized fatty acid pathway proteins using in vitro enzymatic assays to determine the specific target of these molecules. We also aim to take forward these inhibitors to animal models of Leishmaniasis.

13:45 (15 mins)

Pan-Phylum Characterisation of Helminth Endocannabinoid Signalling Systems*A23306*

Presenter: **Miss Bethany Crooks**, *PhD student , Queenâ€™s University Belfast*

B Crooks[1]; D McKenzie[1]; M Castelletto[2]; N J Marks[1]; A Maule[1]; E Hallem[2]; A Mousley[1]; L Atkinson[1];
[1] Queen's University Belfast, UK; [2] University of California, United States

Parasitic helminths are responsible for a range of debilitating neglected tropical diseases (NTDs) and agricultural infections, inflicting a significant global burden on human, plant and animal health. Overreliance on a handful of frontline anthelmintics has accelerated the threat of drug resistance, highlighting an urgent need for novel drug target identification and validation. Endocannabinoid signalling (ECS) is currently a hot topic in vertebrate medicine where ECS therapeutics are becoming attractive options for the treatment of many conditions. Our knowledge of helminth ECS systems is limited; in nematodes data is primarily derived from the model species *Caenorhabditis elegans*, where the ECS appears to modulate several facets of neurobiology (e.g., motility, growth, lifespan and fertility). Most interestingly, homologs of the mammalian EC G-protein coupled receptors (EC-GPCRs) CB1 and CB2 appear absent in nematodes including *C. elegans*, instead the nematode-specific EC-GPCRs NPR-19 and NPR-32 have been implicated in nematode EC signalling. We have no information on ECS system presence or function in flatworms. To broaden our understanding of helminth ECS systems and identify putative novel targets for helminth control we employed publicly available genome and transcriptome data and *in silico* bioinformatics approaches to examine the presence, conservation and life-stage specific expression profiles of ECS pathway proteins (biosynthesis/degradation enzymes and EC receptors) in all helminths that possess genome/transcriptome information (93 nematode spp, 33 flatworm spp (134 and 44 genomes respectively). The data demonstrate that: (i) Nematode ECS pathways exhibit increased complexity in comparison to vertebrate systems; (ii) ECS signalling effectors display broad patterns of conservation across phylum Nematoda and Platyhelminthes, including in therapeutically and agriculturally important species; (iii) Flatworms possess a putative novel EC-GPCR that is broadly conserved pan phylum (present in 82% of 33 flatworms investigated), has key EC-binding domains and displays ~40% homology to vertebrate CB1; (iv) EC-effectors are expressed in therapeutically relevant parasitic nematode life stages (i.e. infective larval and intra-mammalian life stages) suggesting a role for the ECS in parasite host-seeking, invasion and infection biology. These data have informed our understanding of the complexity of helminth ECS pathways and will seed follow-on functional studies underpinning ECS drug target validation in parasitic helminths of importance.

14:00 (15 mins)

Repurposing trypanocidal drugs to tackle amoebic gill disease in Atlantic Salmon*A23536*

Presenter: **Dr Bachar Cheaib**, *Post-doctoral Reasearch Associate, University Of Glasgow*

B Cheaib[1]; L Morrison[4]; P McGinnity[5]; N Ruane[5]; S Martin[6]; M Cook[7]; R Williams[2]; F Hernandez[2]; J Archibald[8]; M Barrett[4]; M S Llewellyn[3];

[1] University of Glasgow , UK; [2] University of Aberdeen, UK; [3] Institute of Biodiversity, Animal Health and comparative Medicine, University of Glasgow, UK; [4] Institute of Infection, Immunity & Inflammation, University of Glasgow, UK; [5] Marine Institute, Newport, Ireland; [6] University of West Scotland, UK; [7] CSIRO Agriculture and Food, Queensland Bioscience Precinct, Brisbane, Australia; [8] Dalhousie University, Halifax, Canada

Amoebic gill disease (AGD), caused by Neoparamoeba perurans, is as a threatening disease in salmonid aquaculture associated with substantial annual losses (20%). The amoeba N. perurans has a unique cellular and evolutionary biology that can readily exploited given the right molecular tools. Enclosed in the cytoplasm N. perurans hosts an endosymbiotic aflagelate kinetoplastid called Perkinsela or Perkinsela-Like Organism (PLO). Genome sequence of this indicates that the basic physiology of the kinetoplastid endosymbiont contains many of the same biochemical features as those found in other kinetoplastid pathogens of man and domestic livestock (Trypanosoma brucei sp., T. cruzi, Leishmania sp.), as well as a high level of metabolic interdependence between host and symbiont. After Omics characterization of the functional associations between host and its endosymbiont, our existing state-of the-art drug discovery pipeline for kinetoplastids, the aim of this project is to test the potency of existing licensed and experimental drugs used against the kinetoplastid diseases for activity against N. perurans in culture, working on the hypothesis that inhibiting or killing the endosymbiont will lead to the death of its host. A candidate drug will then be tested for activity against amoebic gill disease in vivo. Drug residue accumulation in sediment samples at the trial site will be established to assay the potential environmental impact of therapeutant use. In addition to providing a much-needed new tool for aquaculture, our approach, which aims to repurpose drugs effective against neglected tropical disease but often too expensive to deploy, has the potential drive down their cost. Keywords: endosymbiosis, kinetoplastid, amoeba, amoebic gill disease, Omics

Diagnosis and Biomarkers I - (Conference room 1)

22-June-2021, at 15:00 (30 mins)

Metabarcoding and amplicon sequencing in helminth diagnostics and surveillance*A23534*

Presenter: **Prof John Gilleard**, *Professor , University of Calgary*

TBC

Schistosome Biology I - (Conference room 2)

15:00 (30 mins)

A non-ribosomal peptide pheromone controls male-induced female sexual development in schistosomes*A23167*

Presenter: **Dr Jim Collins**, *Associate Professor, UT Southwestern Medical Center*

J Collins[1]; R Chen[1]; J Wang[1]; E Ross[1];
[1] UT Southwestern Medical Center, United States

Schistosome egg production is the primary driver of morbidity due to infection, thus it is paramount that we establish a better understanding of the molecular mechanisms that control sexual development. Interestingly, female schistosomes require close physical contact with male worms to become sexually mature and to maintain the ability to produce eggs. Although this phenomenon was described nearly 100 years ago, the molecular mechanisms are unresolved. Here, we show that the transcription factor GLI1 is essential in male schistosomes to induce the expression of a non-ribosomal peptide synthetase (SmNRPS) expressed in ciliated neurons along the males ventral surface where the male worms interface with the female. Loss of either GLI1 or SmNRPS renders males incapable of inducing female sexual development. Using a combination of in vitro biochemistry and metabolomics, we find that SmNRPS produces a dipeptide exclusively in paired male worms and that this dipeptide is capable of stimulating virgin female sexual development in the absence of the males. Not only do these studies discover a novel flatworm pheromone and signaling molecule, they provide a molecular mechanism for male-induced female sexual development in schistosomes.

15:30 (15 mins)

Excretion patterns of Schistosoma mansoni circulating antigens CAA and CCA by adult male and female worms, using a mouse model and ex vivo parasite culture*A23331*

Presenter: **Miss Miriam Casacuberta Partal**, *PhD student, Leiden University Medical Center*

M Casacuberta Partal[1]; L van Lieshout[1]; A Van Diepen[1]; J C Sijtsma[1]; A Ozir-Fazalalikhan[1]; J P Koopman[1]; C J de Dood[1]; P L Corstjens[1]; G J van Dam[1]; C H Hokke[1]; M Roestenberg[1];
[1] Leiden University Medical Centre, Netherlands

Assays which enable the detection of schistosome gut-associated circulating anodic (CAA) and cathodic (CCA) antigen are increasingly used as a diagnostic tool on serum or urine of the host. However, very little is known about the excretion patterns of these circulating antigens in particular in relation to the sex and reproductive maturity of the parasite. Here we describe CAA and CCA excretion patterns by exploring a mouse model after exposure to male-only, female-only and mixed (male/female) *Schistosoma mansoni* cercariae. We found that serum and urine CAA levels, analysed at 3 weeks intervals, peaked at 6 weeks. Recovered worms were cultured for another 8 days after perfusion at week 14. Male parasites were found to excrete more circulating antigen than females, in the mouse as well as in culture. In mixed infections, serum CAA levels correlated better to the number of recovered worms than to eggs or *Schistosoma* DNA in stool. In culture, CAA levels were higher than CCA levels. This study confirms that CAA levels reflect worm burden and shows that CAA allows detection of low level single sex infections where no eggs are present.

Diagnosis and Biomarkers I - (Conference room 1)

15:30 (15 mins)

A novel immunoassay to measure human blackfly exposure in onchocerciasis endemic areas *A23421*

Presenter: **Dr Laura Willen**, *Post-doctoral researcher, University of Antwerp*

L Willen[2]; P Milton[3]; M G Basáñez[3]; V Dvorak[2]; F B Veriegh[4]; F T Aboagye[4]; B Idun[4]; M E Osman[5]; M Y Osei-Atweneboana[4]; O Courtenay[1]; P Volf[2];
[1] University of Warwick, UK; [2] Charles University, Czech Republic; [3] Imperial College London, UK; [4] Council for Scientific and Industrial Research Water Research Institute, Ghana; [5] National Centre for Research, Khartoum, Sudan

Background: Blackflies of the *S. damnosum sensu lato* (s.l.) complex are the main vectors of human onchocerciasis in Africa. Vector biting rates and heterogeneity in exposure to vector bites are important epidemiological determinants. To date, the only way to estimate blackfly biting rates and exposure patterns is by performing human landing catches (HLCs). Since this is a labour-intensive technique associated with ethical concerns, novel alternatives to measure blackfly exposure are required. We aimed to develop IgG- and IgM-based immunoassays to quantify human antibody responses to blackfly saliva in onchocerciasis endemic communities and to examine demographic patterns in human blackfly exposure using the measured anti-blackfly antibody responses.

Methods: Blackflies were collected by HLCs in an onchocerciasis-endemic area in Ghana from which 940 salivary glands were dissected. The salivary glands were used as antigen to develop two enzyme-linked immunosorbent assays (ELISA) to measure anti-*S. damnosum* s.l. salivary IgG or IgM antibodies. Also, blood samples from 958 people (aged 5 to 95 years) living in 4 endemic villages were collected. Samples from people living in Accra, a blackfly-free area, were used as negative controls together with samples from blackfly-free locations in Sudan. The relationship between anti-blackfly antibodies and village, sex, and age was investigated using generalized linear models.

Results: Both immunoassays were successfully developed and were able to differentiate negative controls from village residents. Overall, males showed a significantly lower IgG response than females. A significant decline in antibody response with increasing age was observed for both IgG and IgM responses. The decline in IgG appeared steeper for adult males than adult females.

Discussion/Conclusion: In the present study, human IgG and IgM immunoassays were successfully developed as a novel tool to quantify exposure to blackfly bites and better understand patterns of exposure. Anti-blackfly antibody responses were shown to differ between sexes and to decline with age. This trend has been previously observed for *Anopheles* mosquitoes, indicating an age-associated desensitization in areas with high biting pressures.

15:45 (15 mins)

Glycomic analysis of the filarial nematode Brugia malayi and characterization of anti-glycan antibody responses during infection. *A23293*

Presenter: **Ms Laudine Petralia**, *PhD student, Leiden University Medical Center*

L Petralia[1]; L Nguyen[1]; A Van Diepen[1]; C H Taron[2]; J M Foster[2]; C Hokke[1];
[1] Leiden University Medical Centre, Netherlands; [2] New England Biolabs Inc., United States

Around 75 million people worldwide are infected with filarial nematodes, responsible for lymphatic filariasis (LF) and other diseases causing chronic disablement. Elimination programs have resulted in a substantial reduction of the rate of infection in certain areas creating a need for sensitive and reliable diagnostic tools in order to establish a proper population surveillance, avoid LF resurgence and meet the World Health Organization 2030 NTD roadmap objectives. Glycans from parasitic helminths are emerging as potential antigens for use in diagnostic serological assays. Thus, we investigated the glycan repertoire of the filarial nematode *Brugia malayi* aiming to identify species-specific elements. Glycosphingolipid (GSL), N-linked and O-linked glycans were extracted from several *Brugia malayi* life-stages using enzymatic and chemical release. Glycans were purified and characterized using a combination of ultra-high performance liquid chromatography, mass spectrometry (MALDI-TOF-MS) and glycan sequencing techniques. Parasite GSL and N-glycans were printed onto microarrays so that the anti-glycan antibody response of the host during infection could be assessed. The comprehensive glycomic analysis of Brugia malayi revealed the presence of several antigenic motifs such as phosphorylcholine, widespread in filarial nematodes, and interestingly, some more specific components such as terminal glucuronic acid-containing glycans. In parallel, glycan microarray screening showed a preferential recognition of most glycan structures by immunoglobulin (Ig) G from *Brugia malayi* infected individuals, relative to uninfected donors. To evaluate the potential of glycans as diagnostic antigens, cross-reactivity with other filarial parasites, as well as differences in recognition for current and past infections were addressed. Finally, a longitudinal set of rhesus macaque plasma allowed us to study the dynamics of anti-glycan IgG and IgM responses during establishment of brugian filariasis.
Altogether, our work highlights a specific antibody response from the host to *Brugia malayi* N-linked and GSL-glycans that could be exploited as potential diagnostic markers to detect LF.

Schistosome Biology I - (Conference room 2)

15:45 (15 mins)

In vitro-matured schistosomes, a valuable tool for drug discovery and studying schistosome development*A23332*

Presenter: **Dr Helmut Haas**, ., *helminGuard*

H Haas[5]; S Haeberlein[2]; E Robb[1]; A G Maule[1]; M Sombetzki[4]; C G Grevelding[2]; G Schramm[3];
[1] Queen's University Belfast, UK; [2] Justus-Liebig-University Giessen, Germany; [3] Research Center Borstel, Germany; [4] University Medical Center Rostock, Germany; [5] helminGuard, Germany

Drug screening against *in vitro*-grown worms enables compound effects on the pathogen to be monitored in real time. Using a modified Basch protocol, *Schistosoma mansoni* larvae can mature *in vitro* into adults including pairing and deposition of vital eggs. Worms were exposed to compounds from various drug libraries to identify anti-schistosomal agents. Several compounds with functional, morphological and/or toxic effects on schistosomes were identified. The effects varied between different groups of drugs: there were early vs. late drug effects, hyperactivity vs. paralysis, shrinkage vs. extension, empty vs. filled guts, circular contractions vs. “ballooning” of the worms. The so far unknown anthelminthic effects of two approved drugs identified in this system were confirmed with *in vitro*-cultured *Fasciola hepatica* juveniles. This suggests that – similar to praziquantel – anti-schistosomal compounds may have a broader anthelminthic spectrum. *In vitro*-matured schistosomes were, moreover, used for studying schistosome development. Knockdown of a pairing-influenced and testis-preferentially-expressed G-protein-coupled receptor (GPCR) during growth from the somule to the adult stage prevented the production of spermatozoa, which suggests a role in sperm maturation. The knockdown of this GPCR (efficiency 60-80%) did not influence the proliferative activity of stem cells suggesting a blockade of other processes further downstream during cellular differentiation. Together, the use of *in vitro*-matured schistosomes is a valuable reductionist approach that – apart from contributing to the 3Rs concept by saving mammalian animal lives – facilitates drug screening and may help to unravel schistosome biology.

16:00 (15 mins)

Cell signalling during Schistosoma mansoni male-female interactions *A23198*

Presenter: **Miss Eman Shakir**, *PhD student, Kingston University*

E SHAKIR[1]; [3]; R Kirk[1]; [3]; G Rinaldi[2]; A J Walker[1]; [3];
[1] Kingston University, UK; [2] Wellcome Trust Sanger Institute, UK; [3] Kingston University, UK

Schistosomes are blood flukes that infect approximately 250 million people and kill more than 100,000 annually in Low and Middle-income countries. Unusual among parasitic flatworms, schistosomes are dioecious (separate sexes) with heterogametic females (2n=16, ZW), and homogametic males (2n=16, ZZ). The genome of *Schistosoma mansoni* encodes over 260 protein kinases, well conserved regulatory proteins through the evolution of eukaryotes. To understand protein kinase signal transduction and function during male-female interactions of *S. mansoni*, we investigated the temporal effects of excretory-secretory products (ESPs) produced by adult male worms over 20 h culture on protein kinase activities in female worms, and *vice versa*. Western blotting with anti-phospho tyrosine/serine/threonine antibodies revealed that the phosphorylation status of multiple proteins changed over 60 min in response to ESP molecules released from worms of the opposite sex. Exchange of male/female ESPs between groups of single sex worms resulted in a rapid activation of protein kinase pathways, particularly p38 mitogen-activated protein kinase (p38 MAPK) and extracellular signal-regulated kinase (ERK) pathways where activation was evident as early as 5 min. Phosphorylation (activation) of p38 MAPK and ERK was significantly attenuated by the inhibitors SB203580 and U0126, respectively. Immunofluorescence and confocal laser scanning microscopy revealed that the activation occurred throughout different tissues including the parasite tegument. In addition, the motility of the parasites was enhanced in response to opposite sex ESPs, and expectedly, the inhibition with SB203580 and U0126 for 1 h prior to exposure to opposite sex ESPs profoundly reduced worm motility. Using biotinylated-ESPs and fluorescence confocal laser scanning microscopy we observed that the adult male ESP bound to the surface membrane of female worms and *vice versa*. Finally, cell proliferation was investigated using Click-it EdU and Alexa Fluor staining. Whereas single sex adult worm in culture showed low levels of cell proliferation over six days, there was a striking cell proliferation increase in the testes, ovaries and surface layer of worms when exposed to opposite sex ESPs. The male/female ESPs were further investigated by proteomics and 896 and 469 proteins were identified in crude and extracellular vesicle-depleted preparations, respectively. To the best of our knowledge, this research represents the first report on male-female ESPs activating signal transduction in opposite sex adult worms and driving cell proliferation in both reproductive and somatic tissues. These findings may expose tentative targets to develop novel strategies for schistosomiasis control.

Diagnosis and Biomarkers I - (Conference room 1)

16:00 (15 mins)

Developmental and secretory regulation of microRNAs in an expanded Fasciola hepatica dataset *A23495*

Presenter: **Miss Caoimhe Herron**, *PhD Student, Queen's University Belfast*

C Herron[1]; E McCammick[1]; M Robinson[1]; A G Maule[1]; P McVeigh[1];
[1] Queen's University Belfast, UK

Fasciola hepatica is a ubiquitous veterinary parasite that costs the UK agriculture industry over £20 million annually, and a Neglected Tropical Disease pathogen in humans with over 90 million people at risk worldwide. Fluke control is threatened by resistance to four of the five available flukicides; improved understanding of fluke biology could lead to new therapies. Micro (mi)RNAs are non-coding RNAs proposed as therapeutic and diagnostic targets in biomedicine. While parasite miRNAs have attracted interest, in general, parasite miRNA complements remain poorly profiled. Here we describe an expanded set of *F. hepatica* miRNAs, and the first developmental profile of miRNAs in this species. Small RNA sequencing of fluke life stages, coupled with published data, identified a total of 151 mature miRNAs. We have used Locked Nucleic Acid based qPCR assays to profile expression of all of these across metacercariae, juvenile and adult tissue samples, as well as adult- and juvenile-derived extracellular vesicles (EVs). A total of 144 miRNAs were validated by qPCR, with 57 present in all life stages. Several miRNA were restricted to individual life stages including 11 specific to metacercariae and 13 specific to adults. These are the first data demonstrating the developmental importance of individual fluke miRNAs. 58 miRNAs were detected in EVs; we are currently establishing whether these are detectable in *in vivo* samples and performing in silico predictions of their potential host mRNA binding partners. These data will contribute to understanding of host parasite interactions and may lead to new diagnostic and therapeutic avenues for fasciolosis.

2020 Wright Medal Lecture - (Conference room 1)

23-June-2021, at 10:00 (45 mins)

The private life of malaria parasites: Strategies for survival & reproduction *A23115*

Presenter: **Prof Sarah Reece**, *Chair of Evolutionary Parasitology, University of Edinburgh*

Research in the Reece lab sits at the interface of parasitology, chronobiology and evolutionary ecology, motivated by the questions of "what makes a successful parasite" and "what are the evolutionary limits on their success"? Specifically, we investigate the strategies that parasites have evolved to cope with the challenges of their lifestyle, and exploit the opportunities it brings. Our research focuses on malaria parasites, which not only cause globally devastating infections in humans, livestock, and wildlife, but whose complex interactions with hosts and vectors can be manipulated and studied in controlled lab experiments. There is a great deal of research into the genetics, cellular and molecular biology, and immunology of these parasites, but conspicuously less from whole-organism, ecological, and evolutionary perspectives. Consequently, malaria parasites persist despite widespread and continuous efforts to eradicate them. Our research discovers surprising sophistication in parasite strategies for surviving in the host and for reproduction in mosquito vectors. These strategies include optimising the trade-off between transmission versus replication, optimising investment in each sex of transmission stages, and getting the timing of replication and transmission right. Understanding these strategies informs the search for the molecular mechanisms underpinning parasite phenotypes, can explain epidemiological patterns, and may uncover new approaches for interventions and how to make them as evolution-proof as possible.

Interactions with Hosts and Vectors - (Conference room 1)

23-June-2021, at 11:00 (30 mins)

Secreting and communicating: lessons from a parasite and vaginal bacterial commensals *A23437*

Presenter: **Dr Augusto Barbosa**, *The University of Auckland*

tbc

Schistosome 'omics' - (Conference room 2)

11:00 (30 mins)

Towards a chromosomal view of schistosome genome evolution *A23208*

Presenter: **Dr Matthew Berriman**, *Senior Group Leader, Wellcome Sanger Institute*

M Berriman[1];
[1] Sanger Institute, UK

It's more than a decade after the first draft genomes of Schistosomes were published. Although highly fragmented and incomplete, these gene catalogues provided a much-needed boost to the schistosomiasis research field. But their inaccuracies hampered data mining and large scale investigations of gene function and genome variation. Our group, along with several others, has continued to sequence and improve the schistosome reference genomes. Transformed by longer range sequencing and scaffolding approaches, we are getting close to the goal of full chromosomal sequences for all major schistosome species. Focussing on two major areas of our work, I will present an update on the *S. mansoni* reference genome and the preliminary stages of a broad exploration of the genomes of Schistosomatidae. In *S. mansoni*, both the Z and W chromosomes are resolved enabling the gene content of sex-specific regions to be explored. Across the genus, comparisons of high-contiguity genome assemblies are enabling us to define a "core schistosome" as well as explore differences that in some cases may represent adaptive changes in the evolution of different schistosome lineages.

11:30 (15 mins)

Life stage-specific glycosylation of schistosome-derived extracellular vesicles (EV) directs interactions of EV with lectin receptors on host cells *A23357*

Presenter: **Prof Cornelis Hokke**, *Professor of Glycobiology, Leiden University Medical Center*

M E Kuipers[2]; E N Nolte-'t Hoen[3]; K F Hoffmann[1]; H H Smits[2]; **C H Hokke**[2];
[1] Aberystwyth University, UK; [2] Leiden University Medical Centre, Netherlands; [3] Utrecht University, Netherlands

Glycans play essential roles in pathogen-host interactions. Larvae and adult worms from *Schistosoma mansoni* release distinct subsets of glycoconjugates as excretory/secretory (ES) products. Extracellular vesicles (EVs) are also among the ES products. We previously found that schistosomula-derived EVs are glycosylated and bind to human dendritic cells (hDC) via the C-type lectin receptor (CLR) DC-SIGN, leading to increased IL-10 and IL-12 release. Here, we investigated the glycosylation of EVs released by *S. mansoni* adult worms, compared this to schistosomula EVs, and addressed how glycans affect EV-host interactions via CLRs. EVs were obtained by ultracentrifugation from cultured *S. mansoni* parasites and purified with iodixanol density gradients. Isolated EVs were analysed by NTA and cryo EM showing that adult worm EVs have a different appearance and size distribution than schistosomula EVs, lacking the long thin filaments characteristically observed in the case of EV from schistosomula. N-glycan and lipid glycan content of EVs was determined by mass spectrometry. In contrast to schistosomula EVs, glycolipids could not be detected in the adult worm EVs. The most abundant N-glycans on the surface of adult worm EVs contained GalNAc-beta1–4GlcNAc (LacDiNAc, LDN) motifs, whereas the Gal-beta1–4(Fuc-alpha1–3)GlcNAc (Lewis X) motif dominated in the surface N-glycans of schistosomula EV. Other differences in EV glycosylation between the two life stages were observed by Western blot using anti-glycan mAbs. In line with these structural observations, the adult worm derived EV bind to cells that express macrophage galactose-type lectin (MGL), an LDN-binding CLR expressed on hDCs and macrophages, whereas schistosomula EV primarily interact with hDC via DC-SIGN. Overall, our observations suggest that specific glycosylation of EVs from helminths and from their different developmental stages plays a critical role in differential recognition of, and response to, helminth EVs by host immune cells.

Interactions with Hosts and Vectors - (Conference room 1)

11:30 (15 mins)

The intimate and evolutionarily conserved relationship between Trichomonas and Mycoplasma*A23541*

Presenter: **Mr Nick Bailey**, *PhD student, Newcastle University*

The anaerobic protozoan parasite Trichomonas vaginalis is the most common non-viral sexually transmitted disease, and the closely related species Trichomonas gallinae is an avian parasite of ecological and economic importance. T. vaginalis shares a strong clinical association with the independent sexually transmitted pathogen Mycoplasma hominis, and the uncultured bacterium Mycoplasma girerdii, with the latter association being an order of magnitude stronger. M. hominis has been shown to profoundly influence T. vaginalis growth, energy production and virulence-associated mechanisms. We aimed to investigate the molecular basis of symbiosis between T. vaginalis and Mycoplasma spp. through transcriptomic profiling. The results showed major shifts in parasite gene expression in response to the bacterium, including genes associated with pathogenesis and energy generation, providing a solid framework for further experimental characterisation. In addition, we will present evidence for a new undescribed Mycoplasma sp., related to M. girerdii, and associated with T. gallinae in the upper digestive tract of domestic pigeons. This new finding suggests a long-term association between Trichomonas and Mycoplasma spp. which has been conserved across evolutionary time and the host species barrier.

11:45 (15 mins)

What insect resistance against fungal biopesticides can teach us about G x E in host-pathogen interactions*A23515*

Presenter: **Dr Matthew Tinsley**, *Senior Lecturer, Stirling University*

M Tinsley[2]; R Mangan[1]; R Polanczyk[3]; L Bussiere[4];
[1] University of Stirling, UK; [2] Stirling University, UK; [3] Universidade Estadual Paulista, UK; [4] University of Gothenburg, Sweden

Pathogens frequently place strong selection on host populations to evolve resistance. Nevertheless, natural host populations frequently contain considerable genetic variation for pathogen defence traits. This raises fundamental questions about what factors maintain this genetic variation, and in some applied settings demands understanding of how this evolutionary potential can be managed.< Insect pests represent an ever-present threat to agricultural production. Farmers are increasingly adopting biological pesticides formulated from the pathogens of insects to enable a move away from ecologically damaging chemical insecticides. However, as biopesticide use increases, so does selection pressure on target insects to evolve resistance. We investigated the potential for the major lepidopteran agricultural pest *Helicoverpa armigera* to evolve resistance against fugal pathogens used as biocontrol agents. We then tested how this evolutionary potential could be managed in

agricultural landscapes by investigating genotype by environment interactions for pathogen susceptibility. We assessed how simultaneous manipulation of fungal pathogen strain and the crop plant on which larvae feed decreases selection consistency to prevent resistance evolution. First, we identified multiple fungal isolates that kill *H. armigera* and studied the impact of field conditions on viability and virulence of spores. Then we quantified host genetic variation for fungal isolate susceptibility using 2198 *H. armigera* larvae from 32 females mated to 18 males. Larvae were reared on 1 of 3 plants (soybean, maize, or tomato) and inoculated with 1 of 3 fungal isolate treatments (*Metarhizium*, *Beauveria* or a control). We demonstrate that *H. armigera* populations harbour extensive genetic variation for fungal pathogen resistance, which if not appropriately managed could facilitate biopesticide resistance evolution. However, we show that selection for resistance is inconsistent between different fungal isolates, an effect enhanced by applying spores to larvae feeding on different crop species. Perhaps surprisingly, the efficacy of resistance genotypes in preventing insect death was more strongly affected by the diet of the larvae than it was by the pathogen strain. We argue this knowledge could be used in agriculture to develop practical solutions for long term proactive biopesticide resistance management.

Schistosome 'omics' - (Conference room 2)

11:45 (15 mins)

Genomic landscape of introgression between blood flukes infecting livestock (Schistosoma bovis) and humans (S. haematobium) across Africa*A23407*

Presenter: **Mr Roy Platt**, *Staff Scientist, Texas Biomedical Research Institute*

R N Platt II et al.[1];
[1] Texas Biomedical Research Institute, United States

Hybridization between human and animal parasites may transfer novel pathogenic traits between species, increasing virulence, host range and negatively impacting human health. Knowing when and how often these events occurs is an essential step in achieving optimal health outcomes within a One Health framework. The human parasitic blood fluke, *Schistosoma haematobium* infects millions of people across sub-Saharan Africa. *S. bovis*, a sympatric and closely related species, parasitizes livestock. Initial genetic analyses showed discordance between rDNA and mtDNA markers and indicate that these species are capable of interbreeding. Laboratory crosses between these species also suggested few reproductive barriers. To date, early generation *S. bovis* X S. *haematobium* hybrids have not been identified in studies using microsatellite, genome, or exome-wide single nucleotide variants. In the samples examined so far, it appears that hybridization between *S. bovis* and *haematobium* occurred in the relatively distant past with subsequent selection on introgressed alleles in *S. haematobium*. In particular an invadolysin gene of *S. bovis* origin has reached near fixation in West African populations of *S. haematobium* but is absent in East Africa. Here, we scored 9.6 million genome-wide, single nucleotide variants in 161 *S. bovis* and *S. haematobium* samples collected from 18 countries across the African continent. Our goals were to (1) examine hybridization and introgression events within a large-scale, biogeographic context, (2) more precisely date the admixture event(s), and (3) identify introgressed regions that may be experiencing ongoing selective pressures in different populations.

12:00 (15 mins)

Simultaneous genotyping of snails and infecting trematode parasites using high-throughput amplicon sequencing. *A23258*

Presenter: **Mrs Cyril Hammoud**, *PhD. candidate, Ghent University*

C Hammoud[3]; S Mulero[4]; B Van Bocxlaer[5]; J Boissier[4]; D Verschuren[3]; C Albrecht[2]; T Huyse[1];
[1] Royal Museum for Central Africa, Belgium; [2] Justus-Liebig-Universität Gießen, Germany; [3] Ghent University, Limnology Unit, Department of Biology, Belgium; [4] IHPE, Univ. Montpellier, CNRS, IFREMER, Univ. Perpignan Via Domitia, France; [5] CNRS, Univ. Lille, UMR 8198 Evo-Eco-Paleo, France

Several methodological issues currently hamper the study of entire trematode communities within populations of their intermediate snail hosts. Here we develop a new workflow using high-throughput amplicon sequencing (HTAS) to simultaneously genotype snail hosts and their infecting trematode parasites. We designed primers to amplify 4 snail and 5 trematode markers in a single multiplex PCR. While also applicable to other genera, we focused on medically and economically important snail genera within the Superorder Hygrophila and targeted a broad taxonomic range of parasites within the Class Trematoda. We tested the workflow using 417 *Biomphalaria glabrata* specimens experimentally infected with *Schistosoma rodhaini*, two strains of *Schistosoma mansoni*,and combinations thereof. We evaluated the reliability of infection diagnostics, the

robustness of the workflow, its specificity related to host and parasite identification, and the sensitivity to detect co-infections, immature infections, and changes of parasite biomass during the infection process. Finally, we investigated the applicability of the workflow in wild-caught snails of other genera naturally infected with diverse trematode assemblages. After stringent quality control the workflow allows the identification of snails to species level, and of trematodes to taxonomic levels ranging from family to strain. Our HTAS workflow is sensitive to detect immature infections and changes in parasite biomass described in previous experimental studies. Co-infections were successfully identified, opening the possibility to examine parasite-parasite interactions such as interspecific competition. Altogether, these results demonstrate that our HTAS workflow provides a powerful tool to analyze the processes shaping trematode communities within natural snail populations.

Interactions with Hosts and Vectors - (Conference room 1)

12:00 (15 mins)

Heligmosomoides polygyrus produces homologues of HpARI and HpBARI which have increased activity against human immune targets*A23517*

Presenter: **Dr Adefunke Ogunkanbi**, *Postdoctoral research fellow, University of Dundee*

A Ogunkanbi[1]; A Jamal[2]; Z Sekne[2]; M Higgins[2]; S Cohen[3]; H J McSorley[1];
[1] The division of Cell Signalling and Immunology, University of Dundee, Dundee, United Kingdom, UK; [2] Department of Biochemistry, University of Oxford, Oxford, United Kingdom, UK; [3] Bioscience Asthma, Research and Early Development, Respiratory & Immunology, BioPharmaceuticals R&D, AstraZeneca, Cambridge, United Kingdom, UK

Infection with parasitic helminths is known to be associated with the reduction of allergic asthma. This has been linked to the ability of parasites to release molecules with immunomodulatory ability, thus promoting their own survival. *H. polygyrus* is a gastrointestestinal parasitic helminth which causes chronic infections in mice, and has multiple known immunomodulatory activities. IL-33 is a key cytokine involved in the activation of type-2 anti-parasite and allergic responses. *H. polygyrus* releases HpARI and HpBARI: proteins capable of suppressing IL-33-induced allergic asthma. Here, we show that these proteins show suppressive effects against allergic asthma irrespective of their route of administration, either locally or systemically. Furthermore, data from *H. polygyrus* infections suggests that HpBARI can act in the peritoneal cavity and lung after release from this purely enteric parasite. These data suggest modulation of immune responses by these parasite proteins can be systemic as well as local. Homologues of both HpARI and HpBARI exist in the *H. polygyrus* genome, which have increased activity against human IL-33 responses. Surface Plasmon Resonance (SPR) experiments were used to assess affinity of the homologues for their immune targets, showing that these homologues have 10-100-fold higher affinity for the human targets, compared to the prototypic HpARI and HpBARI proteins. Furthermore, when tested in a humanised mouse model, or on in vitro human PBMCs, these homologues showed much increased activity in blocking human IL-33 responses. Our findings offer the possibility to develop new parasite-derived therapeutics against human allergic diseases which could be administered systemically.

Interactions with Hosts and Vectors - (Conference room 1)

23-June-2021, at 13:00 (30 mins)

Disparate immunogenic properties of malaria pre-erythrocytic stage antigens and their susceptibility to vaccine-induced CD8+ T cells*A23438*

Presenter: **Dr Julius Hafalla**, *Associate Professor of Immunology, London School of Hygiene and Tropical Medicine*

K Mueller[5]; M P Gibbins[4]; M Roberts[2]; A Reyes-Sandoval[1]; A V Hill[1]; S Draper[1]; K Matuschewski[5]; O Silvie[3]; **J C Hafalla**[2];
[1] University of Oxford, UK; [2] London School of Hygiene and Tropical Medicine, UK; [3] Université Pierre et Marie Curie, France; [4] London School of Hygiene & Tropical Medicine, UK; [5] Humboldt University, Germany

Antigen selection is crucial for malaria vaccine discovery. Immunogenicity is regarded as one vital criterion for progression of candidate vaccines to clinical trials. We investigated this assumption in an infection and vaccination model for malaria pre-erythrocytic stages. We genetically engineered *Plasmodium berghei* parasites that harbour a well-characterised epitope for stimulation of CD8+ T cells, either as an antigen in the sporozoite surface-expressed circumsporozoite protein or the parasitophorous vacuole membrane associated protein

upregulated in sporozoites 4 (UIS4) expressed in exo-erythrocytic forms (EEFs). We demonstrate that the antigen origin results in disparities in immunogenicity with a sporozoite antigen evoking robust, superior antigen-specific CD8+ T-cell responses, whilst an EEF antigen induces poor responses. Regardless of their differing immunogenic properties, both sporozoite and EEF antigens access antigen presentation pathways in hepatocytes, as recognition and targeting by vaccine-elicited effector CD8+ T cells results in high levels of protection when targeting either antigen. Our study is the first demonstration that poorly immunogenic EEF antigens do not exclude their vulnerability to antigen-specific CD8+ T-cell killing, which has important implications on antigen prioritisation for next-generation pre-erythrocytic malaria vaccines.

Schistosomiasis - Immunology & host-parasite interactions - (Conference room 2)

13:00 (30 mins)

Pulmonary and intestinal immune responses during Schistosoma mansoni infection*A23175*

Presenter: **Prof Andrew MacDonald**, *University of Manchester*

A S MacDonald[1];
[1] University of Manchester, UK

Infection with the parasitic worm *Schistosoma mansoni* causes considerable global morbidity, affecting over 200 million people, particularly in sub-Saharan Africa. Following skin penetration, these parasites migrate through the lung vasculature before maturation in the mesenteric vessels, where they reach patency and begin to produce eggs. Many of these eggs transit from the mesenteric blood vessels, rupturing across the intestinal wall and into the lumen. Remarkably, even though this process causes chronic tissue damage, it does not lead to sepsis in immunocompetent hosts. Thus, these parasites have evolved potent strategies to promote 'regulated' mucosal inflammation to ensure host survival in the face of chronic tissue damage. However, pulmonary and intestinal immune responses against schistosomes are currently poorly understood. We have begun to characterise schistosome-induced mucosal responses, focussing on the immune features that dominate in the lungs and intestines at different stages of infection, and interplay between the parasite and the host microbiota. Our data are beginning to reveal how immunity and tissue repair are regulated in these sites during infection, information that may aid future design of therapies against schistosomiasis, or other mucosal inflammatory diseases.

13:30 (15 mins)

Nitric oxide harms the neuropathogenic schistosome Trichobilharzia regenti in mice, partly by inhibiting its vital peptidases*A23294*

Presenter: **Miss Barbora Šmídová**, *Research assistant, Charles University, Prague*

B Šmídová[1]; **T Macháček**[1]; J Pankrác[1]; M Majer[1]; J Bulantová[1]; P Horák[1];
[1] Charles University, Prague, Czech Republic

Avian schistosomes, the causative agents of human cercarial dermatitis (or swimmer's itch), die in mammals, but the mechanisms responsible for parasite clearance are unknown. Here, we examined the role of nitric oxide (NO) in the immune response of mice experimentally infected with *Trichobilharzia regenti*. It is a model species of avian schistosomes remarkable for its neuropathogenicity. First, we confirmed NO production in the infected skin and spinal cord by immunohistochemical staining of inducible NO synthase (iNOS). We detected iNOS around the parasites in the early phases of the infection, specifically at 8 hours post-infection in the epidermis and at 3 days post-infection (dpi) in the spinal cord. However, 3-nitrotyrosine, a marker of nitrosative stress, was present only in the spinal cord at 14–21 dpi. Here, the tyrosine nitration might have been mediated by a myeloperoxidase-dependent pathway which does not require NO produced by iNOS. Second, we examined the impact of iNOS inhibition by aminoguanidine on parasite burden and growth *in vivo*. Inhibition of iNOS resulted in slower parasite growth 3 dpi, but the opposite effect was observed later, at 7 dpi. We also noticed a moderately increased parasite burden in the spinal cord at the latter time point. These data suggested a possible protective effect of NO, so we next examined the vulnerability of *T. regenti* schistosomula to NO *in vitro*. Interestingly, the NO treatment did not directly alter the viability and the ultrastructure of the schistosomula. Therefore, we tested the effect of NO on the activity of *T. regenti* vital peptidases *in vitro* using a fluorogenic substrate. Of note, NO inhibited the activity of *T. regenti* cathepsins B1.1 and B2, the peptidases essential for parasite digestion and migration, respectively. To conclude, our results suggest that although NO is produced in mice infected with *T. regenti*, it does not affect the parasite directly. Indeed, it rather disrupts its proteolytic

machinery, which could lead to suspended parasite growth and migration. Such a mechanism of chronic parasite debilitation might represent a novel mode of NO action against helminths.

Interactions with Hosts and Vectors - (Conference room 1)

13:30 (15 mins)

Turning trypanosomes into a vaccine: The design and application of a brucei-based carrier platform for the targeting of a wide variety of "difficult" antigens*A23417*

Presenter: **Mr Joseph Verdi**, *Post-Doc, Deutsches Krebsforschungszentrum*

J Verdi[1]; G Triller[1]; P Vlachou[1]; S Kruse[1]; Y Kelemen[2]; M Pravetoni[3]; C E Stebbins[1]; N Papavasiliou[1];
[1] Deutsches Krebsforschungszentrum, Germany; [2] Hepione Therapeutics Inc., United States; [3] University of Minnesota, United States

Many previous attempts to generate vaccines against small molecules, such as nicotine and cocaine, have employed conventional antigen carrier systems that have so far proven insufficient in this space. We have developed a novel carrier platform that is characterized by extraordinary epitope focusing and does not require the addition of any adjuvants to generate strong responses. The platform is based on the uniquely repetitive and antigenic surface coat of *Trypanosoma brucei*, comprised in large part by variant surface glycoprotein (VSG). The repetitive and dense nature of the coat provides a highly-antigenic surface, leading to an extremely epitope-focused immune response. We have most recently applied our platform, the *VAST* (VSG-immunogen Array by Sortase Tagging), to the opioid fentanyl in hopes of designing both an overdose preventing vaccine and overdose stopping passive therapies. The platform is generated through the sortase-mediated tagging of fentanyl (or any other “sortaggable” antigen) to VSG, followed by inactivation of the parasites prior to injection. We show that our vaccine reproducibly protects rodents from fentanyl intoxication by trapping fentanyl in the serum and thus preventing access to the brain-resident opioid receptors. We have also harvested B cells from the vaccinated animals, sequenced those cells, and identified candidate antibodies that could be used as passive therapies. This trypanosome-based antibody elicitation platform offers a new avenue to design immunotherapeutics and diagnostics specific to “difficult” antigens like fentanyl, other small molecules, and unique but otherwise "untargetable" glycan epitopes such as those produced exclusively by various protozoan species.

13:45 (15 mins)

Combining a Novel Immunoassay to Quantify Antibodies to Salivary Antigens with Antibody Acquisition Models to Estimate Exposure to Simulium damnosum s.l. Bites*A23383*

Presenter: **Mr Philip Milton**, *Doctoral Student, Imperial College London*

P Milton[3]; L Willen[4]; M Walker[5]; J Hamley[3]; P Volf[2]; M E Osman[7]; M Y Osei-Atweneboana[6]; O Courtenay[1]; M G Basáñez[3];
[1] University of Warwick, UK; [2] Charles University, Czech Republic; [3] Imperial College London, UK; [4] University of Antwerp, Belgium; [5] The Royal Veterinary College, UK; [6] Council for Scientific and Industrial Research Water Research Institute, Ghana; [7] National Centre for Research, Khartoum, Sudan, Sudan

Background: Human onchocerciasis is caused by the filarial nematode *Onchocerca volvulus* and spread by the bites of *Simulium* blackfly vectors. Exposure to blackfly bites is a key driver of transmission and success of interventions. We combine a novel enzyme-linked immunosorbent assay (ELISA) that measures IgG antibody levels against salivary antigens of *S. damnosum* s.l. collected from four onchocerciasis-endemic villages of the Bono East region of Ghana with antibody acquisition models designed to capture the change in antibody levels with age and sex, as a tool to identify patterns of exposure to vector bites.

Methods: Three alternative antibody acquisition models, described by ordinary differential equations, were constructed to model the dynamics of anti-blackfly salivary IgG antibody titre by age and sex. The models assume that exposure to blackfly bites (and concurrently to salivary antigens) increases antibody levels, with antibody decaying at a constant rate through time. The models are: (**1**) *exposure only*, age- and sex-specific exposure to blackfly bites, such that exposure to bites can increase or decrease with age independently for either sex; (**2**) *desensitisations in antibody acquisition*, age- and sex-specific exposure to blackfly biteswith cumulative past exposure to bites reducing antibody acquisition for a given exposure; (**3**) *desensitisation in antibody decay*:

age- and sex-specific exposure to blackfly biteswith cumulative past exposure to bites accelerating antibody decay. All three models were fitted to ELISA-derived standardised optical density titres of anti-blackfly saliva IgG antibodies from 958 individuals. The exposure functions derived from each model were incorporated into an individual-based, stochastic, onchocerciasis transmission model (EPIONCHO-IBM) to evaluate how the different exposure functions to blackfly bites alter the predicted age- and sex-specific profiles of microfilarial load by comparing to data from the same region in Ghana. We also assessed the impact on onchocerciasis community-directed treatment with ivermectin (CDTI) programmes.

Results: All three antibody acquisition models captured the observed IgG dynamics but resulted in different predicted patterns of exposure to blackfly bites. Models (2) and (3) fitted the IgG data better, producing patterns of exposure that were consistent with previous estimates, and resulted in predicted age and sex profiles of microfilarial load resembling pre-intervention infection patterns from the same region in Ghana when incorporated into EPIONCHO-IBM. The different exposure patterns thus generated produced different predicted age and sex infection profiles after multiple years of CDTI, notably in children.

Discussion/Conclusion: Human antibody responses to blackfly salivary antigens have the potential to represent an invaluable tool to measure exposure to blackfly bites at both individual and population levels, with implications for onchocerciasis morbidity, control, elimination and surveillance. The antibody acquisition models offer a way to link antibody data to exposure functions, that can be used within transmission models. The precise inference of exposure from such assays depends on immunological assumptions that warrant further study.

Schistosomiasis - Immunology & host-parasite interactions - (Conference room 2)

13:45 (15 mins)

In-depth exploration of Trichobilharzia regenti neuroinvasion in mice: host immune response and helminth-induced neuropathogenicity *A23291*

Presenter: **Dr Tomas Machacek**, *Postdoc, Charles University, Prague*

T Macháček[1]; R Leontovyč[1]; B Šmídová[1]; M Majer[1]; O Vondráček[1]; I Vojtěchová[2]; T Petrásek[2]; P Horák[1];
[1] Charles University, Prague, Czech Republic; [2] National Institute of Mental Health, Klecany, Czech Republic

Helminths do often invade the central nervous system (CNS) of mammals, including humans. Such infections might represent serious medical conditions, but the host-parasite interplay within the nervous tissue often remains poorly understood. Here, we thoroughly explored mechanisms of *Trichobilharzia regenti* (Schistosomatidae) neuroinvasion in mice. Active migration of *T. regenti* schistosomula through the mouse spinal cord induced motor deficits in hindlimbs but did not affect the general locomotion or working memory. Histological examination of the infected spinal cord revealed eosinophilic meningomyelitis with eosinophil-rich infiltrates entrapping the schistosomula. Flow cytometry and transcriptomic analysis of the spinal cord confirmed massive activation of the host immune response. Of note, we recorded striking upregulation of the MHC II pathway and M2-associated markers, such as *Arg1* and *Chil3* (*Ym1*). Arginase-1 also dominated among the proteins found in the microdissected tissue from the close vicinity of the migrating schistosomula. Our findings indicate that the previous concept of microglia/macrophages actively fighting against the schistosomula needs to be reconsidered. Next, we also evaluated the pathological sequelae of *T. regenti* neuroinvasion. While no demyelination was noticed, our transcriptomic data suggested alterations in permeability and blood-brain barrier integrity, especially in the early stage of the infection. Additionally, we detected DNA fragmentation at the host-schistosomulum interface, but schistosomula antigens did not affect the viability of neurons and glial cells *in vitro*. Taken together, our comprehensive characterisation of *T. regenti* neuroinvasion broadens the range of animal models available to study pathogen-related neuroinflammatory processes. A complex insight into their diversity is a prerequisite for the development of better protective measures, treatment strategies, and diagnostic tools.

14:00 (15 mins)

Harnessing the diagnostic potential of highly specific anti-glycan antibodies in schistosomiasis *A23345*

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

A Kildemoes[1]; T Veldhuizen[1]; M Tanaka[3]; L van Lieshout[1]; D Camprubí-Ferrer[4]; J Munoz[4]; L Visser[1]; S Hamano[3]; S Njenga[2]; M Roestenberg[1]; A Diepen[1]; C Hokke[1];
[1] Leiden University Medical Centre, Netherlands; [2] Kenya Medical Research Institute, Kenya; [3] Nagasaki University, Japan; [4] University of Barcelona, Spain

Infection or exposure to schistosomes induce a multitude of antibodies specific for a wide range of antigens expressed by parasite larvae, adult worms and eggs. A large proportion of these antibodies recognise antigenic glycans that are part of the parasite's glycoprotein and glycolipid repertoire. While the role of these anti-glycan antibodies in immunity remains poorly understood, they present a so far untapped diagnostic potential as extensive glycomics work has shown that schistosomes contain several unique glycan elements. Identification of single or a combination of few defined glycan candidate antigens is central for future development of a highly accurate anti-glycan antibody detection tool. In order to select such candidate antigens, we applied an iterative target selection process based on custom-made glycan microarrays combined with well-characterised sample sets. We have assessed the specificity and sensitivity of candidate antigens by analysing schistosome non-endemic area samples from a controlled human schistosome infection model, from primary infection traveller samples, from presumed schistosome naïve donor samples as well as samples from a soil-transmitted helminth endemic area. Furthermore, samples from schistosomiasis endemic areas in Kenya were investigated. Through this process a candidate target with promising accuracy for primary schistosomiasis infection has been found. Importantly, we have also gained knowledge on longevity of specific antibody responses as well as relationship between exposure dose and timing of antibody response induction for both IgM and IgG. Development of a highly sensitive and specific antibody detection assay would be a beneficial addition to the existing diagnostic tool repertoire for schistosomiasis. An accurate antibody detection tool would have particular impact and use in traveller diagnostics as well as in very low endemic, near- and post-elimination settings for transmission monitoring purposes.

Interactions with Hosts and Vectors - (Conference room 1)

14:00 (15 mins)

Identification and RNA profiling of ovine tuft cells in response to gastro-intestinal nematode infections *A23128*

Presenter: **Miss Katie Hildersley**, *PhD Student, University of Glasgow*

K A Hildersley[4]; T N McNeilly[1]; V Gillan[3]; T D Otto[2]; R M Maizels[2]; E Devaney[3]; C Britton[3];
[1] Moredun Research institute, UK; [2] Institute of Infection, Immunity & Inflammation, University of Glasgow, UK; [3] Institute of Biodiversity, Animal Health, & Comparative Medicine, University of Glasgow, UK; [4] Moredun Research Institute and Institute of Biodiversity, Animal Health & Comparative Medicine, University of Glasgow, UK

Gastrointestinal (GI) nematodes are a major health and economic concern in production animals such as sheep. As anthelmintic resistance is becoming an increasing challenge for controlling livestock parasites, it is important to improve our understanding of host immune mechanisms to aid development of new control methods. Tuft cells (TCs) are of interest in mucosal immunology due to their proposed function in sensing changes in the environment of the gut lumen. Tuft cells are the sole source of IL-25 in the intestine and are key in initiating the type 2 immune response to GI nematodes. Tuft cells have been characterised from the murine small intestine (SI) by immunohistochemistry (IHC) and their frequency was shown to increase significantly during infection with *Nippostrongylus brasiliensis* and *Heligmosomoides polygyrus.* Single cell RNA-sequencing (scRNA-seq) of murine SI epithelial cells has provided additional insight into murine TC function and how they interact with the lumen of the GI tract. However, little is known about TCs in other species and in other regions of the GI tract. In this project, we demonstrated the presence of TCs in the ovine abomasum (true stomach) by IHC using antibodies to murine TC markers POU2F3 and GFI1B. We confirmed that ovine POU2F3+ cells also significantly increased in number over the course of infection with the important livestock GI nematodes *Teladorsagia circumcincta* and *Haemonchus contortus.* Next, we characterised ovine abomasal tuft cells following *T. circumcincta* infection by scRNA-seq. Gene expression profiling demonstrated that many murine TC genes are conserved in ovine abomasal TCs e.g., *il17rb, avil* and *alox5,* but that the surface receptor repertoire differed from those of murine SI TCs e.g., succinate receptor *sucnr1* was not expressed in ovine TC. We also identified distinct sub-populations of ovine tuft cells at different stages of maturation. The scRNA-seq experiment was validated using RNAscope *in situ* hybridisation, which confirmed co-expression of tuft cell genes identified by scRNA-seq. For the first time, TCs have been identified in the ovine abomasum and shown to increase in number over the course of GI nematode infections with a distinctive gene expression profile marking their differentiation and maturation.

Interactions with Hosts and Vectors - (Conference room 1)

23-June-2021, at 15:00 (30 mins)

Scientist at play; artful science to explore Leishmania, sand flies and their gut microbiota.*A23439*

Presenter: **Dr Rod Dillon**, ., *Lancaster University*

The idea that Phlebotomine sand flies act as vectors for *Leishmania* that are transmitted to the mammal has been accepted for over 90 years. We know that this triad of relationships is too simplistic to explain many of the transmission events. The concept that bacteria play a significant role in *Leishmania* establishment in the gut of the sand fly has come to the fore in the past 20 years. More recent research has uncovered the important role for bacteria in *Leishmania* co-infection of the mammalian host. The first part of my talk will focus on the role of bacterial species in the Leishmania-sandfly-mammalian network.

The second part of my talk will introduce some of the arts/ public engagement projects that I have developed in parallel with my scientific research. These artistic projects are an essential part of my approach to working with parasites, insects and microbes. I will argue that the creative arts have helped me develop a 'playful' creative approach that benefited my science research. This also provided a bridge to engage the public and policy makers about the critical scientific issues facing us today.

Schistosomiasis - Chemotherapy/new drugs/drug screening - (Conference room 2)

15:00 (30 mins)

Schisto drug discovery in Sunny San Diego – tools and technologies*A23168*

Presenter: **Dr Conor Caffrey**, *Center for Discovery and Innovation in Parasitic Diseases, Skaggs School of Pharmacy and Pharmaceut*

C Caffrey[2]; M Arkin[1]; S Chen[1]; B M Suzuki[2]; R Singh[3]; B Bibo-Verdugo[2]; A P Ta[2]; Z Jiang[2]; C Liu[2]; N El-Sakkary[2]; P Fatjová[2]; L Liu[2]; W Gerwick[4]; J Almaliti[4]; A J O'Donoghue[2];
[1] Small Molecule Discovery Center, Department of Pharmaceutical Chemistry, University of California, United States; [2] Center for Discovery and Innovation in Parasitic Diseases, Skaggs School of Pharmacy and Pharmaceutical Sciences, University of California, United States; [3] Department of Computer Science, San Francisco State University, United States; [4] Scripps Institute of Oceanography, University of California, United States

The CDIPD at UC San Diego (http://cdipd.org/) is engaged in drug discovery for parasitic diseases of poverty. For schistosomiasis, treatment and control precariously rely on just one partially effective drug, praziquantel. New drugs are needed. The CDIPD and collaborators have designed an automated, high-content drug-screening platform to quantify the chemically-induced, multi-parametric static and kinetic responses of Schistosoma mansoni. I will describe the platform's development and implementation, as well as the interrogation of the data arising using a custom-built, graphical user interface called SchistoView. Screening data for high-value small molecule collections will be presented. Among the compounds identified in one screen were proteasome inhibitors. This prompted an investigation of the proteasome as a possible drug target. Our early forays into designing proteasome inhibitors based on a marine natural product chemical scaffold will be briefly discussed. Supported by a UCSF Clinical and Translational Science Institute T1 catalyst award, and by the NIH awards, R01AI089896, R21AI107390, R21AI133393 and R21AI126296.

15:30 (15 mins)

Docking-based virtual screening identification of multi kinase-targeting inhibitors with in vitro phenotypic activity against Schistosoma mansoni*A23509*

Presenter: **Dr Bernardo Moreira**, *Research Fellow, Justus-Liebig-University Giessen*

B Moreira[3]; I C Batista[2]; N C Tavares[2]; T Armstrong[1]; S G Gava[2]; G P Torres[2]; M M Mourao[2]; F H Falcone[3];
[1] University of Nottingham, UK; [2] Instituto René Rachou - Fiocruz Minas, Brazil; [3] Justus-Liebig-University Giessen BFS, Institute for Parasitology, Germany

Currently, praziquantel (PZQ) is the only available drug that is effective against all *Schistosoma* species, even considering its low efficacy against early stages of the worm. In the search for new drugs to tackle schistosomiasis, computer-aided drug design has proven a helpful tool to enhance the search and initial identification of schistosomicidal compounds, allowing fast and cost-efficient progress in drug discovery. The combination of *in silico* high-throughput screening followed by *in vitro* phenotypic assays allows the assessment of enormous libraries of compounds with the potential to inhibit biological targets. Besides, the drug discovery field has witnessed a shift from traditional approaches of finding potent selective inhibitors against individual

targets, towards identifying promiscuous compounds with multi-target efficacy and less toxicity ("Multi-target drugs"). In order to explore this paradigm, we employed molecular docking for *in silico* screening of five predicted homology models of *Schistosoma mansoni* kinase proteins (SmJNK, Smp38, SmERK1, SmERK2, and SmFES) against approximately 85,000 molecules from the Managed Chemical Compounds Collection of the University of Nottingham (UK). Based on molecular docking scores, we selected 169 molecules, 78 of which were single kinase-targeting compounds and 91 predicted to target all MAP kinases. All compounds were screened *in vitro* against larval and adult stages of *S. mansoni*. In total, 88 (52%) molecules were considered active in at least one of the assays. This approach shows a much higher efficiency when compared to using only traditional high-throughput *in vitro* screening assays, where initial positive hits are retrieved from testing thousands of molecules. Additionally, when we focused on compound promiscuity over selectivity, we were able to efficiently detect 36 active compounds that are predicted to target four SmMAP kinases at the same time. This approach reinforces the concept of selecting multi-target inhibitors aiming for one 'drug-many targets'. Moreover, at least 49 active compounds presented satisfactory druggability score when compared to PZQ, allowing further optimisation to improve potency. In conclusion, our data support the hypothesis that compound prioritization against many targets is a helpful alternative for drug discovery against schistosomiasis. **Keywords:** *Schistosoma mansoni* protein kinases, computer-aided drug design, phenotypic screening, multi-target drugs

Interactions with Hosts and Vectors - (Conference room 1)

15:30 (15 mins)

High throughput single-cell genome sequencing gives insights into the generation and evolution of mosaic aneuploidy in Leishmania donovani*A23351*

Presenter: **Mr Gabriel Negreira**, *Junior research fellow/PhD Student, Institute of Tropical Medicine Antwerp*

G Negreira[3]; P Monsieurs[3]; H Imamura[1]; I Maes[3]; N Kuk[2]; A Yagoubat[2]; F Van den Broeck[1]; Y Sterkers[2]; J C Dujardin[1]; M Domagalska[1];
[1] Institute of Tropical Medicine, Antwerp, Belgium; [2] University of Montpellier and Centre Hospitalier Universitaire, France; [3] Institute of Tropical Medicine Antwerp, Belgium

Aneuploidy, i.e., an imbalance in the copy number of chromosomes in a cell, is a ubiquitous feature of *Leishmania*, a protozoan parasite responsible for the group of diseases known as leishmaniasis. In these organisms, chromosome copy number (CCN) alterations represent an adaptive mechanism, modulating gene expression and possibly impacting phenotypes. Moreover, variations in CCN within single parasites in clonal populations was previously observed in a small subset of chromosomes using fluorescence hybridization methods. This phenomenon, termed mosaic aneuploidy (MA), have important evolutionary and functional implications which remains under-explored, as current methods are not capable of revealing the complete karyotype of individual *Leishmania* cells. To overcome this limitation, we applied and validated a high throughput single-cell genome sequencing method to study for the first time the extent and dynamics of whole karyotype heterogeneity in two *Leishmania* clonal populations representing different stages of MA evolution in vitro. In these two populations, we identified 117 and 208 different karyotypes co-existing among 2378 and 1516 promastigotes respectively. We observed that drastic changes in karyotypes quickly emerge in a population stemming from an almost euploid founder cell. The presence of polyploid cells at early stages suggests that these initial drastic changes may be generated by polyploidization/hybridization followed by assorted ploidy reduction, as has been observed in yeasts. During further stages of expansion, MA increases by moderate and gradual karyotypic alterations. We also observed that MA usually affected a defined subset of chromosomes, of which some display an enrichment in snoRNA genes which could represent an adaptative benefit to the amplification of these chromosomes. Our data provide the first complete characterization of MA in *Leishmania* and pave the way for further functional studies.

15:45 (15 mins)

Functionally mapping the diversification of African trypanosomes using spatial proteomics*A23341*

Presenter: **Dr Nicola Moloney**, *Postdoctoral research associate, University of Cambridge*

N Moloney[1]; K Barylyuk[1]; L Breckels[1]; K Lilley[1]; R F Waller[1]; P MacGregor[1];
[1] University of Cambridge, Department of Biochemistry, UK

African trypanosomes are dixenous unicellular parasites that cause disease with devastating impact in sub-Saharan Africa. Diversity between species and life-cycle stages is concomitant with distinct host and tissue

tropisms within this group. Understanding the molecular biology that underpins the diversity in cell biology requires a comprehensive functional map of each organism which, collectively, is currently lacking.

Protein function is often intimately linked with localisation and as a consequence the subcellular distribution of a protein provides information on its role in the cell. We have optimised a method for resolving subcellular compartments in *Trypanosoma brucei* and *Trypanosoma congolense* and implemented it in the spatial proteomics strategy of hyperLOPIT (hyperplexed localisation of organelle proteins by isotope tagging). Between the insect and vertebrate stages, represented by procyclic and bloodstream forms respectively, we have detected over 7000 in both *T. brucei* and *T. congolense*. Of these, 6171 T. brucei proteins (n = 3) and 6324 T. congolense proteins (n = 3) are included in a spatial proteome characterisation and classified to over 15 subcellular compartments using a machine learning approach based on a t-augmented Gaussian mixture model.

This work provides a comprehensive map of the *T. brucei* and *T. congolense* spatial proteomes. Individually, these data sets guide the determination of uncharacterised protein function, particularly for *T. congolense*, where high-throughput functional analysis lags behind that of *T. brucei*. Further, comparative analysis yields insight into the evolutionary diversification of these species and the effects of speciation on the molecular biology and architecture of the parasite cell.

Schistosomiasis - Chemotherapy/new drugs/drug screening - (Conference room 2)

15:45 (15 mins)

From bugs to drugs: discovery of novel antischistosomal compounds from insects*A23344*

Presenter: **Dr Simone Haeberlein**, *PostDoc, Institute of Parasitology, University Giessen*

S Haeberlein[2]; J Kellershohn[2]; M Tonk[1]; A Vilcinskas[1]; C G Grevelding[2];
[1] Fraunhofer Institute for Molecular Biology and Applied Ecology, Germany; [2] Institute of Parasitology, Justus Liebig University Giessen, Germany

Natural products represent a treasure trove for the discovery of new drugs including anti-infectives. With respect to antischistosomal compounds, plant-derived products have been extensively studied while insect-derived compounds have received little attention. This is surprising, knowing that insects represent the most species-rich class of animals known on earth, and they produce a wide spectrum of compounds with biological activities. Examples are antimicrobial peptides (AMPs), alkaloids, or complex venoms that comprise more than hundred active compounds that are used to defend against insect pathogens, predators, or competitors. In insect biotechnology, the invasive harlequin ladybird *Harmonia axyridis* raised high interest as a rich source of antimicrobials such as the alkaloid harmonine. This compound is thought to act as a chemical weapon keeping pathogenic microsporidia in the beetle under control. Another interesting insect family are assassin bugs, predaceous hemipteran insects known for their potent venom that is injected into invertebrate preys.

In recent studies, we made first steps towards exploring insects as source for antischistosomals and investigated whether ladybird-derived harmonine, venom from the European predatory assassin bug *Rhynocoris iracundus*, or various AMPs from different insect families display activity against *S. mansoni* in *in vitro*-assays (Kellershohn et al. 2019, Tonk et al. 2020). While AMPs had only weak activity, harmonine (5 µM) and venom (10-50 µg/ml) significantly inhibited motility and egg production of schistosome couples. In addition, we observed pleiotropic effects on tissues essential for survival and reproduction of schistosomes that included tegumental damage, gut dilatation, and degradation of gonads. To address possible modes of action, we used EdU-proliferation assays to measure effects on schistosome stem cells, which are essential for survival and reproduction. Both insect products arrested stem-cell proliferation in different tissues, including parenchymatic neoblasts and gonadal stem cells. This was further supported by a downregulated expression of the stem-cell markers *nanos-1* and *nanos-2* in treated worms revealed by quantitative real-time PCR. For harmonine, we additionally obtained first evidence for acetylcholinesterase as one potential molecular target, whose activity was partially inhibited by the compound. One drawback especially of insect venoms is their tendency to lyse eukaryotic cells, which would preclude their therapeutic application. To address this important point, we conducted hemolysis assays using porcine red blood cells, which revealed that *R. iracundus* venom had no significant effect at a concentration of 43 µg/ml.

In summary, besides their natural role to tackle endogenous pathogens or invertebrate preys, insect-derived products might also have the capacity to im

16:00 (15 mins)

Anti-schistosomal activities of quinoxaline-containing compounds: from hit identification to lead optimisation*A23392*

Presenter: **Dr Gilda Padalino**, *PDRA, Ibers Aberystwyth University*

G Padalino[1]; N El-Sakkary[4]; L Liu[4]; C Liu[4]; D Harte[2]; E Sayers[3]; J Forde-Thomas[1]; H Whiteland[1]; G Johnson[2]; A Jones[3]; M Bassetto[3]; C Caffrey[4]; A Brancale[3]; K F Hoffmann[1];
[1] IBERS, Aberystwyth University, UK; [2] Swansea University Medical School, UK; [3] School of Pharmacy and Pharmaceutical Sciences, Cardiff University, UK; [4] Center for Discovery and Innovation in Parasitic Diseases, Skaggs School of Pharmacy and Pharmaceutical Sciences, University of California, United States

Schistosomiasis is a neglected disease of poverty that is caused by infection with blood fluke species contained within the genus Schistosoma. For the last 40 years, control of schistosomiasis in endemic regions has been predominantly facilitated by administration of a single drug, praziquantel. Due to limitations in this mono-chemotherapeutic approach for sustaining schistosomiasis control into the future, alternative anti-schistosomal compounds are increasingly being sought by the drug discovery community. Herein, we describe a multi-pronged, integrated strategy that led to the identification and further exploration of the quinoxaline core as a promising anti-schistosomal scaffold.

Firstly, phenotypic screening of commercially available small molecules resulted in the identification of a moderately active hit compound against *Schistosoma mansoni* (**1**, EC_{50} = 4.59 µM on schistosomula). Secondary exploration of the chemical space around compound 1 led to the identification of a quinoxaline-core containing, non-genotoxic lead (compound **22**). Compound **22** demonstrated substantially improved activities on both intra-mammalian (EC_{50} = 0.44 µM and 84.7 nM, on schistosomula and adult worm, respectively) and intra-molluscan (sporocyst) *S. mansoni* lifecycle stages. Further medicinal chemistry optimisation of compound **22**, resulting in the generation of 20 additional analogues, improved our understanding of the structure-activity relationship and resulted in considerable improvements in both anti-schistosome potency and selectivity (e.g. compound **30**; EC_{50} = 2.59 nM on adult worms; selectivity index compared to the HepG2 cell line = 348). Some compound **22** derivatives (e.g. compounds **31** and **33**) also demonstrated significant activity against the two other medically important species, *Schistosoma haematobium* and *Schistosoma japonicum*. Further optimization of this class of anti-schistosomal is ongoing and could lead to the development of an urgently-needed alternative to praziquantel for assisting in schistosomiasis elimination strategies.

Interactions with Hosts and Vectors - (Conference room 1)

16:00 (15 mins)

Rapid egress of Trypanosoma cruzi follows actin cytoskeleton rearrangement and membrane rupture*A23086*

Presenter: **Dr Eden Ferreira**, *Dr, Federal University of Sao Paulo*

E R Ferreira[3]; A Bonfim-Melo[2]; K M Tyler[1]; R A Mortara[3];
[1] Norwich Medical School at UEA, UK; [2] The University of Queensland, Australia; [3] Federal University of Sao Paulo, Brazil

The protozoan parasite *Trypanosoma cruzi* is the etiological agent of Chagas' disease, a deadly and vector-borne zoonotic disease of poverty that affects 6-7 million people mostly in South and Central America and which lacks vaccines and effective therapeutics. Chagas' disease arises as a direct consequence of the lytic cycle of *Trypanosoma cruzi* in the mammalian host. While invasion are well studied for this pathogen, study of egress has been largely neglected. Here we provide the first description of *T. cruzi* egress documenting a co-ordinated mechanism by which *T. cruzi* engineers its escape from the host cells in which it has proliferated, and which is essential for maintenance of infection and pathogenesis. Our results indicate that this parasite egress is a sudden event involving co-ordinated remodeling of host cell cytoskeleton and subsequent rupture of host cell plasma membrane. We document that host cells maintain plasma membrane integrity until immediately prior to parasite release and report the sequential transformation of the host cell's actin cytoskeleton from normal meshwork in non-infected cells to spheroidal cages - a process initiated shortly after amastigogenesis. Quantification revealed a gradual reduction in F-actin over the course of the lytic cycle and using cytoskeletal preparations and electron microscopy we were able to observe disruption of the F-actin proximal to intracellular trypomastigotes. Furthermore, western blotting experiments revealed actin degradation driven by parasite proteases, suggesting stage-regulated degradation of cytoskeleton as a principal component controlling the initiation of egress. Taken together our results provide the first description of the cellular mechanism which regulates the lytic component of *T. cruzi* lytic cycle. We show graphically how it is possible to preserve the envelope of the host cell plasma

membrane during intracellular proliferation of the parasite and how in cells packed with amastigotes differentiation into trypomastigotes may trigger sudden egress.

2020 President's Medal Lecture - (Conference room 1)

24-June-2021, at 10:00 (30 mins)

R-loops of the Trypanosoma brucei genome and single cell transcriptomic reconstruction of bloodstream form differentiation *A23161*

Presenter: **Dr Emma Briggs**, *University of Glasgow*

T. brucei, along with other kinetoplastids, has an unusual genome structure with implications for transcription, mRNA processing and gene expression regulation. Genes are transcribed in large tandem arrays from common promoters and are processed by trans splicing of the 5' cap and polyadenylation to generate mature individual transcripts. This negates gene expression regulation at the level of transcription for nearly all genes. The first part of the talk will focus on R-loops, three stranded nucleic acid structures. Mapping R-loops, via DRIP-seq, genome-wide reveals their association with intergenic sequences between tandemly arranged genes, promoters and repeat sequences. Genetic knockout or knockdown of R-loop processing enzymes RNase H1 and 2A increases levels of R-loops at specific loci. These are associated with specific DNA damage as well as switching of the variant surface glycoprotein, which is essential for immune evasion in the mammalian host. Despite this genome arrangement, T. brucei regulates transcript levels via post-transcriptional mechanisms such as degradation. These transcript levels can be profiled with single cell transcriptomics (scRNA-seq), which will be discussed in the second part of the talk. In the mammal, T. brucei differentiates from replicative slender forms to cell cycle arrested stumpy forms. Using oligopeptides to induce asynchronous differentiation in vitro, scRNA-seq was used to capture individual transcriptomes of slender, stumpy and intermediate stages, allowing a trajectory of differentiation to be reconstructed. Analysis of gene expression dynamics across the trajectory revealed several details of the process. These include: the lack of a discrete intermediate transcriptome; the precise timing of cell cycle exit, immediately prior to late G1; the transient expression of several genes not identified by bulk-analysis; and the expression timing of known and putative differentiation factors during the developmental processes including ZC3H20. The truncated development of ZC3H20 null T. brucei in response oligopeptides was also profiled by scRNA-seq, revealing the position of this regulators action in stumpy development.

BES: Ecology and Evolution I - (Conference room 1)

24-June-2021, at 11:00 (30 mins)

Sequencing Protists directly from the environment for the Darwin Tree of Life Project*A23066*

Presenter: **Prof Neil Hall**, *Earlham Institute*

The Darwin Tree of Life (DToL) Project aims to generate reference genomes for all described species 70,000 species of eukaryotic organisms in Britain and Ireland. It is a collaboration between biodiversity, genomics and analysis partners led by The Sanger Institute . These genomes will be made freely available to the public on production and will therefore be a transformative resource that will change how we do biology. Since its inception numerous similar projects have been spet awned around the world. Here I will describe the structure of the DToL, its progress and how the data is being released. I will also focus on our parallel effort as part of the DToL to sequence protist genomes directly from the environment. The Protists are a paraphyletic and highly diverse grouping of eukaryotic life, forming the sisters of plants, animals and fungi. They have evolved many different solutions to survive in a multitude of environments and are essential for the function of most ecosystems. Despite this and given the enormity of their diversity, they are relatively understudied, with most species remaining undescribed and with no genomic sampling. The reason for their poor sampling is in part due to methodological difficulties in isolating species from the environment into stable culture, usually a requirement for tractable DNA recovery enabling genome sequencing.

Schistosome Biology II - (Conference room 2)

11:00 (30 mins)

The WEome of Schistosoma mansoni – a non-coding DNA resource shaping schistosome biology, variability, and evolution?*A23207*

Presenter: **Prof Christoph G. Grevelding**, *Professor for Parasitology, Justus-Liebig-University Giessen*

M Stitz[3]; C Chaparro[2]; Z Lu[3]; J Olzog[4]; C Weinberg[4]; J Blom[5]; A Goesmann[5]; C Grunau[1]; **C G Grevelding**[6];
[1] University of Perpignan via Domitia, France; [2] IHPE, France; [3] Institute of Parasitology, Justus Liebig University Giessen, Germany; [4] Institute of Biochemistry, University Leipzig, Germany; [5] Bioinformatics and Systems Biology, Justus Liebig University Giessen, Germany; [6] Institute of Parasitology, Justus-Liebig-University Giessen, Germany

A large part of eukaryote genomes consists of non-coding DNA. This part includes tandemly repeated sequences, which gained attention because they offers exciting insights into genome biology. We investigated satellite DNA-like elements, called W-elements (WEs), of the platyhelminth Schistosoma mansoni. Schistosomes are the only trematodes that have evolved separate genders, and the sexual maturation of the female depends on constant pairing with the male. The schistosome karyotype comprises eight chromosome pairs, males are homogametic (ZZ), females heterogametic (ZW). Former studies identified the WEs W1 and W2 in Puerto Rican isolates of Schistosoma mansoni as female-specific satellite DNAs, which are located in the heterochromatic block of the W-chromosome. Unexpectedly, W1 and W2 occurred in a Liberian strain of S. mansoni also in males. Subsequent studies based on genome version 5 of the S. mansoni genome described a total of 36 WE families (WEFs), and first evidence was obtained for WE transcripts in the free-living larval stages (miracidium, cercaria). Based on new genome (version 7) and transcriptome data, we performed a comprehensive reanalysis of the WEFs of S. mansoni. Besides a new classification into 19 WEFs, we provide first evidence for stage-, gender-, pairing-, gonad-, and strain-specific/preferential transcript occurrence of WEs. Furthermore, we revealed their mobile nature, deduced from the identification of autosomal copies of full-length and partial WEs and sequence features typical for the activity of mobile elements. Advanced structural analyses suggested potential roles of WEFs as sources of non-coding RNAs like hammerhead ribozymes (HHRs). For the latter we obtained biochemical evidence. Finally, we also investigated WEF occurrence in different schistosome species and discovered remarkable divergence. From all obtained results we conclude that WEs exert enduring influence on the biology of S. mansoni. Their variable occurrence in different species, strains as well as among biological replicates and within clonal populations suggests that the WEome of schistosomes represents one of the sources of heritable and spontaneuos variation associated with the evolution of sexual dimorphism and diversification of the family Schistosomatidae.

11:30 (15 mins)

Diversity and Evolution of Antigens in the Tetraspanin Protein Family of Schistosoma japonicum*A23075*

Presenter: **Mr Daniel Parsons**, *PhD Student, Kingston University*

D Parsons[3]; A M Emery[1]; A J Walker[3]; J P Webster[2]; J Buxton[3]; S P Lawton[4];
[1] Natural History Museum, UK; [2] Royal Veterinary College, University of London, UK; [3] Kingston University, UK; [4] Scottish Rural University College, UK

Asiatic schistosomiasis, caused by the zoonotic blood fluke Schistosoma japonicum, results in chronic and debilitating symptoms across China, Indonesia and the Philippines, with approximately 750 thousand people infected across China alone. Despite strenuous control efforts over the past 60 years, a resurgence of the parasite has been demonstrated since the start of the 21st century. This recent resurgence, and subsequent rise in morbidity, has prompted a call for a revolutionised integrated control methodology, with a clinical and/or transmission-blocking vaccine at the forefront of this strategy. Yet, vaccination trials have seen variable success and do not infer long term immunity, and several studies have highlighted variation in schistosome antigen coding genes (ACGs) as possibly accounting for the lack of vaccine efficacy shown thus far. Therefore, efficacious and robust ACGs must be selected as candidates for vaccine development. Tetraspanins (TSPs) are a family of transmembrane cell surface-anchored proteins with a vast array of functions that have been shown to have potential as vaccine targets. Many have been shown to be antigenic, directly interacting with the hosts immune system in parasites such as *Schistosoma japonicum*. However, the full diversity of tetraspanins in *S. japonicum* remains unknown, and the impact of diversifying selection acting on the protein family is unclear. In other pathogens the diversification of ACGs has been implicated in alterations in antibody binding affinity, and thus the ability of the host's immune system to recognise infection. This study aims to elucidate the genetic diversity of TSP proteins in *S. japonicum* via a phylogenetic analyses and to highlight the influence of selection on the protein family and how this impacts their antigenic properties.

BES: Ecology and Evolution I - (Conference room 1)

11:30 (15 mins)

Who's to blame? Host-vector-parasite interactions in timing transmission.*A23425*

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

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

The daily rhythms of malaria parasite development in the blood of the vertebrate host is famous for causing fever rhythms. Previous research suggests that these rhythms result in the production of sexual transmission stages (gametocytes) whose maturation coincides with the time-of-day that mosquito vectors are most likely to bite. Indeed, daily rhythms in the infectiousness of gametocytes to mosquitoes have been observed, with gametocytes being more infectious during their night time. But parasites, hosts and vectors all display daily rhythms, so it's difficult to determine their relative contributions to the infectiousness of gametocytes. Because parasite and host time are inherently confounded in wild-type mice, we used *Per1/2* knock-out mice which do not display any circadian rhythms when kept in constant darkness. By separately disrupting parasite and mosquito rhythms, we tested their relative impacts on transmission efficiency, in the absence of host rhythms. Our results reveal that mosquitoes are less susceptible to infection during their night time. However, night time gametocytes from arrhythmic mice did not display enhanced infectiousness compared to daytime gametocytes. Could enhanced infectivity of night time gametocytes in wildtype mice be the result of rhythmic host factors impeding / enhancing transmission at different time of day?

11:45 (15 mins)

A new Plasmodium species in African apes reveals the origin of human Plasmodium malariae*A23379*

Presenter: **Dr Lindsey Plenderleith**, *Postdoctoral Research Fellow, University of Edinburgh*

L J Plenderleith[1]; W Liu[2]; Y Li[2]; D E Loy[2]; A Ayouba[5]; A Esteban[5]; M Peeters[5]; C M Sanz[3]; D B Morgan[6]; N D Wolfe[7]; S Calvignac-Spencer[4]; F H Leendertz[4]; B H Hahn[2]; P M Sharp[1];
[1] University of Edinburgh, UK; [2] University of Pennsylvania, United States; [3] Washington University, St Louis, United States; [4] Robert Koch-Institute, Germany; [5] University of Montpellier, France; [6] Lincoln Park Zoo, United States; [7] Global Viral Forecasting Initiative, United States

The malaria parasite *Plasmodium malariae* infects humans across Africa, Asia and South America, and has relatives infecting monkeys in the New World (*Plasmodium brasilianum*) and apes in Africa (*Plasmodium rodhaini*). The genetic relationships among these parasites, and even whether they represent separate species, are unclear. Combining DNA sequences newly derived from ape faecal and blood samples with others obtained by mining *Plasmodium* sequence read databases, we have investigated the evolutionary history of *P. malariae* and its relatives. We find that this group of parasites comprises three distinct lineages, one of which represents a previously unknown, distantly related species that infects wild-living chimpanzees, bonobos and gorillas across central and west Africa; we were able to assemble a very partial genome sequence (~500 kb) for this parasite. A second lineage infecting apes is much more closely related to human *P. malariae*, but there was little evidence of genetic exchange between the ape and human parasites, suggesting that these should be considered separate species. Patterns of nucleotide polymorphism suggest that the human parasite has undergone a severe genetic bottleneck, followed by population expansion. Together, these data suggest that the *P. malariae* lineage has a long history in Africa, and the human parasite may have arisen through a recent cross-species transmission from apes. Finally, our analysis places *P. brasilianum* as a lineage within the radiation of human *P. malariae* strains, confirming that *P. brasilianum* emerged following a recent anthroponotic transmission to New World monkeys.

Schistosome Biology II - (Conference room 2)

11:45 (15 mins)

Establishing a Female-only Controlled Human Schistosoma mansoni Infection Model: a safety and dose finding study*A23418*

Presenter: **Mr Jan Pieter Koopman**, *PhD Student, Leiden University Medical Centre*

J P Koopman[1]; J J Janse[1]; M Casacuberta-Partal[1]; J C Sijtsma[1]; C J de Dood[1]; O A Lamers[1]; A van Diepen[1]; A Ozir-Fazalalikhan[1]; L van Lieshout[1]; G J van Dam[1]; P L Corstjens[1]; M Yazdanbakhsh[1]; C H Hokke[1]; M Roestenberg[1];
[1] Leiden University Medical Centre, Netherlands

A controlled human infection model with schistosomiasis (CHI-S) has the potential to speed up vaccine development and can provide useful insights into immune responses following exposure to schistosomes. Recently, a CHI-S model was successfully established using only male *Schistosoma mansoni (Sm)* cercariae in Dutch *Schistosoma*-naïve individuals. In this current study, we aimed to establish a single-sex, female-only CHI-S model to identify which dose of female *Sm* cercariae is safe and leads to patent infection. To this end, we enrolled 13 healthy, S*chistosoma*-naïve volunteers who were challenged with 10 (n=3) or 20 (n=10) female cercariae. Subsequently, participants were followed up for 20 weeks, receiving treatment with praziquantel twice at 8 and 12 weeks after exposure. Throughout, safety data and samples were collected. We used serum circulating anodic antigen (CAA) levels to determine infection status (≥1.0 pg/mL). In addition, we monitored eosinophil levels and *Schistosoma* serology. So far, 6 participants have completed the 20 week follow-up, while the remaining 7 participants are scheduled to complete week 8 mid-June. Similar to the male CHI-S, we observed a rash at the site of infection in nearly all participants. Starting three weeks after exposure, participants reported systemic symptoms probably related to acute schistosomiasis. None of the participants exposed to 10 cercariae showed CAA levels above 1.0 pg/ml, while in the 20 cercariae dose group 2 out of 3 did. Based on these preliminary data, the safety profile of female cercariae seems similar to that of male cercariae. This female CHI-S model together with the previous male CHI-S model provide unique opportunities to dissect sex-specific immune responses to *Schistosoma mansoni* that can further vaccine development.

12:00 (15 mins)

Schistosoma mansoni lacks the homologue of the human telomerase reverse transcriptase (hTERT), and relies on the snail enzyme for its survival.*A23450*

Presenter: **Dr Matty Knight**, *Professor, University of the District of Columbia*

M Knight[3]; N Pels[3]; O Elhelu[3]; S Parn[3]; G Rinaldi[2]; V Mann[1]; P Brindley[1];
[1] The George Washington University, United States; [2] Wellcome Sanger Institute, UK; [3] University of the District of Columbia, United States

The human telomerase reverse transcriptase, hTERT, is the catalytic sub-unit of telomerase. Together with telomerase RNA, the enzyme complex participates in the maintenance of telomeres at the proximal ends of chromosomes. The regulation of hTERT is tightly linked to cell growth states governing either malignancy or senescence and is a prospective therapeutic target in cancer. Malignancy and parasitic disease share many characteristics, such that we posit that the snail host/schistosome relationship provides a facile model to examine the regulation of transcription of cancer-related genes including the snail ortholog of hTERT. To test the hypothesis in relation the development of larval Schistosoma mansoni in the snail Biomphalaria glabrata, we utilized an in-silico approach to identify the snail hTERT ortholog. From the comparative analysis of the human hTERT amino acid sequence (ID 014746) to the B. glabrata ortholog (733 amino acids, accession XP_013074763.1), a strong homology was evident between amino acid sequences of the telomerase of both species (E-value of 2e-86). BLASTp searches using Schistosoma mansoni as the query suggest that the parasite lacks a putative hTERT, even though the parasite chromosomes do possess telomeres. Concerning the regulation of the snail hTERT ortholog in relation to schistosome intra snail development, real time qPCR analysis revealed temporal regulation of B. glabrata hTERT before and after S. mansoni infection in the snail, with upregulation of B. glabrata hTERT transcription 18 hours after schistosome infection. Treatment of snails with the anti-telomerase drugs before infection blocked subsequent cercarial development. These findings suggest that schistosomes rely on the snail telomerase for productive infection establishment and parasite transmission.

BES: Ecology and Evolution I - (Conference room 1)

12:00 (15 mins)

Diversity of Strongylid Nematode Communities in Wild Western Lowland Gorillas*A23113*

Presenter: **Miss Bethan Mason**, *PhD Student, Department of Botany & Zoology, Masaryk University*

B Mason[2]; K J Petrzelkova[1]; T Bohm[3]; B Cervena[1]; T Fuh[4]; A Gomez[5]; S Knauf[6]; J Kreisinger[7]; U Maloueki[3]; D Modry[8]; N Tagg[9]; N Wangue[10]; B Pafco[1];
[1] Institute of Vertebrate Biology, Czech Academy of Sciences, Czech Republic; [2] Department of Botany & Zoology, Faculty of Science, Masaryk University, Czech Republic; [3] African Parks, Odzala-Kokoua National Park, Congo; [4] WWF Central African Republic, Central African Republic; [5] Department of Animal Science, University of Minnesota Twin Cities,, United States; [6] Department of Animal Sciences, Georg-August-University, Germany; [7] Department of Zoology, Faculty of Science, Charles University, Czech

Republic; [8] Department of Pathology and Parasitology, Faculty of Veterinary Medicine, University of Veterinary Sciences Brno, Czech Republic; [9] Project Grands Singes, Centre for Research and Conservation, Royal Zoological Society of Antwerp;, Belgium; [10] WWF Kudu-Zumbo Programme, Cameroon

There is growing concern that changes in parasite communities can significantly affect the survival of fragile wildlife host populations. Western lowland gorillas (*Gorilla gorilla gorilla*) are among the most critically endangered mammalian species. They are phylogenetically closely related to humans (*Homo sapiens*) and, as large terrestrial herbivores, are keystone species for their ecosystems. As such, it is of mounting importance to understand their ecology and conservation threats, including those encompassed by parasitic diseases. Current understanding of wildlife helminths is scarce compared to knowledge on human and livestock helminths, including application of epidemiological modelling.

Gastrointestinal parasite infections are typically asymptomatic in primates, but alterations to transmission mechanisms or host susceptibility can exacerbate the clinical implications of infection. Ongoing habitat disturbance or reduction, changing climate and shifts in group dynamics may all influence the impact of parasite infections on the western lowland gorilla. While *Gorilla* host a broad spectrum of parasites, strongylid nematodes are particularly prevalent, occurring in complex communities within host individuals, as is typical for large terrestrial herbivores. However, little is known on the diversity or epidemiology of these strongylid communities in non-human primates, with traditional coproscopic methods unable to distinguish strongylid nematodes to the species-, or even genus-, level due to indistinguishability of eggs. Modern advances in high-throughput sequencing (HTS) techniques allow analysis of these complex strongylid communities, including identification of both dominant and rare species. We employed an HTS-methodology, utilising ITS-2 metabarcoding within the MiSeq Illumina platform, for strain-level identification of strongylid communities. We successfully applied this approach, previously optimised by our team, to describe the genetic diversity of gastrointestinal strongylid communities in 208 faecal samples from western lowland gorillas, spanning four countries within the Congo basin. Alongside, we also employed 16S rDNA sequencing to describe the gut bacterial community, allowing us to investigate interactions between the two communities within the gastrointestinal system.

We established baseline data of strongylid nematodes infections in wild western lowland gorillas, identifying 134 strongylid haplotypes, comprising six genera. We found that *Necator* and *Oesophagostomum* were dominant genera across localities, with alpha diversity consistent across all localities except one. Though, greater variations were seen in beta diversity between localities, when concerning strongylid community compositions. We also identified interactions between certain strongylid species and gut bacterial genera. Our presented work provides the framework for ongoing research on the comparison of strongylid nematode diversity across all four *Gorilla* subspecies, hoped to provide insight into strongylid epidemiology in the context of host ecology and phylogeny.

BES: Ecology and Evolution II - (Conference room 1)

24-June-2021, at 13:00 (30 mins)

Environmental Parasitology: relevance of parasites in ecotoxicological studies *A23065*

Presenter: **Prof Bernd Sures**, *Universität Duisburg-Essen*

Despite the progress in understanding the ecological significance of parasites that we have made in recent years, we are still far away from having a thorough understanding of the ecological and ecotoxicological implications of parasites. There is an increasing number of papers showing how parasitism and pollution can interact with each other in aquatic organisms. In addition to synergistic negative effects of both stressors, there is also evidence of antagonistic interactions. The latter are related to the reduction of pollutant levels in infected hosts compared with uninfected conspecifics. As reduced contaminant concentrations are usually correlated with less adverse effects, it might be advantageous to be infected if hosts are confronted with environmental pollution. On the other hand, possible pathological effects might reduce a potentially beneficial effect of parasites. There are also examples, however, which show that parasites may enhance toxic effects of pollutants by interfering with the host's protection mechanisms. In these cases, parasites would have exclusively negative effects on the physiological homeostasis of their hosts. In the present talk selected key issues are highlighted that illustrate important contributions of parasites in the field of environmental toxicology and the implications of parasites in pollutant transfer and accumulation with subsequent effects within food-webs. By using selected examples from aquatic ecosystems, an insight into selected ecotoxicological implications of parasites will be provided.

Schistosomiasis - Control, epidemiology and One Health I - (Conference room 2)

13:00 (30 mins)

How does one go from schistosome granulomas to schistosomiasis control programs?*A23171*

Presenter: **Prof Dan Colley**, *University of Georgia*

TBC

BES: Ecology and Evolution II - (Conference room 1)

13:30 (15 mins)

Using high throughput sequencing to detect the presence of multiple parasite strains in the rapidly declining European turtle dove (Streptopelia turtur)*A23330*

Presenter: **Miss Rebecca Young**, *PhD student, Cardiff Univrsity*

R Young[3]; J Dunn[1]; I Vaughan[3]; J Mallord[2]; W Symondson[3];
[1] University of Lincoln, UK; [2] RSPB, UK; [3] Cardiff Univeristy, UK

Trichomonas gallinae is a widespread protozoan parasite infecting a diverse range of avian orders, in particular, free ranging Columbiformes and Falconiformes, and has been found to cause mortality in the rapidly declining European turtle dove. At least 19 strains of *T. gallinae* have been identified, with certain strains found to be more virulent, resulting in a high rate of mortality in infected individuals, whilst other, less virulent stains often result in asymptomatic infection. As a key aspect of parasite ecology is understanding the dynamics of co-infection, we consider the rate of infection with multiple strains of *T. gallinae* in the rapidly declining European turtle dove (*Streptopelia turtur*). This study is one of very few utilising high throughput sequencing to identify the presence of multiple strains of *T. gallinae* within a single host. Birds were sampled across one wintering (Senegal) and two breeding (France and Hungary) sites. We detected a higher rate of co-infection with multiple strains of *T. gallinae* than previous studies, with multiple strains being detected in 16% of birds sampled. Four significant interactions were detected among the four dominant strains of *T. gallinae* identified in this study, all of which were negative. This indicates that, despite a higher rate of co-infection being observed in this study than previously, co-infection occurs less frequently than would be expected if infection were random, suggesting there is a mechanism acting to reduce the presence of multiple strains within the host.

Schistosomiasis - Control, epidemiology and One Health I - (Conference room 2)

13:30 (15 mins)

The potential of citizen science to tackle the wicked problem of snail-borne diseases*A23523*

Presenter: **Dr Tine Huyse**, *senior researcher - parasitologist, Royal Museum for Central Africa*

T Huyse[1];
[1] Royal Museum for Central Africa, Belgium

Citizen science, where non-specialists are contributing to scientific research, has proven its merits in many scientific disciplines, as it can boost data collection and stimulate informal learning. In the ATRAP project we harness this untapped potential by developing a novel snail monitoring approach that can be executed by non-specialists. Both in DRCongo and Western Uganda we trained a network of 25 citizens to collect and identify snail species belonging to the genera that are involved in the transmission of schistosomiasis and fasciolosis. They report on a weekly basis on snail host abundances in predefined water contact sites, add GPS location, key water chemistry parameters, and photographs of the identified snails. Data is submitted using the freely available mobile phone application KoBoToolbox, followed by semi-automatic validation by trained researchers. By doing so, we hope to increase our understanding on snail population dynamics and generate the much-needed data to support local targeted snail control measures in remote and/or resource-limited environments. At the same time, these citizen scientists will act as communicator to the wider community using contextualized communication tools developed in the social strand of the ATRAP project.

BES: Ecology and Evolution II - (Conference room 1)

13:45 (15 mins)

On snail-borne hippo parasites: do artificial lakes and biological invasions pose a burden on Hippopotamus amphibius?*A22951*

Presenter: **Mr Ruben Schols**, *PhD candidate, Royal Museum for Central Africa*

R Schols[1]; H Carolus[2]; C Hamoud[1]; K C Muzarabani[3]; M Barson[4]; T Huyse[1];
[1] Royal Museum for Central Africa, Belgium; [2] Laboratory of Molecular Cell Biology, KU Leuven-VIB center for microbiology, Belgium; [3] University of Zimbabwe, Harare, Zimbabwe; [4] University of Botswana, Gaborone, Botswana

Background

Humans impose a significant pressure on large herbivore populations in Africa through hunting, poaching and habitat destruction. Indirect anthropogenic disturbances such as artificial lake creation and the subsequent introduction of invasive species that alter the ecosystem have been less studied. Still, these events can lead to drastic changes in parasite diversity and transmission.

Results

In order to document and identify trematode parasites of hippopotami in artificial water systems of Zimbabwe, we applied an integrative taxonomic approach, combining molecular diagnostics and morphometrics on archived and new samples. In doing so, we provide DNA reference sequences of the hippo liver fluke *Fasciola nyanzae*, enabling us to construct the first complete *Fasciola* phylogeny. We describe parasite spillback of *F. nyanzae* by the invasive freshwater snail *Pseudosuccinea columella*, as a consequence of a cascade of biological invasions in Lake Kariba, one of the biggest artificial lakes in the world. Additionally, we report an unknown stomach fluke of the hippopotamus transmitted by the non-endemic snail *Radix* aff. *plicatula*, an Asian snail species that has not been found in Africa before, and the stomach fluke *Carmyerius cruciformis* transmitted by the native snail *Bulinus truncatus*. Finally, *Biomphalaria pfeifferi* and two *Bulinus* species were found as new snail host records for the poorly documented hippo blood fluke *Schistosoma edwardiense*.

Conclusions

Our findings indicate that artificial lakes are breeding grounds for endemic and non-endemic snails that transmit trematode parasites of the common hippopotamus. This has important implications, as existing research links trematode parasite infections combined with other stressors to declining wild herbivore populations. Therefore, we argue that monitoring the anthropogenic impact on parasite transmission should become an integral part of wildlife conservation efforts.

Schistosomiasis - Control, epidemiology and One Health I - (Conference room 2)

13:45 (15 mins)

Citizen scientists versus malacologists: comparing schistosome snail collections in Lake Albert, Uganda*A23448*

Presenter: **Mr Julius Tumusiime**, *Scientist, Mbarara University of Science and Technology*

J Tumusiime[4]; J Brees[1]; G Kagoro-Rugunda[4]; C Tolo[4]; C Albrecht[3]; D Namirembe[4]; L Jacobs[1]; T Huyse[2];
[1] KU-Leuven, Belgium; [2] Royal Museum for Central Africa, Belgium; [3] Justus-Liebig-Universität Gießen, Germany; [4] Mbarara University of Science and Technology, Uganda

Snail-borne diseases like schistosomiasis and fasciolosis have proven a major challenge in their control with some scholars referring to them as ‘wicked problems’. For instance, traditional control strategies like mass drug administration (MDA) have not yielded to expectations with the disease re-emerging soon after the intervention. The WHO recommends therefore to (add a) focus on sustainable snail control, but this relies on the availability of high-quality snail distribution data, a major gap in developing countries like Uganda. As such, the citizen science approach, which has proven its worth in other fields, has been proposed in this project as a possible solution to the data gap. To what extent can we rely on data collected by citizen scientists in snail-borne disease control? In this study, a cohort of 25 community members were selected and trained in snail sampling and identification. Each one of them monitors 2 to 4 water contact sites on a weekly basis, covering 82 sites over a total area of ~750 km^2. Data on the presence and abundance of the genera *Biomphalaria*, *Bulinus* and *Lymnaea* (*Radix*) are entered using the mobile phone app KoboCollect, while an experienced malacologist monitors the same sites on a monthly basis using the same sampling effort of 30 minutes per site. Here we report the results for data collected over an 8 month period. Pairwise comparison of the data, based on closeness of sampling date, was done to estimate the extent of agreement between the data sets in presence/absence of snails, and their counts using binomial probability tests and Pearsons χ^2 tests

respectively. For the 375 paired observations, we could not detect significant differences in presence or absence of snails at a site between the citizen scientist and expert collected data ($p<0.001$). The extent of agreement varied for different snail species, with 85.7% for *Bulinus*, 80.1% for *Biomphalaria*, and 70% for *Radix.* The extent of disagreement is largely dependent on the site, with sites at the lake (lower abundance) more likely to disagree in snail occupancy between the datasets. Overall, a higher snail abundance is reported by the expert malacologists compared to the citizen scientists, when the data agree in presence of snails at a site ($p<0.001$). Data mostly disagreed in presence when snail abundance was low, being at least four times lower than when both datasets agreed in snail presence. Thus, citizen collected data can be reliable for detecting presence of snails at a potential snail-borne disease transmission site. Based on the current data we conclude that malacological surveys by experts provide more reliable data for studying freshwater snail abundances.

Key words: *Snail-borne diseases; citizen science; Lake Albert; schistosomiasis; fasciolosis*

14:00 (15 mins)

The current and future predicted status of schistosomiasis in South Africa under climate change *A23178*

Presenter: **Dr Lizaan de Necker**, *Postdoctoral Researcher, North-West University*

L de Necker[1]; D Cilliers[2]; R Burger[2]; N J Smit[1]; V Wepener[1];
[1] Water Research Group, Unit for Environmental Sciences and Management, North-West University, Potchefstroom, South Africa, South Africa; [2] Unit for Environmental Sciences and Management, North-West University, Potchefstroom, South Africa

Climate change is predicted to modify global air temperatures and precipitation. This poses a significant threat to human health as it may alter the distribution and occurrence of vector-borne diseases. This is of particular concern for regions already burdened by many tropical diseases such as sub-Saharan Africa. As a result of these concerns, tropical diseases have gained new traction in the public health discussions. Schistosomiasis, caused by the parasitic trematodes *Schistosoma* spp., is a neglected tropical disease transmitted to humans and animals through snail vectors that are present in still to slow-flowing water bodies. Climate change and continued human population growth in developing countries may alter the distribution of this disease and continuous evaluation thereof is therefore imperative. In South Africa, little research on the distribution of schistosomiasis has occurred since the 1960s and, as a result, the present status of the vectors and parasites are unknown. It is also unclear how climate change and human population growth may alter the distribution of the parasitic disease in the future. The present study will address these concerns with the use of a combined desktop and field-based assessment. Thus far, the first digital map of the distribution of the snail vectors in South Africa has been created using 50 years of distribution records available from the National Freshwater Snail Collection hosted by North-West University. From here, computer-based models will be used to determine the present distribution of *Schistosoma* transmitting snail vectors and parasites in endemic regions in South Africa by evaluating climatic changes from the 1960s to the present. Further models will be used to assess the potential future distribution of the vectors and parasites in relation to climate change and population growth. Field based assessment surveys of snails and parasites will take place simultaneous along with interviews with local communities to assess the accuracy of the model and evaluate the knowledge of people regarding schistosomiasis.

BES: Ecology and Evolution II - (Conference room 1)

14:00 (15 mins)

Zoonotic Implications of parasite helminths among domestic animals in selected communities of Caraga Region, Philippines *A23429*

Presenter: **Dr Sheina Macy Manalo**, *University Research Associate, University of the Philippines Los Baños*

B Divina[2]; V G Paller[2]; S Manalo[3]; M Bandal[3]; M Betson[1];
[1] University of Surrey, UK; [2] University of the Philippines, Los Baños, Philippines; [3] University of the Philippines Los Baños, Philippines

Domestic animals are sources of livelihood, food, companionship, and security for humans. However, this close association with animals allows for the transmission of zoonotic helminths that negatively impact human health. In marginalized areas in the Philippines, very little is known about zoonotic parasites in domestic animals. In this study, fecal samples from 146 dogs, 34 cats, 211 pigs, 154 water buffaloes, and 18 cattle in selected rural communities in Caraga Region, Philippines were examined using standard parasitological

techniques. Furthermore, 341 animal owners were interviewed regarding animal management practices and awareness of zoonotic helminth exposure. An additional 100 water buffalo owners were included in the survey of management practices. Seventeen species of zoonotic helminths were identified, with an overall prevalence of 55.1%. Hookworms and *Toxocara* spp. were most prevalent in companion animals while *Fasciola* spp. and strongyles in farm animals. Molecular analysis will be done to confirm identity of the parasites. Several factors such as animal age, sex, location, housing and feeding practices showed significant association for infections. The high prevalence of zoonotic infections in domestic animals and low awareness of animal owners poses health threats to the community. The results highlight the importance of a One Health approach in addressing concerns about helminth zoonoses.

Diagnosis and Biomarkers II - (Conference room 1)

24-June-2021, at 15:00 (30 mins)

Application of environmental DNA analysis for Fasciola hepatica control in livestock*A23520*

Presenter: **Dr Rhys Jones**, *Lecturer , IBERS*

Controlling fasciolosis in livestock is becoming an increasing challenge globally as climate change and anthelmintic resistance increase liver fluke prevalence and reduces treatment efficacy, respectively. With this, there is growing interest in applying alternative fasciolosis control strategies such as grazing and land management practices on farms. To effectively apply these practices, an understanding of where Fasciola hepatica's intermediate snail host, Galba truncatula resides on farmland is required to enable infection risk areas to be targeted to reduce snail presence and infections in grazing livestock. However, our understanding of G. truncatula spatial ecology is limited, with traditional survey methods used to map G. truncatula habitats on farmland inconsistent, time consuming, costly and requires significant expertise to be applied efficiently. In recent years, we have developed and optimised an environmental DNA assay to detect G. truncatula eDNA in small water bodies on farmland. Optimisation of this assay has created a protocol where 500 ml of water is collected from small water body habitats on farmland and filtered through 3 um pore filters, with DNA extracted from filters prior to DNA amplification. This assay has been used map G. truncatula habitats on farmland, enabling farmers to apply alternative fasciolosis control strategies to control fluke infections in grazing cattle and sheep. We have also used eDNA analysis to identify factors associated with G. truncatula presence in small water body habitats and to monitor interaction between grazing livestock, fluke infection risk areas and subsequent infection burdens. We believe that eDNA analysis has potential to become a valuable tool for intermediate snail host research and trematode control in future.

Schistosomiasis - Molluscan biology & ‘omics’ - (Conference room 2)

15:00 (30 mins)

Snail vector biology, perspectives from genome mining*A23169*

Presenter: **Prof Coen Adema**, *University of New Mexico*

With discovery of snails as vectors of trematode parasites first in the 1880s, distribution of snail hosts was recognized as critical aspect of epidemiology of trematode-caused infectious diseases, making snails a logical target for integrated control efforts. In depth studies, mostly of the Biomphalaria snail/Schistosoma mansoni parasite combination, showed additional complexity in transmission patterns due to variable host competence among and within vector snail species caused by genetic variation in snail (immune)biology. Motivation to gain broader, more comprehensive understanding of vector biology led to characterization of the genome of the snail B. glabrata in 2017. Genome annotation yielded unprecedented details of snail communication, neuroendocrinology, immunity, reproduction and regulation of gene expression. This information helps to interpret distribution and persistence of snail vectors in the field, as well as determinants of host competence to S. mansoni. The genomic data continue to provide access into B. glabrata biology, enabling large scale proteomics, linkage studies for anti-parasite resistance, and characterization of (novel) immune genes. Continued genome mining, also supported by long read sequencing of select BAC clones has improved description and assembly of major anti-trematode immune lectins, belonging to the gene family of VIgLs (Variable Immunoglobin and Lectin domain containing molecules). Genome analyses also disclosed that B. glabrata snails, employing hemoglobin as oxygen carrier, retain an evolutionary relic of a gene for ancestral respiratory hemocyanin named Hcl-1 (hemocyanin-like 1). Functional transcriptomics indicate that Hcl-1 has undergone neofunctionalization toward influencing the reproductive success of B. glabrata: RNAi knockdown of Hcl-1 negatively impacts viability of snail eggs. The value of genome analyses for exploring B. glabrata snail vector biology increases with novel (future) genome assemblies of additional B. glabrata strains, and of other

pulmonate and prosobranch snail vectors of trematode parasites. Comparative genome mining will identify unique and shared biological features of snails that govern snail distribution and transmission of particular trematodes, providing leads that may be targeted for vector- or transmission control. Integrative, synthetic consideration of such findings will inform parasitology by revealing general determinants of trematode virulence and snail host competence.

15:30 (15 mins)

Bulk segregant analysis of host specificity in schistosome parasites*A23519*

Presenter: **Dr Frédéric Chevalier**, *Staff Scientist, Texas Biomedical Research Institute*

F Chevalier[1]; W Le Clec'h[1]; P T LoVerde[2]; B Gourbal[3]; G Mitta[3]; T J Anderson[1];
[1] Texas Biomedical Research Institute, United States; [2] University of Texas Health San Antonio, United States; [3] Université de Perpignan Via Domitia, France

Interactions between parasitic trematodes and their aquatic snail hosts provide a classical example of gene-for-gene co-evolution. Trematode infections typically castrate snails, leading to selection of costly defense mechanisms, while parasites evolve to circumvent these defenses. We used a genetic approach to identify the parasite genes involved in overcoming snail defenses in the *Biomphalaria glabrata - Schistosoma mansoni* system. We performed genetic crosses between two schistosome populations (SmBRE and SmLE) with distinctive patterns of host specificity: while both parasite populations infect BgBRE snails, only SmLE can infect the BgBS90 snail population. The F1 parasite progeny from our crosses were unable to infect BgBS90, while ability to infect BgBS90 snails was recovered in some F2 progeny, consistent with recessive inheritance. To identify the regions of the S. mansoni genome involved in snail host specificity we used a bulk segregant analysis (or extreme QTL (X-QTL)) approach. We (i) allowed pooled F2 progeny to infect either BgBRE or BgBS90 snails, (ii) collected the cercariae emerging from each of these snail populations and (iii) quantitatively genotyped pools of selected and unselected schistosome progeny to measure allele frequencies exome-wide. Two genome regions (on chromosome 2 and 3) showed dramatic enrichment in parasites genotypes able to infect BgBS90, and clearly underlie host specificity. These two genome regions span multiple genes: the challenge now is to identify the specific genes and mutations involved. Our long-term aim is to identify interacting genes in both parasite and snail to understand host-parasite interaction and evolution at the molecular level.

Diagnosis and Biomarkers II - (Conference room 1)

15:30 (15 mins)

SHERLOCK4HAT: a new CRISPR-based tool for Human African Trypanosomiasis diagnosis*A23195*

Presenter: **Dr Nuria Sima Teruel**, *Post-doctoral researcher, Institut Pasteur*

N Sima[1]; A Dujeancourt-Henry[1]; A Crouzols[1]; B Rotureau[1]; L Glover[1];
[1] Institut Pasteur, Paris, France

Human African Trypanosomiasis (HAT) is a debilitating, and often fatal, neglected tropical disease, caused by two subspecies of *Trypanosoma brucei* (T. b.) - *T. b. gambiense*, responsible for 98% of cases, and *T. b. rhodesiense*, accounting for the remaining 2%. Due to a concerted effort over the past 20 years, HAT is now approaching elimination, with the number of cases reported in 2019 dropping below 1,000. In this context, gambiense HAT was targeted for elimination as a public health problem by 2020 and sustainable elimination of transmission (zero cases) by 2030. These efforts are at risk to be undermined as the current field-based HAT diagnostic tools may lack the sensitivity and specificity required to meet the harsh constraints imposed by the WHO in the HAT elimination phase. We have adapted the recently developed Specific High-sensitivity Enzymatic Reporter unLOCKing (SHERLOCK) for the detection of *Trypanosoma* parasites and optimized the methodology for mass screening, surveillance of active infections and point of care testing. SHERLOCK is a CRISPR-based approach that relies on the collateral RNase activity of Cas13 upon target activation. With our assay, we are able to distinguish between three *T. brucei* subspecies without cross-reactivity and with sensitivity of 0,1 parasite/uL using *in vitro* as well as *in vivo* experimental and field isolated samples. We are currently able to detect parasitaemia lower than 100 parasites/mL in simulated human infections. We are now optimizing one-tube reactions coupled to a lateral flow assay making this a simple portable diagnostic to be used at point of care.

15:45 (15 mins)

Evaluating the diagnostic test accuracy of molecular xenomonitoring methods for the surveillance of lymphatic filariasis and onchocerciasis*A23143*

Presenter: **Mr Joseph Pryce**, *Mr, Liverpool School of Tropical Medicine*

J D Pryce[1]; L J Reimer[1];
[1] Liverpool School of Tropical Medicine, UK

Background

Molecular xenomonitoring (MX) is the detection of parasite DNA in vector populations. In lymphatic filariasis (LF) and onchocerciasis elimination settings, MX is a recommended surveillance tool for verifying interruption of transmission and monitoring for disease resurgence. However, the sensitivity of MX for detecting communities positive for either disease has not been evaluated. Due to the limitations of other surveillance tools, MX may have utility for a range of additional programmatic goals, but its use is currently restricted by a limited understanding of the relationship between MX results and human prevalence.

Methods

We conducted a systematic review of studies reporting the prevalence of filarial worm DNA in wild-caught mosquitoes or black fly vectors (MX rate) and the corresponding prevalence of microfilaria (mf) in humans. We estimated the sensitivity of MX for detecting positive communities at a range of mf prevalence values and vector sample sizes. We evaluated the relationship between mf prevalence and MX rates using linear regression models.

Results

LF: We identified 24 studies comprising 144 study communities. MX had an overall sensitivity of 98.3% (95% CI 41.5, 99.9%) and identified 28 positive communities that were negative in the mf survey. Low sensitivity in some studies was attributed to small mosquito sample sizes (<1,000) and very low mf prevalence (<0.25%). Human mf prevalence and mass drug administration status were significantly associated with MX rate measurements, accounting for approximately half of the variation in MX rate ($R^2 = 0.49$, $p<0.001$). Data from longitudinal studies showed that, within a given study area, there is a strong linear relationship between MX rate and mf prevalence ($R^2 = 0.78$, $p < 0.001$).

Onchocerciasis: We identified 15 studies comprising 34 study communities that were included in the quantitative analyses. Most communities were at advanced stages towards elimination and had no or extremely low human prevalence. MX detected positive flies in every study area with >1% mf prevalence, with the exception of one study where comparisons between entomological and epidemiological surveys were complicated. We identified a significant relationship between the two measurements, with mf prevalence accounting for half of the variation in MX rate (R^2 0.50, $p<0.001$).

Conclusion

MX shows clear potential as a sensitive tool for detecting LF and onchocerciasis-positive communities, and as a predictor of human mf prevalence. Further data is required to understand how this relationship can be used to support the evaluation of programmatic goals.

Schistosomiasis - Molluscan biology & 'omics' - (Conference room 2)

15:45 (15 mins)

Lack of functional chromatin dynamics through nuclear motor proteins in aged Biomphalaria glabrata snails reveals a mechanism of interest with respect to controlling schistosomiasis. *A23415*

Presenter: **Dr Daniel Horton**, *unemployed, unemployed*

D A Horton[3]; R Torres Pereira[3]; H D Arican-Goktas[3]; P Driguez[2]; G Rinaldi[2]; M Knight[1]; **J Bridger**[3];
[1] George Washington University, United States; [2] Wellcome Trust Sanger Institute, UK; [3] Brunel University London, UK

We have previously demonstrated that in the interphase nuclei of the intermediate snail host, Biomphalaria glabrata, specific genes, such as the (Heat shock protein) Hsp70 loci are relocated rapidly to new non-random nuclear locations with minutes of the presence of Schistosoma mansoni parasites. This relocation is correlated with the subsequent upregulation of the gene in susceptible snails, which is not apparent in resistant snails or in susceptible snails that have been exposed to irradiated attenuated parasites (miracidia). This active and

functional relocation of the Hsp70 loci can be recapitulated by heat-shocking snails at 32oC. However, in aged snails the gene loci relocation is not possible neither in the presence of parasite nor heat-shock. We have evidence to support that the rapid relocation of gene loci is due to the presence of nuclear motor activity in young snails which is lacking in aged snails. Interference with this mechanism negatively affects chromatin dynamics and gene expression in response to an infection or a heat shock stimulation. This lack of chromobility recapitulates a recent finding in aged human cells (senescent) that normal nuclear motor activity for rapidly relocating chromosomes is also lacking, making B. glabrata a new model organism in which to study genome behaviour in relation to ageing. Since we know this gene movement and subsequent upregulation of gene expression are involved in an active schistosome infection, we hypothesis that aged snails would be less able to be infected by S. mansoni, making this nuclear motor complex and dynamics mechanism a target with respect to controlling infection of this human parasite in the snail.

16:00 (15 mins)

First molecular identification of Bulinus africanus in Lake Malawi with discussions on its transmission potential for human schistosomes *A23328*

Presenter: **Mr Mohammad Alharbi**, *phd student, Liverpool school of tropical medicine*

M Al-Harbi[1]; S Kayoni[1]; J LaCourse[1]; **J R Stothard**[1];
[1] Liverpool School of Tropical Medicine, UK

The freshwater snail genus *Bulinus* plays a vital role in transmitting parasites of the *Schistosoma haematobium* group. Three species within the *S. haematobium* group cause urogenital schistosomiasis while five others typically infect wild and domestic ruminants. Using DNA-based identification methods, a hybrid schistosome between *S. haematobium* and *S. mattheei* has been recently detected in school children along the Lake Malawi shoreline in Mangochi District. This finding raised the need for contemporary revaluation of local interactions between schistosomes and snails, with particular focus on snail species within the *Bulinus africanus* group. In 2017, 2018 and 2019, malacological surveys sampled several freshwater sites in Mangochi District. Collected snails (n= 250) were first characterised using shell morphology before closer inspection of the cytochrome oxidase subunit 1 gene (*cox*1), with DNA barcoding of the 'Folmer' region and a rapid PCR-RFLP typing assay with double digestion with *Hae*III and *Sac*I restriction enzymes. DNA *cox*1 sequence analysis, with phylogenetic tree construction, suggested the presence of at least three taxa in Lake Malawi, *B. globosus* alongside first reports of *B. africanus* and *B. angolensis* which could be differentiated by PCR-RFLP methods. The latter species is morphologically unusual for it is typically placed with the *B. truncatus/tropicus* complex. Further to *B. nyassanus* which plays a key role in the transmission of *S. haematobium* within the lake, the distribution of *B. globosus* was only present in small water bodies around its margins whereas *B. africanus* and *B. angolensis* were found within it. This study provides new insight into the recent changes in the epidemiology of urogenital schistosomiasis as likely driven by a new diversity of *B. africanus* group snails within the lake. Inspection of additional DNA loci is needed to further characterise *B. angolensis,* comparing this population more broadly.

Diagnosis and Biomarkers II - (Conference room 1)

16:00 (15 mins)

Diagnosis of sheep fasciolosis caused by Fasciola hepatica using Cathepsin L ELISA and lateral flow technologies *A23416*

Presenter: **Dr Amber Dorey**, *Post-Doctoral Researcher, Molecular Parasitology Laboratory, NUI Galway*

A Dorey[1]; J López Corrales[1]; K Cwiklinski[1]; C De Marco Verissimo[1]; R Lalor[1]; H Jewhurst[1]; A McEvoy[2]; M Diskin[2]; C Duffy[3]; L Cosby[3]; O Keane[2]; S Doyle[4]; J P Dalton[1];
[1] National University of Ireland, Galway (NUI Galway), Ireland; [2] Teagasc, Ireland; [3] Agri-Food Biosciences Institute, Belfast, UK; [4] Maynooth University, Ireland

Fasciolosis, a global parasitic disease of agricultural livestock, is caused by the liver fluke *Fasciola hepatica.* Management and strategic control of fasciolosis depends on early assessment of the extent of disease on farms to allow control measures to be rapidly implemented. Traditionally, this has relied on the detection of eggs in the faeces of animals, a laborious method that lacks sensitivity (especially for sub-clinical infections) and identifies chronic infections only. Molecular tools such as enzyme linked immunosorbent assays (ELISA) offer a faster and more sensitive serological means of diagnosis, with the potential to detect early acute infection before significant liver damage occurs. We evaluated the performance of three functionally-active recombinant forms of *F. hepatica* secreted cathepsin L's as antigens in an indirect ELISA to serologically diagnose liver

fluke infection in experimentally infected sheep. We found that these enabled detection of fasciolosis in sheep as early as three weeks after experimental infection, at least five weeks earlier than both coproantigen and faecal egg tests. Furthermore, we developed a lateral flow assay capable of detecting infection as soon as 7 weeks post-infection. The lateral flow assay provides significant time and cost-saving advantages compared to the ELISA, while still demonstrating high levels of sensitivity. With the potential to be used at point-of-care and provide results within 30 mins, lateral flow technology represents a significant advancement over both the coproantigen ELISA and faecal egg count in the diagnosis of *F. hepatica* infection.

16:15 (30 mins)

Microscopy – relevant or redundant in diagnostic parasitology?*A23176*

Presenter: **Mrs Claire Rogers**, *Principal Biomedical Scientist, London School of Hygiene and Tropical Medicine*

Over the last 130 years the diagnosis of infectious diseases has advanced exponentially since Robert Koch set down his criteria for diagnosis. Development of molecular based methods have given diagnostic laboratories the option of high throughput automation, syndromic diagnosis by microarray and whole genome sequencing. Whilst the disciplines of Bacteriology and Virology have embraced the new technology, Parasitology has lagged behind. Traditionally relying on macroscopic and microscopic identification of parasites in blood, faeces and other specimen types, is it now time to move on and retire our microscopes in favour of PCR, LAMP and point of care tests? I will present my view on the current role of microscopy in the diagnostic parasitology laboratory, including its role in the diagnosis of malaria in an non-endemic setting.

Plenary II - (Conference room 1)

25-June-2021, at 09:00 (45 mins)

Fascioliasis control in human endemic areas: one health action to complement preventive chemotherapy*A23537*

Presenter: **Prof Santiago Mas-Coma**, *Faculty of Pharmacy, University of Valencia*

Introduction: Human fascioliasis is caused by fasciolid flukes using livestock as reservoirs and freshwater lymnaeid snails as vectors. This disease is highly dependent on climate change and influenced by livestock movements. WHO control follows different strategies according to countries, always based on triclabendazole treatments with the main purpose of reducing morbidity by decreasing burdens, including annual campaigns of preventive chemotherapy in the hyperendemic areas. Aim: In human endemic areas, infection is frequent giving rise to reinfections of treated subjects and fluke accumulation increasing burdens in non-treated ones due to premunition lack. One-Health initiatives are considered to complement the yearly preventive chemotherapy campaigns to decrease animal transmission and thus reduce such high human reinfection risk. Methods: Reducing Fasciola transmission implies a multidisciplinary action at the levels of snail vector, livestock reservoirs, and environment, the latter mainly concerning freshwater collections. Efforts should also include activities to decrease/avoid human infection sources and human participation in disease transmission. Results: A One-Health initiative including experimental studies and field surveys is at present being performed in the human hyperendemic area of the Northern Bolivian Altiplano, selected because (i)) it is the area with the more complete knowledge on the disease, (ii) its relative simplicity (well defined flatland endemic area, with only Fasciola hepatica and Galba truncatula involved), (iii) the highest prevalences and intensities reported in humans, and (iv) preventive chemotherapy running after already ten years of triclabendazole mono-dose yearly mass treatments. Conclusion: Many problems appear regarding sustainability. Changing centenary-old traditions and habits of endemic area inhabitants may be very difficult even despite long-term education efforts. Use of animals for transport, as donkeys, opens doors for flukes and lymnaeids entering from outside into the endemic area under control. Climate change may modify the environmental characteristics and give rise to epidemics due to snail population increases after temperature increases and long rainfall. Fasciolids are able to give rise to veterinary drug resistance. A multidisciplinary team should be maintained in place to continuously monitor the efficiency of each one of the measures. This needs long-term efforts and funding, which may not be affordable for remote, rural, poor areas in developing coumtries. Funding: Projects Nos. 2017/ACDE/001583, AECID, Ministry of Foreign Affairs and Cooperation; PI16/00520, AES, ISCIII-MINECO; RD16/0027/0023, RICET, RETICS, Ministry of Health and Consumption, Madrid, Spain; and 2016/099, PROMETEO Program, Generalitat Valenciana, Valencia, Spain.

Drugs, Vaccines and Disease Control III - (Conference room 1)

25-June-2021, at 11:00 (30 mins)

Development of macrofilaricidal drugs for onchocerciasis and lymphatic filariasis *A23535*

Presenter: **Prof Achim Hoerauf**,

Abstract: Control or elimination of the 20 NTDs WHO are a litmus test for the UN's SDGs, indicating in particular whether the countries that signed the SDG agenda 2030 are serious about safeguarding access to essential health care. In order to align their control efforts with the SDG agenda, the WHO at their 73rd WHA (World Health Assembly) meeting has last week adopted a new roadmap for NTD control and elimination. Two major NTDs are onchocerciasis and lymphatic filariasis. Current control and elimination efforts comprise the use of several drugs (ivermectin, albendazole and diethylcarbamazine), using mass drug administration (MDA) in endemic areas. However, these drugs primarily kill worm larvae which are taken up by transmitting insects, but not the long-lived (10-15 years) adult worms which continue to reproduce after drug exposure. Therefore, in the new roadmap, WHO has expressed the need for new drugs that kill the adult worms (adulticidal drugs). In my talk, I will give an overview over the principle of using filarial Wolbachia endosymbionts as targets for novel chemotherapies that are adulticidal (macrofilaricidal) and describe the work of international consortia, funded by the Bill Gates Foundation and others such as DNDi where the institute is a partner, on their way to deliver new macrofilaricidal drugs for human use over the next years.

Schistosomiasis - Control, epidemiology and One Health II - (Conference room 2)

11:00 (30 mins)

Reaching the WHO elimination targets for schistosomiasis: the importance of a One Health perspective*A23170*

Presenter: **Prof Joanne Webster**, *Professor of Parasitic Diseases, Royal Veterinary College*

2021, amidst the global SARS-Covid-19 pandemic, has seen the launch of the new WHO Neglected Tropical Diseases (NTD) 2021-2030 Roadmap and the G7 summit. Across all there is now a clear emphasis on the need to incorporate a One Health approach, recognizing the critical links between human and animal health and the environment. Schistosomiasis, caused by Schistosoma spp. trematodes, is a NTD of global medical and veterinary importance, with over 140 million people currently infected and untold millions of livestock. Despite decades of mass administration of the anthelmintic praziquantel to, predominantly, school-aged children, the burden of schistosomiasis remains extremely high in certain regions, particularly that within sub-Saharan Africa (SSA). Whilst in endemic regions of Asia, animal hosts are acknowledged as important zoonotic reservoirs, within SSA, in contrast, the zoonotic component of schistosomiasis transmission and the implications of the multi-host aspects of schistosomiasis for disease control and reaching the elimination targets has, until recently, been largely ignored. This was particularly the case for S. haematobium, the causative agent of urogenital schistosomiasis in humans, which was assumed to be an exclusively human infection – and thus amenable to elimination by targeting treatment at humans alone. Here, presenting our recent parasitological, epidemiological, experimental, molecular, clinical and environmental work across both Asia and Africa, we illustrate the distribution and transmission dynamics of Schistosoma spp. and notably the emerging risk raised by both wildlife reservoirs and viable hybridization between human with livestock schistosomes. Taken together, our research emphasizes that a truly multi-disciplinary One Health perspective must be implemented in order to achieve the 2030 WHO Roadmap targets of elimination as a public health problem and ultimately towards interruption of schistosomiasis transmission and its subsequent verification.

11:30 (15 mins)

Remaining pockets of moderate to high endemicity of schistosomiasis and soil-transmitted helminthiasis in selected communities in Caraga region, the Philippines*A23372*

Presenter: **Mr Allen Jethro Alonte**, *University Research Associate II, Institute of Biological Sciences, University of the Philippines Los Banos*

V G Paller[3]; V Y Belizario[4]; A I Alonte[2]; B P Divina[3]; R C Ancog[3]; M Betson[1];
[1] University of Surrey, UK; [2] Institute of Biological Sciences, University of the Philippines Los Banos, Philippines; [3] University of the Philippines, Los Baños, Philippines; [4] University of the Philippines, Manila, Philippines, Philippines

Schistosomiasis and soil-transmitted helminthiasis (STH) remain as major public health concerns in developing countries. In the Philippines, interventions recommended by the World Health Organization for their control have been implemented through national control programs. This study, carried out as part of the ZooTRIP project, aimed to determine the prevalence and intensity of schistosomiasis and STH in selected communities in co-endemic provinces of Agusan del Sur and Surigao del Norte, Caraga region, the Philippines. Stool samples, collected from 663 participants ages 10 to 60 years old, were processed by Kato-Katz technique and examined microscopically for the presence of intestinal helminth ova. Results revealed high prevalence and moderate heavy intensity (HI) schistosomiasis, as well as moderate prevalence and HI STH. Remaining pockets of moderate to high prevalence and intensity of schistosomiasis and STH were still observed after more than a decade of program implementation. The results indicate considerable morbidity despite high reported mass drug administration coverage, suggesting the need to revisit the reported coverage rates as well as to identify and address the factors underlying possible low coverage. Challenges in safe water, sanitation, and hygiene (WASH), such as continuing open defecation and lack of access to WASH facilities, promote considerable continuing transmission in the area. Lack of available sensitive laboratory diagnostic techniques and a robust surveillance scheme are likely to have contributed to underdiagnosis, lack of access to treatment, and continuing transmission amidst co-existing challenges in WASH. For schistosomiasis, complementary measures such as promotion of veterinary public health and vector ecology management, will help accelerate its control and elimination.

Drugs, Vaccines and Disease Control III - (Conference room 1)

11:30 (15 mins)

Towards the Structure Based Design of Broad Spectrum Anti-Apicomplexan Drugs*A23216*

Presenter: **Dr Ashwani Sharma**, *Scientist, Paul Scherrer Institute*

A Sharma[1];
[1] Paul Scherrer Institute, Switzerland

Apicomplexan parasites are responsible for several diseases including malaria, toxoplasmosis and cryptosporidiosis. Drug administration remains the preferred treatment strategy for most of these diseases. However, the emergence of resistance in all available therapies necessitates the urgent discovery of novel drug-scaffolds targeting unique parasite proteins and pathways.

Inhibition of cell division by using tubulin targeting, antimitotic compounds has been the most successful strategy for cancer treatment up to now. Implementing a similar strategy to arrest parasite replication using apicomplexan tubulin specific inhibitors offers a completely new and attractive avenue towards anti-apicomplexan drug discovery. However, this strategy has not been explored sufficiently mainly due to the lack of biochemical and structural knowledge on apicomplexan tubulins. In this talk I will present a very first structural description of apicomplexan tubulin drug-binding sites together with the comparison to their mammalian counterparts. Utilizing this structural information, we are developing novel anti-tubulin drugs specific for protozoan parasites. My presentation will highlight how this structural knowledge is enabling the rational development of specific and broad-spectrum anti- apicomplexan drugs.

11:45 (15 mins)

ACT treatment failure and resistance gene variants in African Plasmodium falciparum*A23154*

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

C J Sutherland
[1] ,

As we near the end of a second decade of widespread artemisinin combination therapy (ACT) use for treating human malaria, there are signs of waning efficacy in some African settings. Evidence to date suggests the parasite factors linked to ACT treatment failure in Asia, such as K13 variants and markers of piperaquine drug failure, have not themselves spread to Africa. Rather, a suite of variant *Plasmodium falciparum* loci, experimentally linked to reduced artemisinin susceptibility *in vitro*, are under scrutiny in African parasite populations. These include not only *pfk13* variants, but also variant alleles of *pfcoronin*, *pfk10*, *pfubp1* and *pfap2mu*. I will present recent molecular, epidemiological and *in vitro* data and attempt to provide some mechanistic insights that could help us understand the emerging complexity of the

genetic polymorphisms underlying reduced artemisinin susceptibility. Finally, the importance of such variant loci in resistance surveillance will be considered.

Schistosomiasis - Control, epidemiology and One Health II - (Conference room 2)

11:45 (15 mins)

How much variation in drug response is found in schistosome populations?*A23528*

Presenter: **Dr Winka Le Clec'h**, *Staff Scientist, Texas Biomedical Research Institute*

W Le Clec'h[1]; F D Chevalier[1]; R Diaz[1]; A Strickland[1]; M Morales[1]; T J Anderson[1];
[1] Texas Biomedical Research Institute, United States

Schistosmes are outbred, sexually reproducing parasites and extensive genomic and phenotypic variation is found within natural and laboratory populations.

We have previously demonstrated that there is standing variation for oxamniquine resistance in *S. mansoni* populations that resulted in treatment failure in Brazil and East Africa. As new anti-schistosomal drugs are developed, it is important to determine levels of pre-existing phenotypic variation in response to these compounds.

We hypothesize that there will be extensive phenotypic and genetic variation for drug response within schistosome populations. Using a combination of high throughput phenotyping assays, based either on single worm metabolism (Lactate assay) or a newly developed movement assay (SWAMP - Single Worm Analysis Movement Pipeline), we are quantifying phenotypic variation in drug response to nine drugs in our genetically diverse laboratory schistosome populations. The presence of natural genetic variation in drug response within schistosome populations allows use of whole genome association methods to determine the genomic region(s) involved, and ultimately to decipher the mechanism(s) of action of these drugs.

Drugs, Vaccines and Disease Control III - (Conference room 1)

12:00 (15 mins)

Disentangling the role of Ascaris β-tubulin isotypes in the emergence of anthelmintic resistance.*A23311*

Presenter: **Mr Ben Jones**, *PhD student, University of Surrey*

B P Jones[2]; A H van Vliet[2]; E J Lacourse[1]; M Betson[2];
[1] Liverpool School of Tropical Medicine / UoL, UK; [2] University of Surrey, UK

Ascaris lumbricoides and *Ascaris suum* are intestinal roundworms that infect humans and pigs respectively and cause the disease known as ascariasis. Ascariasis affects nearly one billion people, with chronic infections leading to reduced growth and cognitive ability. Ascariasis affects pigs worldwide and can reduce production yields via decreased growth and condemnation of livers. The predominant drugs used to treat ascariasis are the benzimidazoles (BZ). Despite the farming industry using these drugs for decades, and BZ resistance occurring in numerous livestock helminths, there has been little work into the development of resistance in pig ascariasis. Benzimidazoles work by interacting with β-tubulin and the mutations causing resistance are known in some nematodes. In most nematodes there are multiple β-tubulin isotypes. Only a few of these are expressed at high levels, with others being restricted to specialised cells or specific developmental stages. Seven β-tubulin isotypes were identified by analysis of *Ascaris* genome sequences, and the expression profiles of these were analysed at various developmental stages. Only three of the seven isotypes were highly expressed, making these the most likely to influence drug susceptibility. *In silico* docking simulations were used to model how BZs interact with wildtype and mutated β-tubulin proteins from *Ascaris suum* isotypes. The BZ albendazole sulfoxide was docked within the binding pocket containing the residues associated with resistance. The β-tubulin-BZ models then underwent molecular dynamics simulations. The results showed that interaction between BZs and residue 198 is key to drug binding and mutations in this residue lead to reduced binding energy. Mutations at residue 200 may also lead to resistance by interfering with binding at residue 198. These results highlight the key interactions between BZ and specific residues as well as the direct impact that some mutations have on drug binding.

Schistosomiasis - Control, epidemiology and One Health II - (Conference room 2)

12:00 (15 mins)

Standardising the interpretation of point-of-care circulating cathodic antigen diagnostics for Schistosoma mansoni: A Bayesian latent class analysis study*A23527*

Presenter: **Dr Jessica Clark**, *Post-doctoral Research Associate, University of Glasgow*

J Clark[3]; M Arinaitwe[1]; A Nankasi[1]; C L Faust[3]; M Adriko[1]; D Ajambo[1]; F Besigye[1]; A Atuhaire[1]; A Wamboko[1]; L V Carruthers[3]; R Francoeur[3]; E M Tukahebwe[1]; J M Prada[2]; P H L Lamberton[3];
[1] Vector Control Division, Ministry of Health, Uganda; [2] University of Surrey, UK; [3] Institute of Biodiversity, Animal Health and comparative Medicine, and Wellcome Centre for Integrative Parasitology, University of Glasgow, UK

Background: Schistosomiasis is targeted by the World Health Organisation (WHO) for elimination as a public health problem (EPHP) by 2030, defined as a population having ≤1% heavy infections by the Kato-Katz diagnostic. However, Kato-Katz lack sensitivity. The point-of-care circulating cathodic antigen (POC-CCA) tests are also recommended by WHO for *Schistosoma mansoni* diagnosis, but no guidance exists for their optimal interpretation, or analogous indicators of EPHP.

Methods: We developed a Bayesian latent-class model fit to parasitological data from 210 school-aged-children at four time points from pre-treatment to six-months post-treatment: one with Kato-Katz and POC-CCA+ (the standard POC-CCA scoring method: Negative, Trace, +, ++ and +++) and one Kato-Katz and G-Score (a newly developed scoring method from G1 (negative) to G10). Using parameter estimates, we simulated EPHP settings to establish an EPHP indicator analogous to Kato-Katz.

Findings: The POC-CCA tests saturate at low infection intensities explaining the lack of correlation between WHO infection intensity categories and POC-CCA scores. Optimal positivity thresholds are + and G3. Scoring system performance was comparable, but fluctuated with treatment. The proportion of a population that has scores of ++ or +++, or G7 and above, can be used as cut offs for if a community has likely reached EPHP.

Interpretation: The POC-CCA cannot be aligned to individual-level egg-count morbidity indicators. POC-CCA policy guidelines should be provided in terms of population-level prevalence. That the performance of the POC-CCA fluctuates with time, indicates a changing relationship between egg production and antigen levels.

12:15 (15 mins)

Spatial analysis of Schistosomiasis in Endemic Communities in Southern Mindanao, Philippines*A23482*

Presenter: **Dr Vachel Gay Paller**, *Professor, University of the Philippines Los Banos*

V G Paller[2]; K L Patagnan[2]; M S Calica[5]; S M Manalo[6]; A J Alonte[2]; B Divina[3]; V Belizario[4]; R Ancog[3]; M Betson[1];
[1] University of Surrey, UK; [2] Institute of Biological Sciences, University of the Philippines Los Banos, Philippines; [3] University of the Philippines, Los Baños, Philippines; [4] University of the Philippines, Manila, Philippines, Philippines; [5] School of Environmental Science and Management, University of the Philippines Los Banos, Philippines; [6] 3Department of Paraclinical Sciences, College of Veterinary Medicine, University of the Philippines Los Baños, Philippines

Schistosomiasis remains a major public health problem in some endemic communities in the Philippines. The major endemic areas are located in agricultural areas and marshlands in the Southern regions in the country. Spatial analytical techniques are often used in epidemiology to identify spatial clusters in disease regions. This study assessed the spatial distribution of schistosomiasis and explores high-risk areas in Southern Mindanao to provide guidance on schistosomiasis control in the region. In this study, spatial distribution using QGIS was utilized to describe and map spatial clusters and areas where human *Schistosoma japonicum* infection is prevalent. In addition, logistic regression model was used to determine the characteristics of spatial distribution. Results revealed that high prevalence was observed in areas near irrigations and marshlands. In addition, the knowledge, perception, and practice such as playing and working in the rice field, presence of farm animals, and housing management of water buffalo showed significant associations. The findings indicated that spatial surveillance of *S. japonicum* transmission plays a significant role in schistosomiasis control. Timely and integrated prevention should be continued, especially in marginalized endemic communities.

Surveillance, Epidemiology, Stigma and Public Health I - (Conference room 1)

25-June-2021, at 13:00 (30 mins)

Mathematical modelling and the WHO 2021-2030 roadmap on neglected tropical diseases: Insights and challenges*A23116*

Presenter: **Prof Maria-Gloria Basanez**, *Chair in Neglected Tropical Diseases, Imperial College London, Faculty of Medicine*

The World Health Organization (WHO) has launched a new roadmap to reduce the burden due to Neglected Tropical Diseases (NTDs) and achieve the UN Sustainable Development Goals (SDGs) during the period 2021-2030. Prior to this, the WHO initiated a period of consultation and convened a meeting in April 2019 with NTD modellers to inform the goals of the roadmap. Modellers were asked to assess the technical feasibility and the challenges associated with reaching goals for the control and elimination of NTDs during the proposed time-framework. The goals comprise a spectrum of end-points, from control to elimination of transmission. Our groups contributed with modelling insights for onchocerciasis (ear-marked for elimination--interruption-- of transmission), Taenia solium taeniasis/cysticercosis, and Chagas disease (indicated for control). In this talk, I will discuss the role that modelling played in informing the new WHO roadmap. The discussion will centre around the 3 pillars of the recent roadmap, namely, acceleration of progress (through alternative and complementary intervention strategies); cross-cutting themes (e.g. the need for better access to diagnosis and treatment), and increased endemic country engagement (through collaboration between stakeholders, programme managers, endemic communities, field and quantitative epidemiologists, and NTD modellers) to reach the SDGs by 2030. The impact of COVID-19 on epidemiological trends for onchocerciasis will also be presented and the relative merits of mitigation strategies to help countries get back on track to achieve elimination goals will be discussed.

13:30 (15 mins)

Force of infection and age-profiles of Taenia solium human taeniasis and cysticercosis: global trends and subnational analysis for Colombia*A23376*

Presenter: **Dr Matthew Dixon**, *Visiting researcher, Imperial College London*

M A Dixon[1]; [2]; P Winskill[1]; [2]; W E Harrison[6]; C Whittaker[1]; [2]; V Schmidt[4]; A C Flórez Sánchez[7]; Z M Cucunubá[1]; [2]; A U Edia-Asuke[5]; M Walker[3]; M G Basáñez[1]; [2];
[1] Imperial College London, UK; [2] Imperial College London, UK; [3] Royal Veterinary College, UK; [4] Technical University of Munich, Germany; [5] Ahmadu Bello University Zaria, Nigeria; [6] SCI Foundation, UK; [7] Instituto Nacional de Salud, Colombia

The health and economic burden imposed by the zoonotic cestode, *Taenia solium*, is substantial, posing a major global health challenge across endemic countries. The World Health Organization (WHO) has proposed milestones in the 2021-2030 Neglected Tropical Disease (NTD) roadmap for countries to achieve intensified *Taenia solium* controlin hyperendemic areas by 2030. Successful control and elimination strategies for *T. solium* will likely require tailored interventions based on local epidemiological and socio-economic conditions; therefore, understanding geographical variation in epidemiological patterns such as age-prevalence profiles and force-of-infection (FoI) estimates will be important to inform effective intervention design.

To estimate global FoI estimates for human taeniasis (HTT) and human cysticercosis (HCC), we collated age-(sero)prevalence data from 16 studies in Latin America, Africa and Asia, and fitted catalytic models, incorporating diagnostic performance uncertainty, using Bayesian methods, to estimate the rates of antibody seroconversion, infection acquisition and seroreversion/ infection loss. In addition, FoI estimates were estimated for 23 departments across Colombia (n=29,360 individuals), representing the first sub-national assessment of FoI estimates for *T. solium*.

Substantial variation in all-age seroprevalence was found across settings, with evidence for antibody seroreversion/ infection loss found in most settings for both HTT and HCC, including HCC seroreversion found across all departments in Colombia. Across epidemiological settings, the average duration until humans became seropositive or infected (reciprocal of the FoI) decreased as all-age (sero)prevalence increased. Marked geographical heterogeneity in human *T. solum* transmission rates demonstrate the requirement for setting-specific intervention strategies and parameterisation of transmission models, including at the sub-national level as identified for Colombia.

13:45 (15 mins)

ZooTRIP: Zoonotic transmission of intestinal parasites: implications for control and elimination.*A23380*

Presenter: **Dr Kezia Whatley**, *Post doctoral research fellow, University of Surrey*

K Whatley[1]; R Ancog[2]; V Belizario[3]; B Divina[2]; S Gourley[1]; J M Prada[1]; A H van Vliet[1]; V G Paller[2]; M Betson[1];
[1] University of Surrey, UK; [2] University of the Philippines, Los Baños, Philippines; [3] University of the Philippines, Manila, Philippines, Philippines

Zoonotic intestinal helminthiasis affects more than 949 million people globally, collectively contributing to an estimated 9.68 million disability adjusted life years (DALYs) lost per annum. Endemicity is focused in rural and poor urban areas of low-and-middle-income countries, where access to sanitation, hygiene, health care and education on parasite transmission is lacking. Zoonotic intestinal helminths include the *Schistosoma spp*. (*Schistosoma japonicum*), soil-transmitted helminths, foodborne trematodes, and *Taenia spp*. each having varying degrees of lifecycle complexity, but all utilising animal reservoirs as well as human definitive hosts to maintain transmission, complicating control strategies. Historically the mainstay of control for helminth infections has been mass drug administration of a handful of donated anthelmintic chemotherapies (praziquantel, and benzimidazoles). However, the new World Health Organisation roadmap for neglected tropical diseases directs the need for more holistic, One Health approaches to control, in order to successfully eliminate helminthiasis as a public health problem completely. This project focuses on intestinal helminth endemicity in southeast Asia, applying a multidisciplinary approach to investigate the prevalence of zoonotic intestinal helminthiasis in the Philippines. Sampling from animals, humans and the environment has been integrated with both parasitological, and molecular diagnostics. Further work will utilise genomics and mathematical modelling approaches to investigate helminth transmission dynamics. The ultimate aim is to determine whether a One Health approach involving integrated human/animal control and surveillance programmes can provide more effective management options than solely human-focused control.

14:00 (15 mins)

Parasite-vaccine interactions through the lenses of meta-analysis and field research *A23487*

Presenter: **Ms Liana Wait**, *PhD Candidate, Princeton University*

L Wait[1];
[1] Princeton University, United States

What happens if individuals are infected with parasites when they are vaccinated? I conducted a meta-analysis to explore this question, and found that, in general, parasites tend to interfere with immunisation: individuals infected with helminths, protozoa, and viruses have worse immunisation outcomes compared with uninfected individuals. I also found that chronic helminth infections tend to result in worse immunisation outcomes than acute helminth infections, and that vaccines that are thymus-dependent are more susceptible to parasite interference than thymus-independent vaccines. In parallel to the meta-analysis, I have begun to investigate parasite-vaccine interactions in the field. Raccoons are one of the main vectors of rabies in the United States and are currently subject to a federal vaccination campaign that aims to eliminate raccoon rabies via an oral vaccine. My field research suggests that raccoons that are infected with gastrointestinal nematodes are less likely to become immunised by the rabies vaccine compared with uninfected raccoons. In a cross-sectional survey following vaccine baiting, only 22% of nematode-infected worms had antibodies to rabies, compared with 31% of uninfected raccoons, and nematode infection status was a significant factor in a general linear model of rabies serostatus.

Schistosomiasis - Control, epidemiology and One Health III - (Conference room 2)

25-June-2021, at 14:00 (30 mins)

Schistosomiasis vaccines: their role in disease prevention and elimination*A23172*

Presenter: **Prof Peter Hotez**, *Baylor college of Medicine, Baylor University*

tbc

14:30 (15 mins)

Using choice modelling to identify popular and affordable alternative interventions for schistosomiasis in Uganda*A23529*

Presenter: **Dr Poppy Lamberton**, *Reader, University of Glasgow*

K Meginnis[1]; N Hanley[2]; L Mujumbusi[4]; L Pickering[3]; **P H L Lamberton**
[1] University of Stirling, UK; [2] Institute of Biodiversity, Animal Health and comparative Medicine, University of Glasgow, UK; [3] Institute of Health & Wellbeing, College of Social Sciences, University of Glasgow, UK; [4] Medical Research Council, Uganda Virus Research Institute, Entebbe, Uganda; [5] Institute of Biodiversity, Animal Health and comparative Medicine, and Wellcome Centre for Integrative Parasitology, University of Glasgow, UK

Schistosomiasis is caused by a vector-borne parasite, commonly found in low- and middle-income countries, with over 240 million people infected globally. People become infected by direct contact with contaminated water, through activities such as bathing and fishing. Water becomes contaminated when human waste is not adequately contained. The main control strategy recommended by the World Health Organization (WHO) is mass drug administration with praziquantel. However coverage remains low in many endemic areas, and hotspots exist where MDA alone is not reducing transmission. Additional interventions are needed to reach the ambitious WHO 2030 goals for schistosomiasis. We elicit community preferences towards alternative water access, sanitation and hygiene (WASH) interventions that would reduce individuals' risk of contracting, or transmitting, Schistosoma mansoni. We administered a discrete choice experiment to understand community preferences for improved WASH interventions. We compared interventions that target behaviours that put oneself at higher risk versus behaviours that mainly put others at risk. We used two payment vehicles to quantify what individuals are willing to give up in time and/or labour. Key findings indicate that new sources of potable water and fines on open defection are the highest valued interventions. A large portion of our sample ignored the payment vehicles, which is key for policy analysis.

14:45 (15 mins)

The Enemy of My Enemy is Perhaps My Friend: Intestinal schistosomiasis is associated with reduced malaria intensity in preschool children in Uganda.*A23267*

Presenter: **Mr Daniel McDowell**, *PhD student, Cardiff University*

D McDowell[1]; J R Stothard[2]; L Hurt[3]; J Lello[1];
[1] Cardiff School of Biosciences, Cardiff University, UK; [2] LSTM, UK; [3] Cardiff School of Medicine, Cardiff University, UK

In sub-Saharan Africa, preschool – aged children (<6 years), typically bear the brunt of the malaria burden, constituting the largest number of child deaths. In addition, recent epidemiological surveys in Uganda show that intestinal schistosomiasis can be highly prevalent in this age group and cause significant morbidities. In the context of co-infection, either antagonistic or synergistic, it is essential that we better understand how these parasites interact within these young children. Furthermore, this age group offers a unique opportunity to gain a clearer insight into the interactions between *Schistosoma mansoni* and *Plasmodium falciparum*, as we follow an individual child's infection dynamics and history with these two parasites through time.

Using a mixed modelling approach, applied to previous longitudinal cohort data from the Schistosomiasis In Mothers and Infants (SIMI) study, we assessed the relationship between *S. mansoni* and *P. falciparum* infections in these young children, in the face of regular antiparasitic treatments. Despite the regular treatment in this study, of the 1211 preschool children in the cohort, the prevalence of infection for *P. falciparum, S. mansoni* and co-infected individuals remained constant over the study period. A single *P. falciparum* infection was by far the most prevalent and remained constant from the baseline survey to the 12 month survey (36.2% - 36.8%). Similarly, the prevalence of a single *S. mansoni* infection remained constant (13.7% - 13.4%) whereas the prevalence of co-infected individuals slightly decreased (36.8% - 31.6%).

We conclude, from the mixed models, that infection with *S. mansoni* is associated with a lower intensity of *P. falciparum* infection; however, this relationship becomes more complicated by host infection history, increasing age and the intensity of the *S. mansoni* infection. Looking ahead as treatment of young children with praziquantel is to be up scaled, understanding co-infection interactions in more detail is essential for the success of future public health initiatives to reduce the burden of intestinal schistosomiasis and malaria.

15:00 (15 mins)

New dynamics of schistosomiasis in Lake Malawi*A22981*

Presenter: **Prof Russell Stothard**, *Medical Parasitologist, LSTM*

J R Stothard[2]; S A Kayuni[1]; M Al-Harbi[2]; E J Lacourse[1]; J Musaya[3];
[1] Liverpool School of Tropical Medicine / UoL, UK; [2] LSTM, UK; [3] MLW, UK

We give a brief history of epidemiology of schistosomiasis in Lake Malawi, drawing attention to major ecological changes ongoing within the lake leading to a fulminating outbreak of intestinal schistosomiasis. Furthermore, we highlight the novel occurrence of various hybrid schistosomes placing their current importance within the need to redefine 'OneHealth' surveillance in Malawi. Once control interventions against schistosomiasis can resume after COVID-19, we recommend stepped-up preventive chemotherapy, with increased community-access to praziquantel treatment(s), alongside renewed efforts in appropriate environmental control of intermediate snail hosts, either with existing chemical or biological control methods.

Surveillance, Epidemiology, Stigma and Public Health II - (Conference room 1)

25-June-2021, at 15:00 (30 mins)

Leishmaniasis and Conflict*A23160*

Presenter: **Dr Margriet den Boer**, *NTD advsior, MSF UK*

It may not be surprising that epidemics with mortality occur more frequently during large-scale complex emergencies. A historical analysis demonstrated a very significant dose-response relationship between the incidence of leishmaniasis and levels of conflict and political terror. Further analysis indicates that this association is through a process of population displacement and health system deterioration. Important factors are population movement of non-immune persons to endemic areas, or infected people moving to non-endemic areas where vector is present. Moreover, population displacement is generally associated with crowding, poor housing and sanitation, immune-compromised health status, and increased human-vector interactions. Several case presentations from different conflict contexts (South Sudan, Somalia, Iraq, Syria, Afghanistan, Pakistan, Colombia) are demonstrating the impact of conflict on the incidence of visceral and cutaneous leishmaniasis, and the emergence of leishmaniasis in new areas. The specific mechanisms leading to disruption of health services, increased disease transmission, and disruption of control activities are explained.

15:30 (15 mins)

Are Parasitic Diseases still a Continuing Health Problem in Gaza Strip, Palestine?*A23289*

Presenter: **Prof Adnan Alhindi**, *Research Fellow, Islamic University Of Gaza*

A Al-Hindi[1];
[1] The Islamic University, Gaza, Palestinian Territory

According to the World Health Organization, an estimated 3.5 billion people worldwide continue to be affected by intestinal parasitic infections which to be one of the greatest health problems in the developing world.Most literature states thatIntestinal parasites and other parasitic diseases are endemic in the Gaza Strip for decades, despite the improvement in infrastructure as in other developing countries. Due to the many unfavourable health conditions in the Gaza Strip, these intestinal parasites continue to survive. There are many reports on parasitic diseases in the Gaza Strip, including the epidemiology of intestinal parasites, prevalence, diagnosis, the association between intestinal parasites and malnutrition and environmental contamination caused by these parasites, and sexually transmitted parasitic diseases such as *Trichomonas vaginalis*. This lecture aiming to discusses infections with intestinal parasites and other parasitic diseases in the Gaza Strip, and its treatments in children and adults. The challenges encountered during diagnosis and the associated risk factors are also addressed, followed by some proposed solutions to decrease/minimize further increases in infections with intestinal parasites in the Gaza Strip.

15:45 (15 mins)

Community practices and Environmental Reservoir as risk factor of Soil-Transmitted Helminths in Selected Rural Communities in the Philippines*A23422*

Presenter: **Mrs Kim Louisse Patagnan**, *Senior Science Research Specialist, University of the Philippines Los Banos*

K Patagnan[4]; R Ancog[2]; V Belizario[3]; B Divina[2]; M Betson[1]; V G Paller[2];
[1] University of Surrey, UK; [2] University of the Philippines, Los Baños, Philippines; [3] University of the Philippines, Manila, Philippines, Philippines; [4] University of the Philippines Los Banos, Philippines

Soil plays a significant role in the transmission of STH eggs. Soils from selected households in Caraga Region, Philippines were examined for parasite contamination. A total of 408 soil samples were processed through a modified sucrose flotation technique. Out of 408 samples, 92 (22.6%) were contaminated with parasite eggs, namely *Ascaris* sp. (14.7%), *Trichuris* sp. (2.7%), strongyle/hookworm (2.2%), *Toxocara* sp. (1.23%), *Capillaria* sp. (1.0%), and *Schistosoma* sp. (0.7%). Risk factors such as playing outdoors, working in the field, contact with an unclean water body, type of toilet facility, and how animals are kept showed significant associations with parasite soil contamination. QGIS maps were also generated to demonstrate the extent of soil environment contamination. The socio-economic status of local people had significant impacts on knowledge, attitude, and practices with regard to sanitation, hygiene, and health. The incidence of STH eggs contaminating the environment indicates human and animal activities associated with poor sanitation and hygiene practices, poor husbandry, and farming practices vis-à-vis poor socio-economic conditions. Thus, a coordinated effort involving various sectors in the government working together is needed to educate and build capacities among relevant sectors and stakeholders to control parasitic infections in marginalized communities in the Philippines.

16:00 (15 mins)

Unusual localization of blood-borne Loa loa microfilariae in the skin depends on microfilarial density in the blood: Implications for onchocerciasis diagnosis in co-endemic areas*A23388*

Presenter: **Mr Yannick NIAMSI EMALIO**, *Biostatistician, Centre for Research on Filariasis and other Tropical Diseases (CRFilMT)*

Y NIAMSI EMALIO[1];
[1] Centre for Research on Filariasis and other Tropical Diseases (CRFilMT), Cameroon

Yannick Niamsi-Emalio[1], Hugues C. Nana-Djeunga[1], Cédric B. Chesnais[2], Sébastien D.S. Pion[2], Jules B. Tchatchueng-Mbougua[3], Michel Boussinesq[2], María-Gloria Basáñez[4], Joseph Kamgno[1,5]

1. Centre for Research on Filariasis and other Tropical Diseases (CRFilMT), Yaoundé, Cameroon

2. Institut de Recherche pour le Développement (IRD), UMI233/ INSERM U1175/ Université de Montpellier, 911 avenue Agropolis, BP 64501, 34394 Montpellier Cedex 5, France

3. Service d'Epidémiologie, Centre Pasteur du Cameroun, Membre du Réseau International des Instituts Pasteur, Yaoundé, Cameroun

4. MRC Centre for Global Infectious Disease Analysis and London Centre for Neglected Tropical Disease Research, Department of Infectious Disease Epidemiology, School of Public Health, Imperial College London, London, UK

5. Faculty of Medicine and Biomedical Sciences, University of Yaoundé I, Cameroon

Background:

The diagnostic gold standard for onchocerciasis relies on identification and enumeration of (skin-dwelling) *Onchocerca volvulus* microfilariae (mf) using the skin snip technique (SST). In a recent study, blood-borne *Loa loa* mf were found by SST in individuals heavily infected with *L. loa*, and microscopically misidentified as *O. volvulus* due to their superficially similar morphology. This study investigates the relationship between *L. loa* microfilarial density (*Loa* MFD) and the probability of testing SST positive.

Methods:

A total of 1,053 participants from the (onchocerciasis and loiasis co-endemic) East Region in Cameroon were tested for: i) *Loa* MFD in blood samples; ii) *O. volvulus* presence by SST, and iii) IgG4 antibody positivity to Ov16 by rapid diagnostic test (RDT). A Classification and Regression Tree (CART) model was used to perform

a supervised classification of SST status and identify a *Loa* MFD threshold above which it is highly likely to find *L. loa* mf in skin snips.

Results:

Of 1,011 Ov16-negative individuals, 28 (2.8%) tested SST positive and 150 (14.8%) were *L. loa* positive. The range of *Loa* MFD was 0–85200mf/mL. The CART model subdivided the sample into two *Loa* MFD classes with a discrimination threshold of 4080 (95% CI: 2180–12240) mf/mL. The probability of being SST positive exceeded 27% when *Loa* MFD was >4080mf/mL.

Discussion/Conclusion:

The probability of finding *L. loa* mf by SST increases significantly with *Loa* MFD. Skin-snip polymerase chain reaction (PCR) would be useful when monitoring onchocerciasis prevalence by SST in onchocerciasis–loiasis co-endemic areas.